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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN BRAIN(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the
brain and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

CROSS REFERENCE TO RELATED APPLICATIONS

5 The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S.provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entirety.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20 The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_BRAIN.txt, created
25 24 January 2001, having 25,840,972 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30 The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

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brain and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

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amounts of sequence data (see for example Adams *et al.*,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

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While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

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Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

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et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.
25 There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the brain and nervous system particularly those diseases with polygenic etiology.

30 Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional
35 information derived from genomic sequence. The present

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invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel
5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids
10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single
15 exon nucleic acid probes for measuring gene expression in a sample derived from human brain, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably
25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality
30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000
35 probes, for example, 50 - 5000.

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Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,434 or a complimentary sequence, or a
5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp,
10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least
15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
20

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.
25

Suitable substrates include a filter membrane
30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene,
35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

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polytetrafluoroethylene, polystyrene, polycarbonate,
polyacetal, polysulfone, celluloseacetate,
cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is
5 provided a microarray comprising a spatially addressable
set of single exon nucleic acid probes in accordance with
the first aspect of the invention.

In one embodiment, a genome-derived single-exon
microarray is packaged together with such an ordered set of
10 amplifiable probes corresponding to the probes, or one or
more subsets of probes, thereon. In alternative
embodiments, the ordered set of amplifiable probes is
packaged separately from the genome-derived single exon
microarray.

15 In another aspect, the invention provides genome-
derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
20 probes that include specifically-hybridizable fragments of
SEQ ID Nos. 12,822 - 25,434, wherein the fragment
hybridizes at high stringency to an expressed human gene.
In particular embodiments, the invention provides single
exon probes comprising SEQ ID Nos. 1 - 12,821.

25 Accordingly, in a third aspect of the invention,
there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human brain which is a nucleic acid molecule comprising a
nucleotide sequence as set out in any of SEQ ID NOs.: 1 -
30 12,821 or a complementary sequence or a fragment thereof
wherein said probe hybridizes at high stringency to a
nucleic acid expressed in the human brain.

In one embodiment, a single exon nucleic acid
probe in accordance with the third aspect comprises a
35 nucleotide sequence as set out in any of SEQ ID NOs.:

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12,822 - 25,434 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,435 - 37,811 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high
10 stringency to a nucleic acid expressed in the human brain.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the
15 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
20 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,
25 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

30 In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent
35 labels include dyes such as cyanine dyes, preferably Cy3

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and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

10 In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human brain, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

35 wherein said detectably labeled nucleic acids are

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derived from mRNA from the brain of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon
5 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
10 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
15 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
20 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,434 wherein said sequence encodes a peptide.

25 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,822 - 25,434, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
30 encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,821.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
35 ID NOS.: 25,435 - 37,811.

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Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,435 - 37,811, or fragment thereof.

5 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for
10 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

15

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each
20 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called
25 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
30 Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary
35 planar substrate, as is described, *inter alia*, in Brenner

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et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

5 As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick
10 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

 As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid
15 probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the
20 requirement that the probe hybridize to mRNA.

 As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence
25 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

 As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing
30 the predicted exon.

 As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a
35 natural protein.

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As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a
5 portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a
10 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF
15 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another
20 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit
25 specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

30 As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual
35 object of the display.

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As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

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FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e^{-30}$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e^{-30}$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original

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sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence
5 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A
10 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can
20 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part
25 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100
30 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the
35 National Center for Biotechnology Information (NCBI).

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Databases of genomic sequence from species other than human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic
5 sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by
10 the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of
15 mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into
20 process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will
25 be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental
30 confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the
35 entirety of the input sequence.

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The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

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Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in

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subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is

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possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional

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preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the

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undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired
5 sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower
10 percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest
15 contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*,
20 addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as
25 conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting
30 such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating
35 transcription, regulating message transport after

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transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability
5 or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function
10 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as
15 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for
20 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs)
25 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene
30 finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;
35 and DICTION yielded the least putative coding region, with

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0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, 5 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such 10 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored 15 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further 20 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 25 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three 30 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used 35 approach to exon calling is gene prediction, the process

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can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison
5 can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the
10 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
15 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to
20 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon
25 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene
30 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible
35 secondary structure, and the like can be used to identify

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and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving

5 hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such

10 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process

15 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in

20 process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the

25 sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression

30 of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon

35 nucleic acid microarrays of the present invention.

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Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at

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amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

5 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic
10 sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased
15 commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves
20 to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later
25 sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least
30 about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for
35 amplification will come from the eukaryotic species from

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which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

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Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or

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32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create
5 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.
10 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
15 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
20 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
25 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
30 provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
35 throughput and compatibility with existing readers. For

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example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
5 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
10 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

15 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
20 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
25 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific"
30 libraries targeted at a particular biological question, R.S. Thomas et al., Cancer Res. (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure
35 expression only of those genes found in EST libraries,

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shown herein to represent only a fraction of expressed genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective
5 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be
10 determined – subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the
15 present invention – that is, the one third of sequences that had previously been accessioned in EST or other expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA
20 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays..

25 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present
30 invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
35 transcription and cloning of unknown message in EST

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approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from

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genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly
5 lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through
10 preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-
15 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker
20 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include
25 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to
30 the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without
35 such sequences, and if so constructed, presents an even

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smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
5 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present
10 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual
15 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be
20 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often
25 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized
30 probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

35 In contrast, by virtue of their origin from

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algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 5 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single 10 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression 15 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 20 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention 25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon 30 microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and 35 thus measure such phenomena such as nuclear export control.

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The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large

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percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower
5 percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual
10 probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the
15 present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear
20 genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the
25 ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present
30 invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence
35 drawn from eukaryotes in which at least about 10, 20 or 50%

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of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which
5 the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

10 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization
15 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the
20 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can
25 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see
30 Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
35 nucleotides labeled with a first label, typically a

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fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
5 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

10 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
15 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
20 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
25 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
30 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
35 can be used, greater efficiency is obtained using higher

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density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
5 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-
10 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
15 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

20 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

25 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered
30 set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing
35 information, and that can additionally contain annotation

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information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate
5 that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

10 The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a
15 preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental
20 verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be
25 compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide
30 polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local
35 alignment search tool"). The results of such query -

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including information on identical sequences and
information on nonidentical sequences that have diffuse or
focal regions of sequence homology to the query sequence -
can then be passed directly to process 500, or used to
5 inform analyses subsequently undertaken in process 200,
process 300, or process 400.

Experimental data, whether obtained by physical
or bioinformatic assay in process 400, is passed to process
500 where it is usefully related to the sequence data
10 itself, a process colloquially termed "annotation". Such
annotation can be done using any technique that usefully
relates the functional information to the sequence, as, for
example, by incorporating the functional data into the
record itself, by linking records in a hierarchical or
15 relational database, by linking to external databases, or
by a combination thereof. Such database techniques are
well within the skill in the art.

The annotated sequence data can be stored
locally, uploaded to genomic sequence database 100, and/or
20 displayed 800.

The methods and apparatus of the present
invention rapidly produce functional information from
genomic sequence. Coupled with the escalating pace at
which sequence now accumulates, the rapid pace of sequence
25 annotation produces a need for methods of displaying the
information in meaningful ways.

FIG. 3 shows visual display 80 presenting a
single genomic sequence annotated according to the present
invention. Because of its nominal resemblance to artistic
30 works of Piet Mondrian, visual display 80 is alternatively
described herein as a "Mondrian".

Each of the visual elements of display 80 is
aligned with respect to the genomic sequence being
annotated (hereinafter, the "annotated sequence"). Given
35 the number of nucleotides typically represented in an

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annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left
5 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

10 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
15 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
20 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
25 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
30 fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity
35 or identity to an input query sequence. When visual

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display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection
5 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional
10 sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

15 Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method
20 and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

25 Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c
30 represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.
35 For example, rectangles 83a can represent the results from

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GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

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However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

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Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as

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many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links
5 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be
10 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical
15 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of
20 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of
25 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to
30 depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to
35 indicate expression intensity. As discussed *infra*, such

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relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is

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protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

10 It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,821 of these ORFs in brain.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in brain is currently available for use in measuring the level of its ORF's expression in brain.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.

For example, over the past few decades Alzheimer's disease (AD), once considered a rare disorder,

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has become recognized as a major public health problem; over 4,000,000 people in the United States are now estimated to suffer with various stages of this progressive, degenerative brain disorder.

5 Although there is no agreement on the exact incidence or prevalence of Alzheimer's disease, in part due to varying diagnostic criteria and difficulties of differential diagnosis among dementias, the studies are consistent in pointing to an exponential rise in prevalence
10 of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2
15 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest of tasks. Anatomic
20 changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and
25 internal neurofibrillary tangles.

Alzheimer's disease has been suspected to have a multifactorial genetic etiological component for almost half a century. Sjogren et al., Acta Psychiat. Neurol. Scand. 82(suppl.): 1-152 (1952).

30 At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with the APOE4 allele on chromosome 19; AD3 is caused by mutation in a chromosome 14 gene encoding
35 a 7-transmembrane domain protein, presenilin-1 (PSEN1), and

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AD4 is caused by mutation in a gene on chromosome 1 that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2).

There is strong evidence, however, for additional, as yet uncharacterized, AD loci on other chromosomes.

For example, Daw et al., Am. J. Hum. Genet. 66: 196-204 (2000), estimated the number of additional quantitative trait loci (QTLs) and their contribution to the variance in age at onset of AD, and reported that 4 loci make a contribution to the variance in age at onset of late-onset AD similar to or greater in magnitude than that made by apoE, with one locus making a contribution several times greater than that of apoE. These results suggest that several genes not yet localized may play a larger role than does apoE in late-onset AD.

In accord, three groups recently announced the possible existence of an AD susceptibility gene on chromosome 10. Bertram et al., Science 290(5500):2302-2303 (2000); Ertekin-Taner et al., Science 290(5500):2303-2304 (2000); and Myers et al., Science 290(5500):2304-2305 (2000).

As another example, multiple sclerosis (MS) affects about 350,000 Americans, with approximately 200 new cases diagnosed each week, with an estimated annual monetary cost in the U.S. alone of \$2.5 billion.

Clinically, MS is an unpredictable disorder, with symptoms, presentation and course falling broadly into one of several clinical patterns. In relapsing-remitting (RR) MS, the disease first manifests as a series of attacks followed by complete or partial remissions, with symptoms returning later after a period of stability. In primary-progressive (PP) MS, there is a gradual clinical decline with no distinct remissions, although there may be

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temporary plateaus or minor relief from symptoms.

Secondary-progressive (SP) MS begins with a relapsing-remitting course followed by a later primary-progressive course. Rarely, patients may have a progressive-relapsing

5 (PR) course in which the disease takes a progressive path punctuated by acute attacks. PP, SP, and PR MS are sometimes lumped together and called chronic progressive MS. The waxing and waning course characteristic of RR, SP and PR MS makes differential diagnosis difficult.

10 Anatomically, MS attacks are associated with focal inflammation in areas of the white matter of the central nervous system (CNS), accompanied or followed by demyelination in these areas, termed plaques. Destruction of the myelin sheath slows or blocks neurological
15 transmission, leading to diminished or lost function. Clinical manifestations depend upon the location of the plaques and severity of demyelination, and range from fatigue, the most common symptom of MS, to visual impairment, due to inflammation of the optic nerve, termed
20 optic neuritis, to numbness and paresthesias, to focal muscular weakness, ataxia, and bladder incontinence.

Increasing evidence suggests that genotype contributes to susceptibility to MS.

As early as 1965, McAlpine, in Multiple
25 Sclerosis: A Reappraisal (McAlpine, ed.), Williams and Wilkins Co. pp. 61-74 (1965), concluded that the risk to a first-degree relative of a patient with multiple sclerosis is at least 15 times that for a member of the general population, but could discern no definite genetic pattern
30 of inheritance.

Subsequently, many studies associated MS with HLA (MHC) haplotype. Haines et al., Hum. Molec. Genet.
7:1229-1234 (1998), studying a data set of 98 multiplex MS families, confirmed earlier reports that genetic linkage to
35 the MHC can be explained by association with the HLA-DR2

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allele, but suggested that MHC association explains only between 17% and 62% of the genetic etiology of MS.

From a review of genomic screens, Dyment et al., Hum. Molec. Genet. 6: 1693-1698 (1997), concluded that a number of genes with interacting effects are likely and that no single region has a major influence on familial risk. Chataway et al., Brain 121: 1869-1887 (1998), reporting a follow-up on U.K. studies using a systematic genome screen to determine the genetic basis of MS, stated that a gene of major effect had been excluded from 95% of the genome and one with a moderate role from 65%, results thus suggesting that multiple sclerosis depends on independent or epistatic effects of several genes, each with small individual effects, rather than a very few genes of major biologic importance.

As a yet further example, schizophrenia has long been recognized to have complex, likely polygenic, genetic contributions.

Schizophrenia is a common psychiatric disorder, occurring in 1 to 1.5 percent of the population worldwide, and is characterized by variable constellations of symptoms drawn from a universe of behavioral abnormalities. Although there are accepted alternative diagnostic criteria, primary criteria for diagnosis require two or more of the following, each present for a significant portion of time during a 1-month period (or less if successfully treated): (1) delusions; (2) hallucinations; (3) disorganized speech (e.g., frequent derailment or incoherence); (4) grossly disorganized or catatonic behavior; (5) negative symptoms, i.e., affective flattening, alogia, or avolition. (Diagnostic and Statistic Manual of Mental Disorders DSM-IV-TR, American Psychiatric Association (2000)). Only one such symptom is required if delusions are bizarre or hallucinations consist of a voice keeping up a running commentary on the

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person's behavior or thoughts, or consist of two or more voices conversing with each other.

Three-quarters of persons with schizophrenia develop the disease between 16 and 25 years of age: onset is uncommon after age 30, rare after age 40. In the 16 to 25 year old age group, schizophrenia affects more men than women; in the 25-30 year old group, the incidence is higher in women than in men. Studies have shown that some persons with schizophrenia recover completely, and many others improve to the point where they can live independently, often with the maintenance of drug therapy. However, approximately 15 percent of people with schizophrenia respond only moderately to medication and require extensive support throughout their lives, while another 15 percent simply do not respond to existing treatment.

Schizophrenia has long been known to have a significant genetic component. Studies have consistently demonstrated that the risk to relatives of a proband with schizophrenia is higher than the risk to relatives of controls. Moldin, in Genetics and Mental Disorders: Report of the NIMH Genetics Workgroup (NIH publication 98-4268, (1998), reviewed family and twin studies published between 1920 and 1987 and found the recurrence risk ratios to be 48 for monozygotic twins, 11 for first-degree relatives, 4.25 for second-degree relatives, and 2 for third-degree relatives. He also found that concordance rates for monozygotic twins averaged 46%, even when reared in different families, whereas the concordance rates for dizygotic twins averaged only 14%. The prevalence of schizophrenia is known to be higher in biologic than in adoptive relatives of schizophrenic adoptees.

The mode of inheritance is unclear, however. Susceptibility has been mapped to many loci, including chromosomes 1q21-q22, 5, 6p23, 8p22-p21, 11q, 13q14-q21, 13q32, 15q15, 15q14, 18p, and 22q11. Chromosome

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19 has also been implicated in schizophrenia, at 2
different sites, as have sites on the X chromosome. Wei et
al., Nature Genet. 25:376-377 (2000) report more
specifically that the NOTCH4 locus is associated with
5 susceptibility to schizophrenia.

In general, however, it is believed that
development of schizophrenia involves multiple loci.

For example, Williams et al., Hum. Molec. Genet.
8:1729-1739 (1999) undertook a systematic search for
10 linkage in 196 affected sib pairs (ASPs) with
schizophrenia. Using 229 microsatellite markers at an
average intermarker distance of 17.26 cM, followed in a
second stage by a further 54 markers allowing the regions
identified in stage 1 to be typed at an average spacing of
15 5.15 cM, Williams et al. considered results on chromosomes
4p, 18q, and Xcen as suggestive; however, given the scores,
Williams et al. interpreted their results as suggesting
that common genes of major effect (susceptibility ratio
more than 3) are unlikely to exist for schizophrenia.

20 Similarly, Shaw et al., Am. J. Med. Genet.
81(5):364-76 (1998), in a genome-wide search for
schizophrenia susceptibility genes, found that twelve
chromosomes (1, 2, 4, 5, 8, 10, 11, 12, 13, 14, 16, and
22) had at least one region with a nominal P value <0.05,
25 that two of these chromosomes had a nominal P value <0.01
(chromosomes 13 and 16), and that five chromosomes (1, 2,
4, 11, and 13) had at least one marker with a lod score
>2.0, suggesting the existence of multiple loci that
contribute to schizophrenia susceptibility.

30 As yet another example, multiple genes are
thought to predispose to epilepsy.

Epilepsy is characterized by recurrent,
paroxysmal disorders of cerebral function (seizures); that
is, by sudden, brief attacks of altered consciousness,
35 motor activity, sensory phenomena, or inappropriate

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behavior. The risk of developing epilepsy is 1% in the period from birth to age 20, and 3% at age 75.

Epilepsy is caused by excessive discharge of cerebral neurons. Clinical manifestations depend on the type and location of discharge. In partial seizures, for example, the excess neuronal discharge is contained within one region of the cerebral cortex. Simple partial seizures consist of motor, sensory, or psychomotor phenomena without loss of consciousness; the specific phenomenon reflects the affected area of the brain. In generalized seizures, the discharge bilaterally and diffusely involves the entire cortex. Sometimes a focal lesion of one part of a hemisphere activates the entire cerebrum bilaterally so rapidly that it produces a generalized tonic-clonic seizure before a focal sign appears.

Epilepsy is a family of disorders. Those that are idiopathic are believed to have multiple genetic contributions. For example, idiopathic generalized epilepsy (IGE) is characterized by recurring generalized seizures in the absence of detectable brain lesions and/or metabolic abnormalities. Twin and family studies suggest that genetic factors play a key part in its etiology. Although a mutation in the CACNB4 gene can cause the disorder, linkage to 8q24, Zara et al., Hum. Molec. Genet. 4: 1201-1207(1995), 3q26 and 14q23, Sander et al., Hum. Molec. Genet. 9:1465-1472 (2000), and 2q36 has been also demonstrated, with a multilocus model appearing to fit best the observed familial patterns.

Polygenic contributions to the etiology of various neurologic cancers have similarly been described.

For example, gliomas account for 45% of intracranial tumors, and multiple loci have been implicated in its development, with losses of chromosome 17p, increase in copy number of chromosome 7, structural abnormalities of

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chromosomes 9p and 19q, and genes on chromosome 10 among the suspects.

Other significant diseases of brain and nervous tissue are also believed to have a genetic, typically
5 polygenic, etiologic component. These diseases include, for example, Parkinson's disease, dementia with Lewy bodies, frontotemporal dementia, corticobasal ganglionic degeneration, progressive supranuclear palsy, prion diseases (Creutzfeld-Jakob, Gerstmann-Straussler-Shenker,
10 familial fatal insomnia), Tourette's Syndrome, corticobasal degeneration, multiple system atrophy, striatonigral degeneration, Shy-Drager syndrome, olivopontocerebellar atrophy, spinocerebellar ataxia, Friedreich ataxia, ataxia-telangiectasia, amyotrophic lateral sclerosis, bulbospinal
15 atrophy (Kennedy's syndrome), spinal muscular atrophy, neuronal storage diseases (sphingolipid, mucopolysaccharide, mucolipid), leukodystrophy, Krabbe disease, metachromic leukodystrophy, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Canavan disease,
20 mitochondrial encephalomyopathy, Leigh disease, neurofibromatosis (Type I and Type II), tuberous sclerosis, paraneoplastic syndrome, subacute cerebellar degeneration, subacute sensory neuropathy, opsoclonus/myoclonus, retinal degeneration, stiff-man syndrome and Von Hippel-Lindau
25 disease.

Many neurologic cancers other than gliomas have also been shown or suspected to have genetic bases or contributions. Among these cancers are astrocytoma, fibrillary astrocytoma, pilocytic astrocytoma,
30 pleomorphic xanthoastrocytoma, oligodendroglioma, ependymoma, gangliocytoma, ganglioglioma, medulloblastoma, primary brain germ cell tumor, pineocytoma, pineoblastoma, and meningioma.

Other disorders of brain and central nervous
35 system that likely have genetic components include the

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various forms of neural deafness, catatonia, depression, bipolar (manic-depressive) disorder, Wilson's Disease, Pick disease, neuromyelitis optica (Devic disease), central pontine myelinolysis, Marchiafava-Bignami disease, 5 Guillain-Barre syndrome, sleep disorders (insomnia, myoclonus, narcolepsy, cataplexy, sleep apnea), amnesia, aphasias (including Broca's aphasia and Wernicke's aphasia), cortical blindness, visual agnosia, auditory agnosia, and Kluver-Bucy syndrome.

10 The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human brain, particularly those diseases with polygenic etiology. With each of the single 15 exon probes described herein shown to be expressed at detectable levels in human brain, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

20 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known 25 to be characteristic of a given neurologic disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 30 patient's brain (or other CNS tissues, including cultured tissues) to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating 35 gene expression profiles, without regard to the function of

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the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of neurologic disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human brain. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the brain has been demonstrated are useful for both measurement in the brain and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was

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measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

5 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

10 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

15 Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

20 Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);
35 Voehringer et al., "Gene Microarray Identification of Redox

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and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine
5 abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and
15 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the
20 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

25 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change,
30 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway
35 of which the gene's expressed protein is a part.

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Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena *et al.*

The invention particularly provides genome-derived single-exon probes known to be expressed in brain.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are

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described, for example, in U.S. Patent Nos. 5,142,047;
5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
form and quantity suitable for amplification, where the
5 amplified product is thereafter to be used in the
hybridization reactions that probe gene expression.
Typically, such probes are provided in a form and quantity
suitable for amplification by PCR or by other well known
amplification technique. One such technique additional to
10 PCR is rolling circle amplification, as is described, *inter*
alia, in U.S. Patent Nos. 5,854,033 and 5,714,320 and
international patent publications WO 97/19193 and
WO 00/15779. As is well understood, where the probes are
to be provided in a form suitable for amplification, the
15 range of nucleic acid analogues and/or internucleotide
linkages will be constrained by the requirements and nature
of the amplification enzyme.

Where the probe is to be provided in form
suitable for amplification, the quantity need not be
20 sufficient for direct hybridization for gene expression
analysis, and need be sufficient only to function as an
amplification template, typically at least about 1, 10 or
100 pg or more.

Each discrete amplifiable probe can also be
25 packaged with amplification primers, either in a single
composition that comprises probe template and primers, or
in a kit that comprises such primers separately packaged
therefrom. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
30 common sequence added thereto, and the ORF-specific 3'
primers used for genomic amplification can have a second,
different, common sequence added thereto, thus permitting,
in this embodiment, the use of a single set of 5' and 3'
primers to amplify any one of the probes. The probe
35 composition and/or kit can also include buffers, enzyme,

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etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,822 – 25,434, respectively, for probe SEQ ID NOS. 1 – 12,821. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or

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microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,822 - 25,434 individually by routine experimentation using standard high stringency conditions.

- 5 Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a
- 10 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization
- 15 at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room
- 20 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single

25 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more

30 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more

35 than about 3 kb.

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It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member

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of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human brain.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in

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Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term
5 "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human brain.
10 In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 12,821.

When used for gene expression analysis, the
15 genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray
20 surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a
25 fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means
30 can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon
35 microarray, each of the nucleic acids having SEQ ID NOS.: 1

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- 12,821 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,822 - 25,434, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 12,821 can be used, or that portion thereof in SEQ ID NOS. 12,822 - 25,434 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,822 - 25,434. Such amino acid sequences are set out in SEQ ID NOS: 25,435 - 37,811. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that

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have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

10

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and

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DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding
5 region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a
10 single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

15 PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes
20 were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore,
25 amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3
30 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit
35 subsequent reamplification of the amplicon using a single

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set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant
5 further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

10 Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of
15 agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest
20 directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range
25 of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region,
30 with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process
35 was adjusted to amplify 1000, 1500 or 2000 bp fragments

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from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

- 5 Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and
10 standard protocols.

- Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some
15 submitted sequence data.

- Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression
20 ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not
25 shown).

- The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII
30 Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

- 35 Each of the probe sequences was BLASTed against

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the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal

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45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 25 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 30 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT,

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100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II
enzyme. The reaction was incubated for 2 hours at 42°C.
After 2 hours, the first strand cDNA was isolated by adding
5 1 U Ribonuclease H, and incubating for 30 minutes at 37°C.
The reaction was then purified using a Qiagen PCR cleanup
column, increasing the number of ethanol washes to 5.
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured
10 for dye incorporation. Volumes of both Cy3 and Cy5 cDNA
corresponding to 50 pmoles of each dye were then dried in a
Speedvac, resuspended in 30 µl hybridization solution
containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2
µg/µl human c_ot1 DNA, and 0.5 % SDS.

15 Hybridizations were carried out under a
coverslip, with the array placed in a humid oven at 42°C
overnight. Before scanning, slides were washed in 1X SSC,
0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2%
SDS, at 55°C for 20 minutes. Slides were briefly dipped in
20 water and dried thoroughly under a gentle stream of
nitrogen.

Slides were scanned using a Molecular Dynamics
Gen3 scanner, as described. Schena (ed.), Microarray
Biochip: Tools and Technology, Eaton Publishing
25 Company/BioTechniques Books Division (2000) (ISBN:
1881299376).

Although the use of pooled cDNA as a reference
permitted the survey of a large number of tissues, it
attenuates the measurement of relative gene expression,
30 since every highly expressed gene in the tissue/cell type-
specific fluorescence channel will be present to a level of
at least 10% in the control channel. Because of this fact,
both signal and expression ratios (the latter hereinafter,
"expression" or "relative expression") for each probe were
35 normalized using the average ratio or average signal,

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respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the

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matrix ("EST Hit") contains "bioinformatic" rather than
"physical" expression data — that is, presents the results
returned by query of EST, NR and SwissProt databases using
the probe sequence. The legend for "bioinformatic
5 expression" (i.e., degree of homology returned) is
presented in panel C. Briefly, white is known, black is
novel, with gray depicting nonidentical with significant
homology (white: E values < 1e-100; gray: E values from 1e-
05 to 1e-99; black: E values > 1e-05).

10 As FIG. 7 readily shows, heart and brain were
demonstrated to have the greatest numbers of genes that
were shown to be uniquely expressed in the respective
tissue. In brain, 200 uniquely expressed genes were
identified; in heart, 150. The remaining tissues gave the
15 following figures for uniquely expressed genes: liver, 100;
lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100;
HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more
"novel" genes among those that were up-regulated in only
20 one tissue, as compared with those that were down-regulated
in only one tissue. In fact, it was found that ORFs whose
expression was measurable in only a single of the tested
tissues were represented in sequencing databases at a rate
of only 11%, whereas 36% of the ORFs whose expression was
25 measurable in 9 of the tissues were present in public
databases. As for those ORFs expressed in all ten tissues,
fully 45% were present in existing expressed sequence
databases. These results are not unexpected, since genes
expressed in a greater number of tissues have a higher
30 likelihood of being, and thus of having been, discovered by
EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have
35 high homology to genes present in the GenBank human EST

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database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR)

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and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray
5 experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

10 Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as
15 measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay
20 methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the
25 power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides
30 correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very
35 low (normalized) signal (less than 0.5, determined to be

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biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray

5 hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal Expressed Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system

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AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen

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AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
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Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
20 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
25 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to

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tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2
were similar to actin (AL035701-2; AL034402-1), and 6 were
found to be homologous to glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
5 AC006064-K; AC035604-3; AC006064-L). These genes are often
used as controls or housekeeping genes in microarray
experiments of all types.

Other interesting genes highly expressed in brain
were a ferritin heavy chain protein, which is reported in
10 the literature to be found in brain and liver (Joshi et
al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result
duplicated with the array. Other highly expressed chip
sequences included a translation elongation factor 1 α
(AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
15 chromosome RNA-binding motif (Chai et al., *Genomics*
49(2):283-89 (1998))(AC007320-3). A low homology analog
(AP00123-1/2) to a gene, DSCR1, thought to be involved in
trisomy 21 (Down's syndrome), showed high expression in
both brain and heart, in agreement with the literature
20 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we
selected the BAC AC006064 to be included on the array.
This BAC was known to contain the GAPDH gene, and thus
could be used as a control for the ORF selection process.
25 The gene finding and exon selection algorithms resulted in
choosing 25 exons from BAC AC006064 for spotting onto the
array, of which four were drawn from the GAPDH gene. Table
3 shows the comparison of the average expression ratio for
the 4 exons from BAC006064 compared with the average
30 expression ratio for 5 different dilutions of a
commercially available GAPDH cDNA (Clontech).

Table 3

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Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm
Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe

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sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure,

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it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they

5 show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

red = kallistatin protease inhibitor (P29622);

purple = plasma serine protease inhibitor (P05154);

10 turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

15 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2,

20 *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in brain tissue.

These unique exons are within longer probe

25 sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-

30 incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented

35 fragments of each of the 12,821 single exon probes, each

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fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 12,821 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,821. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID NOS.: 12,822 - 25,434, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the

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observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified
5 control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

10 This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5.
15 Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human brain tissue.

20 The sequence of each of the exon probes identified by SEQ ID NOS.: 12,822 - 25,434 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because
25 the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the
30 three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were
35 found to have no similar sequences.

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As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO:. of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (*i.e.*, highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (*i.e.*, lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (*i.e.* Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

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Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,821) and probe exon (SEQ ID NOs.: 12,822 - 25,434, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

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(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Brain

15

Table 4 (536 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human brain.

20

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CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human brain comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,822 - 25,434.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

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average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human brain.

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14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,822 - 25,434 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
10 SEQ ID NOs.: 25,435 - 37,811, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

16. A single exon nucleic acid probe as claimed in any one
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one
35 of claims 13 - 20, wherein said probe lacks homopolymeric

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stretches of A or T.

22. A method of measuring gene expression in a sample derived from human brain, comprising:

5 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human brain; and then
 measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

 algorithmically predicting at least one exon from
15 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
 wherein said detectably labeled nucleic acids are derived
 from mRNA from the brain of said eukaryote, said probe is a
20 single exon probe having a fragment identical in sequence
 to, or complementary in sequence to, said predicted exon,
 said probe is included within a microarray according to
 claim 12, and said fragment is selectively hybridizable at
 high stringency.

25

24. A method of assigning exons to a single gene, comprising:

 identifying a plurality of exons from genomic
 sequence according to the method of claim 23; and
30 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
 probe with said exon,
35 wherein a common pattern of expression of said exons in

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said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOS: 1 - 25,434 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 25,434.

10 27. A peptide comprising a sequence as set out in any of
SEQ ID NOS: 25,435 - 37,811.

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
437	13223	25858	6.47				
869	13638	26308	15.92				
1022	13782		2.15				
1279	14029	26698	10.88				
1488	14235	26921	1.22				
1488	14235	26922	1.22				
1609	14355	27044	3.19				
1633	14379	27066	6.1				
1718	14461	27160	3.31				
1743	14485	27184	1.44				
1750	14492	27192	6.78				
1884	14621	27331	1.44				
1971	14707	27425	2.14				
2162	14892	27627	2.7				
2277	15003	27743	2.91				
2578	15292	28028	1				
2578	15292	28029	1				
3181	15944	28695	2.83				
3442	16198	28848	1.42				
3505	16261	28915	12.04				
3549	16304		1				
3649	16402	29042	1.67				
3928	16678		1.03				
4173	16913	29543	1.52				
4230	16971	29595	6.4				
4248	16989	29613	0.97				
4248	16989	29614	0.97				
4303	17042		1.07				
4361	17069	29734	0.76				
4784	17516	30138	0.99				
4983	17706	30310	5.38				
4995	17718	30323	1.3				
5176	17885	30500	1.57				
5176	17885	30501	1.57				

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5336	18139		4.3			
5510	18308		6.14			
5593	18139		3.97			
5648	18443	31356	0.6			
5654	18449	31362	3.28			
5932	25082	31673	1.82			
5958	18740	31699	1.76			
6322	19082		1.27			
6454	19222	32220	1.1			
6454	19222	32221	1.1			
7025	19717	32774	1			
7025	19717	32775	1			
7311	18994	33071	1.76			
7311	18994	33072	1.76			
7712	20376		0.81			
7860	20655	33780	1.4			
8384	21077	34214	1.49			
8759	21451	34598	0.59			
8759	21451	34599	0.59			
9434	22112	35287	2.67			
9666	22318	35515	0.77			
9782	22433	36638	1.24			
9922	22570	35767	0.94			
10328	22975	36194	0.82			
10328	22975	36195	0.82			
10592	23277		2.53			
10749	25131	36879	1.34			
10852	23628		2.2			
11030	23701	36968	1.84			
11332	24023	37328	2.02			
11485	24088		2.47			
12313	24735		1.52			
12609	24916	31006	2.36			
5961	18143	31703	17.79	9.9E+00 AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18

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7905	20600	33730	1.74	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9643	22295	35489	0.44	9.8E+00	Y18830.1	NT	Sulfobus solfataricus 281 kb genomic DNA fragment, strain P2
9643	22295	35490	0.44	9.8E+00	Y18930.1	NT	Sulfobus solfataricus 281 kb genomic DNA fragment, strain P2
6901	19639	32684	0.73	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
6901	19639	32685	0.73	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10321	22968	36187	1.17	9.8E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H1 polypeptide 2 (Gtf2h2) genes, complete cds
10321	22968	36188	1.17	9.8E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H1 polypeptide 2 (Gtf2h2) genes, complete cds
2671	15381	28119	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2671	15381	28120	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2924	15690	28334	2.87	9.4E+00	AB043785.1	NT	Mus musculus A13 gene for antithrombin, complete cds
7997	20692	33820	0.91	9.3E+00	AF130990.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8901	21592	34733	3.06	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5214	18022	30645	2.48	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds, mitochondrial gene for mitochondrial product
5214	18022	30646	2.48	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds, mitochondrial gene for mitochondrial product
9330	21997	31685	0.83	9.0E+00	P09241	SWISSPROT	RHODOPSIN
5945	18727	31685	5.55	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834592 3'
6287	19060	32041	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp Tbx3 premature mRNA, partial cds
6287	19060	32042	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp Tbx3 premature mRNA, partial cds
430	13216	25861	2.3	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9355	20426	33545	3.58	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11122	23791	3051	2	8.0E+00	P41620	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8051	20745	3051	0.89	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7246	19931	34080	1.9	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8259	20953	34091	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8259	20953	34091	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5711	18504	31426	2.68	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4285506 5'
8651	21343	34487	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8651	21343	34488	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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2977	15743	28390	3.58	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2977	15743	28391	3.58	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
6831	19667	32713	0.71	7.2E+00	BE170900.1	EST_HUMAN	RCO-HT0613-200300-031-407 HT0613 Homo sapiens cDNA
7049	19740	32800	1.28	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7049	19740	32801	1.28	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9498	22151		8.63	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11359	24047	37350	3.28	7.1E+00	P08850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
9882	22532	35729	3.37	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11215	23878	37165	1.51	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8181	20875	34011	1.92	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10249	22897	36107	1.38	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10267	22915	36125	0.47	6.9E+00	P34226	SWISSPROT	SKT15 PROTEIN
7808	20503	33623	1.53	6.8E+00	W03412.1	EST_HUMAN	zad7c11.11 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291860 5'
7808	20503	33624	1.53	6.8E+00	W03412.1	EST_HUMAN	zad7c11.11 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291860 5'
9031	21721		1.28	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) (CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8)
10109	22757	35969	3.24	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5202	18010		0.72	6.8E+00	Q09028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6450	19218	32216	0.61	6.8E+00	BF672121.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283427 5'
9974	22622	35827	2.36	6.8E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9974	22622	35828	2.36	6.8E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11073	23743		1.97	6.8E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
9079	21768	34931	7	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10203	22851	36067	0.49	6.5E+00	BE86000.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960969 5'
9642	22294	35488	1.55	6.2E+00	AY010901.1	NT	Schizaphyllum commune unknown mRNA
10460	23106	36337	0.5	6.2E+00	6754621	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
6936	19871	32717	1.46	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
9716	22367	35565	0.46	6.0E+00	AP000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt position (8/7)
10411	23057	36274	0.67	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10411	23057	36275	0.67	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6428	19186	32193	7.32	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlx3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
3514	16270		0.99	5.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7061	18752	32816	0.95	5.7E+00	AF302046.1	NT	Mus musculus Immunoglobulin scavenger receptor IgSR mRNA, complete cds

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7061	19752	32817	0.95	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor [gSR mRNA, complete cds
7468	20142		1.13	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11456	23223	36458	2.59	5.6E+00	Q56276	SWISSPROT	LYCOPENE BETA CYCLASE
6157	18934	31901	0.59	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10678	23369		1.28	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11464	23221	36455	3.09	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
6830	19492	32514	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
6830	19492	32515	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7769	20465		1.54	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LPOVITELLIN LV-1N; LPOVITELLIN LV-1C; LPOVITELLIN LV-2]
8698	21390	34534	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8698	21390	34635	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
9636	22584	35784	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
9636	22584	35785	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4734	17466	30102	1.32	5.3E+00	L43126.1	NT	Bovine Immunodeficiency-like virus surface envelope gene, 5' end of cds
7978	20873		3.23	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8882	21573		0.49	5.3E+00	AB034890.1	NT	Homo sapiens HERPUD1 gene for stress protein Hsp, complete cds
11628	24225	37548	3.2	5.3E+00	Q27805	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
5377	18177		0.91	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-186-09 HT0691 Homo sapiens cDNA
10271	22919		0.95	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11150	23817		2	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME1
8861	21552	34698	0.9	5.1E+00	O18005	SWISSPROT	RHODOPSIN
9725	22378	35577	1.19	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6193	18969	31944	0.72	5.0E+00	BF310443.1	EST_HUMAN	607894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10094	22742		0.59	5.0E+00	BF308561.1	EST_HUMAN	607890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10330	22977	36197	3.07	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
11260	23922	37214	8.95	5.0E+00	Z83880.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10132	22780		0.71	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
4039	16784		10.86	4.9E+00	AF185255.1	NT	Emuice australis histone H3 (H3) gene, partial cds
8054	20748	33879	0.47	4.8E+00	BF367909.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8439	21131		5.28	4.8E+00	AW1750067.1	EST_HUMAN	PMD-BT0547-310100-002-404 BT0547 Homo sapiens cDNA
283	13090	25731	1.86	4.7E+00	BF240552.1	EST_HUMAN	601876654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098716 5'

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284	13090	25731	1.89	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098716 5'
3288	16030	28679	2.38	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9095	21783	34948	1.18	4.6E+00	BE646437.1	EST_HUMAN	7686g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292088 3' similar to TR:075140 O75140 KIAA0645 PROTEIN; contains element PTR5 repetitive element;
9095	21783	34949	1.18	4.6E+00	BE646437.1	EST_HUMAN	7686g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292088 3' similar to TR:075140 O75140 KIAA0645 PROTEIN; contains element PTR5 repetitive element;
10287	22935		0.61	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11054	23724		2.31	4.6E+00	D63996.1	NT	Synechocystis sp. PCC6803 complete genome, 18/27, 2257260-2392728
11605	24204	37526	2.59	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11762	24353	37685	1.78	4.5E+00	BF668841.1	EST_HUMAN	602123238F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4280216 5'
3035	15801	28447	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
3035	15801	28448	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
6109	18886		1.66	4.4E+00	X13414.1	NT	Mutrin 1 gene for MHC class II(a) associated invariant chain
6027	18807		0.68	4.3E+00	AF059679.1	NT	Homo sapiens neutrophil collagenase (GLGNA) gene, promoter region and 5'UTR
7338	20019	33097	2.03	4.3E+00	Y13402.1	NT	Plasmodium falciparum R28R+var1 gene, exon 1
7515	20186	33280	0.65	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
10769	23453	36696	7.54	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5430	18229		3.44	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5507	18305	31206	0.87	4.2E+00	P51826	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6674	19591	32627	2.62	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6674	19591	32628	2.62	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8859	21550	34697	4.68	4.2E+00	AJB09013.1	EST_HUMAN	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
9818	22469	35672	1.06	4.2E+00	P31368	SWISSPROT	NUBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10049	22687		0.46	4.2E+00	P40886	SWISSPROT	HEXOSE TRANSPORTER HXT8
5846	25079	31569	0.56	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
5846	25079	31570	0.56	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7012	19704	32760	0.84	4.1E+00	BE253668.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7111	19799	32863	0.65	4.1E+00	BF247939.1	EST_HUMAN	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068758 5'
7559	20229	33332	8.73	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7681	20345		0.62	4.1E+00	AB041523.1	NT	Patinopecten yessoensis mRNA for calcineurin A, complete cds
7683	20347	33459	4.32	4.1E+00	P28994	SWISSPROT	GENE 68 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7683	20347	33460	4.32	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7817	20512	33638	2.53	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9440	22118	35295	0.57	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9571	22224	35409	2.46	4.1E+00	BF692425.1	EST_HUMAN	802247938F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4333209 5'
10205	22853		0.48	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10800	23483		3.06	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLFI
10892	23572		11.69	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3909031 5'
3533	16289		0.95	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5372	19500	32524	0.77	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5372	19500	32525	0.77	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32524	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32525	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7089	19778	32843	1.44	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8772	21464	34611	0.45	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIA0144
9843	22494	35695	0.44	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10065	22713	35931	0.63	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 89 of the complete genome
11453	23220	36454	1.53	4.0E+00	P14546	SWISSPROT	CYTCHROME C OXIDASE POLYPEPTIDE III
11537	24137	37444	2.27	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11537	24137	37445	2.27	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3494	16250	28904	4.61	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4287	17026		8.24	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 89 (MSVSP89) gene, promoter region
5572	18369	31279	2.91	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5572	18369	31280	2.91	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6591	19354	32367	0.55	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6774	19518	32546	4.62	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AID-RP5F INTERGENIC REGION

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7282	19946	33022	4.3	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8218	20910	34046	1.86	3.9E+00	X65865.1	NT	Xi laevis mRNA for M4 muscarinic receptor
11365	23176	36403	3.3	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2635	15347		0.9	3.8E+00	AE001582.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
8297	19070	32054	0.96	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN M0385
8673	19590	32826	0.66	3.8E+00	AI493849.1	EST_HUMAN	q25107 x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030437 3'
8331	21024	34181	1.1	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9694	22345		0.62	3.8E+00	AJ390961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
4001	16748	29379	12.29	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7066	19757		1.03	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8609	21301		0.55	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
9076	21765	34928	0.7	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11408	24057	37363	2.23	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11408	24057	37364	2.23	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
579	13359	25986	5.19	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4745	17477		1.06	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
5174	17983	30498	0.74	3.6E+00	BF316316.1	EST_HUMAN	601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
8450	21142	34280	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM0001B08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8450	21142	34281	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM0001B08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8543	21235	34378	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8543	21235	34379	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
							Escherichia coli glycero-phosphate dehydrogenase (gldP) gene, partial cds; and the translation start site has been verified (gldP), the translation start site has been verified (gldP), and repressor protein (gldP) genes, complete cds
10759	23444		4.07	3.6E+00	M96795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3241	18003	28652	1.1	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
5911	18095		1.17	3.5E+00	L42898.1	NT	y940c08.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
6118	18896	31884	1.18	3.5E+00	R19745.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8383	21076		0.56	3.5E+00	P24557	SWISSPROT	z96600.4 s1 Stragene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element;
8930	21821	34763	1.02	3.5E+00	AA190998.1	EST_HUMAN	z96600.4 s1 Stragene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element;
8930	21821	34764	1.02	3.5E+00	AA190998.1	EST_HUMAN	z96600.4 s1 Stragene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element;
9393	22055	35227	0.96	3.5E+00	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

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10417	23063	36283	0.46	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1501	14247	26933	2.94	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
7261	18945	33021	2.84	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7601	20287	33374	0.69	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8577	21269		0.7	3.4E+00	U65408.1	NT	Human alternatively spliced potassium channels ROMK1, ROMK2, ROMK3, ROMK4, ROMK5, and ROMK6 (KCNJ1) gene, complete cds
8972	21682	34813	0.67	3.4E+00	AJ229042.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9010	21700	34850	0.54	3.4E+00	AJ250587.1	NT	Homo sapiens partial TM6SF2 gene for tetraspanin protein, exon 6
10184	22812	36030	2.97	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11519	24119	37429	1.89	3.4E+00	L77570.1	NT	Homo sapiens Digeorge syndrome critical region, centromeric end
5977	18759	31722	1.57	3.5E+00	Q08669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
5977	18759	31723	1.57	3.5E+00	Q08669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7784	20489	33611	0.79	3.5E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	23008	36223	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	23008	36224	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
488	13273	25908	1.64	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4004	13273	25908	0.9	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4879	17413	30048	1.08	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5481	18280	31176	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5481	18280	31177	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5515	18313	31214	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5515	18313	31215	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6214	18988	31964	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6214	18988	31965	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7505	20176	33270	0.7	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7672	20336	33448	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf4, ycf3, rps18 genes
7672	20336	33449	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf4, ycf3, rps18 genes
8928	21619	35283	4.51	3.2E+00	P13061	SWISSPROT	PERIPLASMIC (NIFE) HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
8430	22108	35283	0.87	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (LV1) gene, complete cds
10041	22689	35907	2.03	3.2E+00	AB016081.2	NT	Oryzias latipes OIGC8 gene for guanylyl cyclase C, complete cds
11948	24500		2.44	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5785	18576	31505	2.46	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7287	19970	33047	0.83	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)

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7627	20293		0.94	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
7886	20681	33807	0.48	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8500	21182	34333	4.38	3.1E+00	P49894	SWISSPROT	TYPE I IODOETHYRONINE DEIODINASE (TYPE I 5-DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
8500	21192	34334	4.36	3.1E+00	P49894	SWISSPROT	TYPE I IODOETHYRONINE DEIODINASE (TYPE I 5-DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
9158	21889		3.85	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9796	22447	35652	0.59	3.1E+00	7524769	NT	Chlorella vulgaris chloroplast, complete genome
9888	22538		0.63	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F62C9.5 IN CHROMOSOME III
10234	22882	36065	5.52	3.1E+00	P48385	SWISSPROT	DEOXYTHYRUSINE SYNTHASE (DHS)
11440	23207		2.66	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11463	24066		3.28	3.1E+00	S56660.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, POC7-MZ1, mRNA, 2971 nt]
2842	15610	28259	1.09	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5254	18060	30689	1.32	3.0E+00	X63096.1	NT	S. aureus genes encoding Sau961 DNA methyltransferase and Sau861 restriction endonuclease
6461	19228	32228	0.83	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6461	19228	32229	0.83	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7055	19746		9.09	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (SCH61)
7096	19785		0.6	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8805	21497		1.2	3.0E+00	X67838.1	NT	B. napus DNA for myosinase
10192	22840	36055	0.82	3.0E+00	Q59605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
10544	23240	36474	1.57	3.0E+00	Q16181	SWISSPROT	GDC10 PROTEIN HOMOLOG
10931	23611	36860	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10931	23611	36861	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11578	24177	37492	2.72	3.0E+00	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2004	14740	27464	2.28	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 94 of the complete genome
6809	19470	32493	1.74	2.9E+00	Z36879.1	NT	F. pringlei gdcPA gene for P-protein of the glycine cleavage system
7110	19798	32861	5.21	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR

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7110	19798	32862	5.21	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7356	20037	33115	8.84	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7767	20463	33587	0.87	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7767	20463	33588	0.87	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7996	20691	33819	1.03	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NC1 CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4153059 5'
1440	14187	26872	4.4	2.8E+00	AF186398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast product
1629	14375		2.74	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7207	19892	32968	5.72	2.8E+00	5393724	NT	Mus musculus endomucin (LOC63423), mRNA
9513	22166		0.54	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10588	19892	32968	1.32	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
224	13036	25672	13.51	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Pbx3), mRNA
224	13036	25673	13.51	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Pbx3), mRNA
5484	18263	31154	1.17	2.7E+00	L14005.1	NT	Homo sapiens apolipoprotein A4, polypeptide chain, exons 1 and 2
8045	20739		0.8	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8867	21558		1.83	2.7E+00	AL118459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9332	20403	33519	0.73	2.7E+00	AW088191.1	EST_HUMAN	xc88e12x1 NC1 CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10397	23043		1.75	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4626	17361	26994	5.15	2.6E+00	AF068749.1	NT	CMD-BT0281-031189-087-h04 BT0281 Homo sapiens cDNA
5460	18259	31149	1.86	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5460	18259	31150	1.86	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5736	18528		0.59	2.6E+00	Y17082.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7454	25424		0.82	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7600	20266		6.04	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-8 genes
7958	20653	33776	1.13	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
7958	20653	33777	1.13	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
9557	22210	33395	2.83	2.6E+00	AL161540.2	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10253	22901		1.87	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10953	23630	36878	1.32	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12560	25304		3.17	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1448	14195	28878	3.73	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TPP), member 4 (ABCB4), mRNA
						NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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1448	14195	26879	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5723	18515	31434	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5723	18515	31435	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6387	18515	31434	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6387	18515	31435	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6630	19392	32408	0.84	2.5E+00	D30052.1	NT	Vibrio cholerae ctxA gene and ctxB gene for cholera toxins, complete cds
7659	20323	33431	0.99	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
7700	20363	33477	0.58	2.5E+00	4502902	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9001	21691	34841	1.53	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9752	22403	35608	0.87	2.5E+00	BE297768.1	EST_HUMAN	601176779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
11528	24128		1.34	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
11943	24498		3.08	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3012	15778	28428	1.13	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4949	17579	30203	6.09	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5920	18705	31657	4.16	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7280	19864	33040	0.78	2.4E+00	BF667502.1	EST_HUMAN	602120859F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7280	19864	33041	0.78	2.4E+00	BF667502.1	EST_HUMAN	602120859F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
8039	20734	33865	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8039	20734	33866	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8110	20804		2.63	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8549	21241		1.61	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031289-011-c05 PT0004 Homo sapiens cDNA
8727	21419	34563	7.36	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
9938	22586	35788	2.56	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9938	22586	35789	2.56	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10007	22655	35888	1.86	2.4E+00	X62511.1	NT	H.sapiens CTGF gene and promoter region
10143	22791		6.55	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
10220	22868	36079	1.62	2.4E+00	BE326702.1	EST_HUMAN	hr6306.x1 NC1 CGAP Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10220	22868	36080	1.62	2.4E+00	BE326702.1	EST_HUMAN	hr6306.x1 NC1 CGAP Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10490	23136	36364	0.87	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11331	24022	37327	2.16	2.4E+00	AF158852.2	NT	Fraxaria x enanassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1231	13980	26560	13.6	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4102	16845		1.35	2.3E+00	AJ401081.1	NT	Bos taurus partial cyb gene for cytochrome b

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5744	18536		0.95	2.3E+00	N88245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7354	20035	33113	2.47	2.3E+00	697854	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7495	28425	P07189	3.07	2.3E+00	P07189	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7679	20343	33455	1.01	2.3E+00	X60265.1	NT	Mimazi dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9008	21698	34849	0.54	2.3E+00	5835317	NT	Polyporus ornamentalis mitochondrion, complete genome
9068	21757	34919	1.8	2.3E+00	Q11127	SWISSPROT	ALPHA(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10704	23395	36632	3.83	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11782	24373	37703	3.03	2.3E+00	BF541987.1	EST_HUMAN	802069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11782	24373	37704	3.03	2.3E+00	BF541987.1	EST_HUMAN	802069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12157	24642	31099	6.84	2.3E+00	BE895237.1	EST_HUMAN	801433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
3898	18746	29378	0.95	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4278	17017	29644	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4278	17017	29645	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5258	18064	30692	12.73	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11)>
5258	18064	30693	12.73	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11)>
5763	18554	31478	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
5763	18554	31479	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
5971	18753	31714	9.84	2.2E+00	BE250383.1	EST_HUMAN	800943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2969777 3'
6261	19035	32010	3.87	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6502	19267	32268	3.16	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6861	17838		3.94	2.2E+00	AA594574.1	EST_HUMAN	n85502.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7217	19902	32976	0.9	2.2E+00	AA137027.1	EST_HUMAN	zn97704.r1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7507	20178	33272	19.2	2.2E+00	AA449012.1	EST_HUMAN	zn05610.r1 Soares fetal_fetus_Nb2HF8_Bw Homo sapiens cDNA clone IMAGE:785634 5'
7589	20267	33365	0.72	2.2E+00	P64918	SWISSPROT	ALANINE RACEMASE
8001	20698	33823	0.58	2.2E+00	BE301580.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);

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8001	20696	33824	0.58	2.2E+00	BE301580.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2883207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9241	21820		11.02	2.2E+00	BE741878.1	EST_HUMAN	601594739F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9468	25124		2.28	2.2E+00	Q04706	SWISSPROT	TRANSPONSON TY1 PROTEIN A
9953	22601	35804	1.1	2.2E+00	A1280373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8tc9weeks_2NHP8tc8w Homo sapiens cDNA clone IMAGE:1883985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
9953	22801	35806	1.1	2.2E+00	A1280373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8tc9weeks_2NHP8tc8w Homo sapiens cDNA clone IMAGE:1883985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
9996	22644	35858	2.68	2.2E+00	BF246782.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8tc9weeks_2NHP8tc8w Homo sapiens cDNA clone IMAGE:1883985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10353	23000	36217	3.11	2.2E+00	AF183416.1	NT	60185559F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
11418	23185	36415	3.47	2.2E+00	P07911	SWISSPROT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11616	24214	37539	5.89	2.2E+00	P10407	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
556	15545	25967	8.3	2.1E+00	AF132612.2	NT	EARLY E1A 28 KD PROTEIN
3575	16330		1.08	2.1E+00	AW449386.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
6041	18821		0.89	2.1E+00	P75357	SWISSPROT	U1H.B13-ak-e-08-Q.U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6710	19825	32669	3.95	2.1E+00	O70159	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6946	19428	32443	5.72	2.1E+00	N29575.1	EST_HUMAN	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
8395	21088		1.97	2.1E+00	AU123630.1	EST_HUMAN	W08a10.s1 Soares_melanocyte 2NHP8 Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M56654 TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
1174	13927	26591	1.44	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1174	13927	26592	1.44	2.0E+00	AF180527.1	NT	Homo sapiens p220kdel (DOKDEL) mRNA, complete cds
1312	14060	26735	0.97	2.0E+00	AF204927.1	NT	Homo sapiens p220kdel (DOKDEL) mRNA, complete cds
1569	14316		2.61	2.0E+00	P25562	SWISSPROT	Oryctolagus cuniculus Na ⁺ ,K ⁺ -ATPase beta 1 subunit mRNA, complete cds
2145	14875	27609	5.98	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2145	14875	27610	5.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4080	16824	29450	2.2	2.0E+00	AW664498.1	EST_HUMAN	R.norvegicus mRNA for collagen alpha1 type I
4080	16824	29451	2.2	2.0E+00	AW664498.1	EST_HUMAN	h13c05.x1 NCL_CGAP_GUI Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7449	20125		0.92	2.0E+00	P07568	SWISSPROT	h13c05.x1 NCL_CGAP_GUI Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7923	20618	33745	3.17	2.0E+00	AB008676.1	NT	STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
7923	20618	33746	3.17	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds
7923	20618	33747	3.17	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds

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8820	21512	34856	3.15	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
12481	25265	30720	7.27	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5511	18309	31209	4.77	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (ltp1), mRNA
5511	18309	31210	4.77	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (ltp1), mRNA
6009	18790	31753	1.32	1.9E+00	BE966895.1	EST_HUMAN	601678636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6556	19321		0.75	1.9E+00	AW845889.1	EST_HUMAN	MRO-CT0063-07 (099-002-g02 CT0063 Homo sapiens cDNA
6650	19412		2.46	1.9E+00	O63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8358	21051	34190	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8358	21051	34191	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8557	21249		2.94	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT0114-010900-328-h12 MT0114 Homo sapiens cDNA
8792	21484		1.33	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9530	22183	35367	0.59	1.9E+00	AA689125.1	EST_HUMAN	ab94904.s1 Stratagene lung (8937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu
10462	23108	36339	0.62	1.9E+00	AF249269.1	NT	repetitive element contains element L1 L1 repetitive element ;
3089	15854	28498	1.3	1.8E+00	P21004	SWISSPROT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3118	15883	28522	1.57	1.8E+00	U04358.1	NT	PROTEIN B8 PRECURSOR
3118	15883	28522	1.57	1.8E+00	U04358.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5777	18568		1.81	1.8E+00	P18502	SWISSPROT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
6013	18784	31757	1.32	1.8E+00	BF311999.1	EST_HUMAN	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6305	19077		1.12	1.8E+00	BF683327.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127384 5'
6641	19403	32418	1.64	1.8E+00	BF305652.1	EST_HUMAN	602138470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298272 5'
6958	19440	32455	1.79	1.8E+00	P21249	SWISSPROT	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4199038 5'
8016	20711	33841	0.93	1.8E+00	P11369	SWISSPROT	MAJOR ANTIGEN
8016	20711	33842	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8368	21061	34201	0.44	1.8E+00	P48634	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8368	21061	34202	0.44	1.8E+00	P48634	SWISSPROT	ENDONUCLEASE
8368	21061	34203	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8753	21445	34593	1.98	1.8E+00	O43281	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9073	21762	34924	0.77	1.8E+00	R31042.1	EST_HUMAN	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9161	21831	34994	0.76	1.8E+00	AW880004.1	EST_HUMAN	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
							YH72a08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:136278 5'
							QV0-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA

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9749	22400	35605	0.75	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10183	22831		3.2	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10452	23098		0.83	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12276	25236		6.29	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12359	24763		3.9	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpct1b), mRNA
1086	13844	26502	2.21	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2269	14995	27734	2.29	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2372	15094	27833	2.56	1.7E+00	A1141067.1	EST_HUMAN	oz43h05.x1 Soares NIH-HMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4426	17162	29792	0.81	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5525	18323	31223	1.77	1.7E+00	BE063548.1	EST_HUMAN	CMO-BT0282-171298-127-e05 BT0282 Homo sapiens cDNA
5525	18323	31224	1.77	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171298-127-e05 BT0282 Homo sapiens cDNA
5927	18711	31666	3.28	1.7E+00	Q81TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
7118	19806	32871	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7118	19806	32872	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7753	20449	33573	0.91	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 2 and gamma 4 gene clusters
7932	20627	33755	1.13	1.7E+00	8755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tall1), mRNA
7961	20656	33781	0.59	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214889 5'
8440	21132	34268	0.5	1.7E+00	AF245613.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8525	21217		2.3	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8605	21297	34440	0.59	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
8605	21297	34441	0.59	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9047	25123	34892	2.18	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9047	25123	34893	2.18	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9066	22169		1.15	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
10071	22719		0.48	1.7E+00	AW963681.1	EST_HUMAN	EST365751 MAGE sequences, MAGE Homo sapiens cDNA
11598	24195	37514	2.57	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp509f-cleaved sublibrary/Homo sapiens cDNA not directional
12231	24684	31074	1.9	1.7E+00	A1078443.1	EST_HUMAN	tue2d07.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257649 3' similar to contains MSR1.t1
12717	24990	30970	1.84	1.7E+00	A198573.1	EST_HUMAN	MSR1 repetitive element;
2027	14762	27491	18.51	1.6E+00	AF189339.1	NT	qf50b01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.t1 L1 repetitive element;
							Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2038	14771	27500	3.75	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2042	14776	27505	1.54	1.6E+00	Y11344.1	NT	Mus musculus ST6Galinacill gene, exon 2
2282	15007		1.24	1.6E+00	X98373.1	NT	B. napus gene encoding endo-polygalacturonase
2981	15727	28377	1.61	1.6E+00	W59426.1	EST_HUMAN	z42501.1 Soares_fetal_jheart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
4011	16757		5.68	1.6E+00	BF570077.1	EST_HUMAN	gb:D28805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN):
4319	17058	28682	1.9	1.6E+00	AF155827.1	NT	602180395T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4319	17058	28683	1.9	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA8) mRNA, complete cds
4942	17688	30277	0.84	1.6E+00	AF075394.1	NT	Homo sapiens cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
4942	17688	30278	0.84	1.6E+00	AF075394.1	NT	Urotrochis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5024	17745	30356	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6Galinacill gene, exon 2
5024	17745	30357	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6Galinacill gene, exon 2
5737	18529	31450	2.16	1.6E+00	L04808.1	NT	Brachydanio rerio MHG class II DA-beta-2'01 gene, 3' end
5823	18612	31543	0.79	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6378	19147	32146	0.69	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6610	19373	32387	1.06	1.6E+00	AW294881.1	EST_HUMAN	UIH-B12-ahr-B-04-Q-UI st NCJ CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7145	19832	32901	2.73	1.6E+00	BE997267.1	EST_HUMAN	RCO-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
7929	20624	34112	1.19	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8277	20971	34112	3.28	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
8788	21490	34636	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8788	21490	34637	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8970	21660	34810	0.47	1.6E+00	BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9360	25121	33549	1.94	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9360	25121	33550	1.94	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9487	22140		0.68	1.6E+00	AF043466.1	NT	Thermomonas thermophilus D-xylose-binding protein (xyf) gene, complete cds
9634	22286	35480	1.32	1.6E+00	T41290.1	EST_HUMAN	ph686_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph686_19/1TV
10047	22695	35911	0.5	1.6E+00	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Iel (IAL), and zinc finger protein (DNZ1) genes, complete cds
10085	22733	35947	1.15	1.6E+00	AW835644.1	EST_HUMAN	QV4-L1 T0016-090200-100-407 LT0016 Homo sapiens cDNA
10085	22733	35948	1.15	1.6E+00	AW835644.1	EST_HUMAN	QV4-L1 T0016-090200-100-407 LT0016 Homo sapiens cDNA
10242	22890	38102	0.47	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10491	23137	38365	0.45	1.6E+00	AF162084.1	NT	Glugea pleocoglossi beta-tubulin 2 (btub2) gene, partial cds

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10670	23381	38602	1.95	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 (CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN)
10728	23416	36657	1.27	1.6E+00	AA216387.1	EST_HUMAN	nc16b02.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008287 similar to contains element MIER4 repetitive element;
10747	18612	31543	5.27	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
11705	24300	37626	3.46	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
31	12859	25476	5.31	1.5E+00	U53449.1	NT	Rattus norvegicus Jun dimerization protein 2 (jdp-2) mRNA, complete cds
225	13037	25674	2.2	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii R1 section 82 of 228 of the complete chromosome 1
606	13384		2.03	1.5E+00	6752981	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagidlin) (Adam15), mRNA
2410	15131	27867	1.95	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2519	15235	27875	2	1.5E+00	6878350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3135	15131	27867	1.85	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3388	16127	28785	0.72	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 228 of the complete chromosome 1
5642	18437	31350	0.83	1.5E+00	A1655301.1	EST_HUMAN	HKF-1.;
5642	18437	31351	0.83	1.5E+00	A1655301.1	EST_HUMAN	HKF-1.;
6312	19083	32068	3.02	1.5E+00	R17878.1	EST_HUMAN	Y010602.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31893 5'
7028	19720		1.37	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7060	19751	32814	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7060	19751	32815	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7245	19930	33006	0.61	1.5E+00	AA888259.1	EST_HUMAN	ak2610.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7493	20165	33257	0.76	1.5E+00	A103254.1	EST_HUMAN	ar07b11.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:595836 SEROTRANSFERRIN PRECURSOR (HUMAN);
7727	20390		0.64	1.5E+00	A8036887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8021	20716	33848	0.89	1.5E+00	BE887446.1	EST_HUMAN	601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8542	21234	34377	0.84	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
8914	21605		0.48	1.5E+00	AB038516.1	NT	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9032	21722	34878	0.46	1.5E+00	BF217818.1	EST_HUMAN	60182662F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9383	22045	35217	0.64	1.5E+00	R81928.1	EST_HUMAN	y03h01.r1 Soares placenta N2b2HP Homo sapiens cDNA clone IMAGE:147697 5'
9535	22188	35374	1.39	1.5E+00	AW375697.1	EST_HUMAN	Q1V3-G10192-261099-008-d09 G10192 Homo sapiens cDNA
9760	22411	35618	6.39	1.5E+00	BF376754.1	EST_HUMAN	RCO-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
9952	22600		1.77	1.5E+00	BF379444.1	EST_HUMAN	60203577F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183865 5'
10096	22744	35958	1.66	1.5E+00	AA017693.1	EST_HUMAN	ze38g08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'

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10096	22744	35959	1.66	1.5E+00	AA017689.1	EST_HUMAN	z839g06.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11375	23982	37282	4.46	1.5E+00	AL134187.1	EST_HUMAN	DKFZP547P243_s1 547 (synonym: hnf1r1) Homo sapiens cDNA clone DKFZP547P243 3'
11530	24130		6.55	1.5E+00	X07380.1	NT	Malze mitochondrial rRNA-Ser gene and rRNA-Phe pseudogene
11628	24228	37549	2.1	1.5E+00	AI400798.1	EST_HUMAN	ig94d09.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
11629	24226	37550	2.1	1.5E+00	AI400798.1	EST_HUMAN	ig94d09.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12222	25325	30713	1.44	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12445	24815		3.38	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
28	12856	25472	2.76	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
28	12856	25473	2.76	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2333	15057		6.92	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2675	15394	28125	2.21	1.4E+00	X74493.1	NT	Human papillomavirus type 7 genomic DNA
2776	15481	28221	2.61	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2776	15481	28222	2.61	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4545	17280		1.81	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287556 5'
5288	18093	30754	1.61	1.4E+00	AW054978.1	EST_HUMAN	wf45g07.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5441	18240		5.57	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6186	18963	31936	2.72	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6202	25420		4.02	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0805 protein, complete cds
6318	19089	32074	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6318	19089	32075	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
7186	19872	32946	2.07	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a and 2b), CAV1 (exons 1 and 2)
7201	19887	32962	1.17	1.4E+00	AW467760.1	EST_HUMAN	he23105.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
7258	19942	33018	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7258	19942	33019	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8233	20927		0.68	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8693	21385		4.47	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8991	21681	34829	1.73	1.4E+00	R20459.1	EST_HUMAN	y93f12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9097	21765	34951	4.65	1.4E+00	BC064687.1	EST_HUMAN	RC1-BT03113-301299-012-05 BT03113 Homo sapiens cDNA
9131	21819	34985	0.51	1.4E+00	AF13484.1	NT	Sceloporus undulatus ornithine decarboxylase (OTC) mRNA, complete cds

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10108	22756	35968	0.79	1.4E+00	BF576546.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10151	22798	36015	0.61	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291089-008-C04 HT0198 Homo sapiens cDNA
10151	22798	36016	0.61	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291089-008-C04 HT0198 Homo sapiens cDNA
10424	23070	36291	1.08	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10424	23070	36292	1.06	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11003	23875	36931	1.34	1.4E+00	AA195528.1	EST_HUMAN	z33609.r1 Soanes_NhIMPu_S1 Homo sapiens cDNA clone IMAGE:565512 5' similar to contains element MER22 repetitive element
11188	23853	37139	6.16	1.4E+00	AB006882.1	EST_HUMAN	Homo sapiens APECED mRNA for AIRE-1, complete cds
11381	23988	37288	4.42	1.4E+00	BE962107.2	EST_HUMAN	601655194R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11381	23988	37289	4.42	1.4E+00	BE962107.2	EST_HUMAN	601655194R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11404	24053	37357	3.46	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. reitzi guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11404	24053	37358	3.46	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. reitzi guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12079	26256		1.48	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
557	13339		1.81	1.3E+00	Z73640.1	NT	M. musculo gene encoding 4-Dihydroxyethyl-trisporate dehydrogenase
882	13651	26320	3.42	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1107	13864		20.26	1.3E+00	Y19213.1	NT	Homo sapiens putative psht-HbA pseudogene for half keratin, exons 2 to 7
1274	14024	26692	13.71	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1274	14024	26693	13.71	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	14083		1.26	1.3E+00	U61730.2	NT	Cox1 lactyma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1605	14351		2.27	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 89 of the complete genome
2239	14867		1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2405	15126	27862	1.27	1.3E+00	P25391	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2553	15268		1.75	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915845 3'
2940	15705	28354	0.73	1.3E+00	6759621	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
3594	16339	28684	0.89	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P56), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5427	18226	30538	1.09	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5822	18418	31330	0.6	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
5863	18850	31590	0.81	1.3E+00	BF663825.1	EST_HUMAN	602145284F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4308095 5'
5928	18712	31667	7.57	1.3E+00	AW362834.1	EST_HUMAN	PIMC-CT0289-291189-004-f03 CT0289 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5928	18712	31688	7.57	1.3E+00	AW362834.1	EST_HUMAN	PMD-CT0289-291199-004-108 CT0289 Homo sapiens cDNA
6323	19093	32081	1.34	1.3E+00	M33496.1	NT	D melanogaster no-on-transient A gene product, complete cds
6652	19414		0.75	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6739	19573	32606	0.82	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
6854	19554	32584	1.17	1.3E+00	BE538819.1	EST_HUMAN	801081420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447865 5'
7000	19692	32743	0.81	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0659 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TC8A Homo sapiens cDNA clone TCBAP0969
7338	20039	33117	1.01	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8187	20891	34029	1.28	1.3E+00	AJ009812.1	NT	Sua scrofa p16 gene
8346	21039	34176	2.78	1.3E+00	BE963378.2	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866185 3'
8459	21151	34294	0.88	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8611	21303		1.78	1.3E+00	9810247	NT	Homo sapiens GL004 protein (GL004), mRNA
8859	21381	34525	0.79	1.3E+00	AB27628.1	EST_HUMAN	wc65607 x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482100 3'
9415	22053		5.24	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9424	22102	35273	2.56	1.3E+00	X72019.1	NT	S.alba pht-1 mRNA for photolyase
9524	22177	35361	0.96	1.3E+00	AF058250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9588	22222	35407	1.56	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMMAN)
9651	22303	35498	1.14	1.3E+00	AB27629.1	EST_HUMAN	wc65607 x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482100 3'
9726	22377	35578	0.79	1.3E+00	AJ223982.1	NT	Lactococcus lactis cremoris NCDO-hv1 chromosomal inversion junction DNA
9726	22377	35579	0.79	1.3E+00	AJ223992.1	NT	Lactococcus lactis cremoris NCDO-hv1 chromosomal inversion junction DNA
9768	22417	35624	4.53	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866185 3'
9826	22477		0.48	1.3E+00	AF559844.1	EST_HUMAN	tg77a12x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:U14723
10050	22698	35913	0.46	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN)
10050	22698	35914	0.46	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10113	22761	35974	1.62	1.3E+00	AE004392.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10130	22778	35991	1.35	1.3E+00	M29963.1	NT	Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome
10483	23128		0.82	1.3E+00	AL163302.2	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10511	23157	36383	0.45	1.3E+00	AB980846.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
10592	23286		4.6	1.3E+00	Q14117	SWISSPROT	wc32a10 x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2488922 3' similar to SW:TRXB_HUMAN Q16881 THIOREDOXIN REDUCTASE ;
							DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10822	23505	36744	1.93	1.3E+00	P26298	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
10846	23528	36772	2.01	1.3E+00	Z18892.2	NT	Mus musculus desmulin gene
11307	23966		1.8	1.3E+00	AW274791.1	EST_HUMAN	xp00603.x1 NC1 CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739866 3'
11527	24127	37433	3.21	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11624	24221	37544	3.16	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment
12210	24675		2.84	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12386	24780	31035	6.3	1.3E+00	BF348043.1	EST_HUMAN	602028185F1 NC1 CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4158452 5'
12397	25163		2.73	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12489	24848		2.15	1.3E+00	AF187035.1	NT	Stumria lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
635	13414	26050	11.05	1.2E+00	AA678248.1	EST_HUMAN	Z22408.s1 Soares_fetal_liver_spleen_1N1LS S1 Homo sapiens cDNA clone IMAGE:431535 3'
804	13576	26239	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26240	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26241	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13627		1.35	1.2E+00	B924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1138	13893	26554	5.64	1.2E+00	AF080245.2	NT	Eleis oleifera sesquiterpene synthase mRNA, complete cds
1183	13935	26600	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1183	13935	26601	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2003	14739	27463	1.22	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3108	15873	28512	1.24	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3163	15926	28573	5.88	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3163	15926	28574	5.88	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3280	16041		2.59	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3699	16452	29091	6.69	1.2E+00	U75602.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3967	16716	29354	1.78	1.2E+00	BF373570.1	EST_HUMAN	MRQ-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4268	18110	28766	1.11	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4438	17174		1.57	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4487	17222	29850	0.98	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4523	17258	29892	1.89	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4548	17283		6.43	1.2E+00	Y06200.1	NT	T. plimatum chloroplast rbcL gene, partial
5351	18154	30836	1.1	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5467	18266	31158	1.91	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5784	18575	31504	0.83	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6060	18940	31801	2.51	1.2E+00	X74885.1	NT	D.hydral aryl repeat cluster DNA, fragment D
6119	18997	31855	4.42	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0080-270400-180-a03 BN0080 Homo sapiens cDNA

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6188	18974	31951	1.94	1.2E+00	X89084.1	NT	C-glutamicum pla gene and ackA gene
6198	18974	31952	1.54	1.2E+00	X89084.1	NT	C-glutamicum pla gene and ackA gene
6241	19015	31989	39.54	1.2E+00	AA759254.1	EST_HUMAN	ah94g12.s1 Soares_festis_NHT Homo sapiens cDNA clone 1322374 3'
6342	19112	32101	0.55	1.2E+00	N83295.1	EST_HUMAN	y69b12.s1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:273569 3' similar to
6408	19177	32175	0.68	1.2E+00	P17671	SWISSPROT	gbIM87935[HJMAALU472 Human carcinoma cell-derived Aliu RNA transcript, (RNA); gb:J04970
6412	19180	32179	2.08	1.2E+00	AW813278.1	EST_HUMAN	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6815	19478	32498	1.17	1.2E+00	AB029010.1	NT	ECDSONE-INDUCIBLE PROTEIN E75-A
6828	19490	32512	3.11	1.2E+00	AJ002141.1	NT	MR3-ST0191-140200-013-005 ST0191 Homo sapiens cDNA
7153	19840	AJ271735.1	0.94	1.2E+00	AJ271735.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7282	25109	33044	4.86	1.2E+00	AV734585.1	EST_HUMAN	Mus musculus DSPP gene
7550	20220	33323	2.49	1.2E+00	X74207.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
7603	20269	33378	0.56	1.2E+00	J05218.1	NT	AV734585 cda Homo sapiens cDNA clone cdaAFH03 5'
7715	20379	33492	0.56	1.2E+00	BE787646.1	EST_HUMAN	L-lactid pyrD and prf genes
8467	21159	34302	3.32	1.2E+00	AB033030.1	NT	Chicken muscarinic acetylcholine receptor (cm4 mAChR) gene, complete cds
8561	21253	34391	0.68	1.2E+00	P38427	SWISSPROT	601481761F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3884270 5'
8776	21467		0.51	1.2E+00	7708271	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
8923	21614	34758	1.87	1.2E+00	AW377210.1	EST_HUMAN	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT
9138	21626	34891	0.5	1.2E+00	H48599.1	EST_HUMAN	(TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE
9298	21985	35138	3.76	1.2E+00	Z32850.1	NT	GLUCOSYLTRANSFERASE)
9505	22158	35339	1.81	1.2E+00	D11745.1	EST_HUMAN	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
9831	22482	35984	2.86	1.2E+00	X56832.1	NT	yc80a08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA
10224	22872		0.73	1.2E+00	AB009666.1	NT	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
11318	24009	37314	3.78	1.2E+00	AW817817.1	EST_HUMAN	HUMHMO1A01 Liver HepG2 cell line. Homo sapiens cDNA clone hmo1a01
11357	24045		10.62	1.2E+00	BE160781.1	EST_HUMAN	H.sapiens ENO3 gene for muscle specific endase
11435	23202	38434	4.36	1.2E+00	U50147.1	NT	Homo sapiens kotho gene, exon 1
12179	25227	30817	17.06	1.2E+00	AL183203.2	NT	PMO-ST0284-181199-001-d01 ST0284 Homo sapiens cDNA
12199	24667		2.8	1.2E+00	AP001515.1	NT	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
451	13237	25878	1.53	1.1E+00	D68980.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
1757	14499	27200	1.33	1.1E+00	AW965393.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
1892	14629	27339	0.98	1.1E+00	AW575889.1	EST_HUMAN	Bacillus halodurans genomic DNA, section 9/14
						NT	Bacillus halodurans genomic DNA, section 9/14
						NT	Human mRNA for KIAA0227 gene, partial cds
						EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
						EST_HUMAN	UJHF-BR0p-ajk-f-02-0-UJ.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'

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3324	16084	28734	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3324	16084	28735	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3480	18236	28892	1.11	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3587	18322	28970	1.01	1.1E+00	AI808360.1	EST_HUMAN	wf54h1.1.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3707	18460	29098	1.05	1.1E+00	AE003896.1	NT	SW_P531_HUMAN Q12888 P33-BINDING PROTEIN 53BP1;
3707	18460	29099	1.05	1.1E+00	AE003896.1	NT	wf54h1.1.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3798	18550		1.02	1.1E+00	X85374.1	NT	Xyella fastidiosa, section 32 of 228 of the complete genome
4190	18931		5.69	1.1E+00	5855331	NT	Xyella fastidiosa, section 32 of 228 of the complete genome
4634	17369		0.81	1.1E+00	U34992.1	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4834	17662	30272	3.45	1.1E+00	U18496.1	NT	R. uniconis complete mitochondrial genome
4935	17663	30273	1.05	1.1E+00	U18496.1	NT	Carcharias plumbeus lg lambda light chain gene, complete cds
5129	17847	30464	1.07	1.1E+00	AJ271740.1	NT	African swine fever virus, complete genome
5224	18031	30657	1.39	1.1E+00	6878530	NT	Drosophila melanogaster D-Tin gene, exons 1-37
5526	18324	31225	16.76	1.1E+00	BE860184.1	EST_HUMAN	Homo sapiens putative GR6 protein (GR6), mRNA
5545	18342	31250	1.2	1.1E+00	AI138582.1	EST_HUMAN	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
6001	18782	31743	1.1	1.1E+00	11419739	NT	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828835 3'
6181	18958	31932	0.62	1.1E+00	AF197861.1	NT	qd55c03.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6313	19084	32069	0.82	1.1E+00	R06037.1	EST_HUMAN	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6616	19379	32394	0.72	1.1E+00	AJ404004.1	NT	Meiostrongylus pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
7155	19842		0.68	1.1E+00	AF101091.1	NT	ye98e03.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:124924 5'
7196	19882	32956	0.72	1.1E+00	X55891.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7389	20068	33146	2.18	1.1E+00	Z72338.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7389	20068	33147	2.18	1.1E+00	Z72338.1	NT	Malva mRNA for endase (2-phospho-D-glycerate hydrolase)
7411	20088	33172	8.94	1.1E+00	AL161598.2	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7490	25115	33247	0.8	1.1E+00	11987860	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
8032	20727	33860	3.01	1.1E+00	BF693996.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8120	20814	33950	0.64	1.1E+00	AI478339.1	EST_HUMAN	Mus musculus ailerin mating type information regulation 2, (S.cerevisiae, homodog)-like (Sir2), mRNA
8636	21328	34471	0.71	1.1E+00	AB003088.1	NT	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8714	21406	34549	0.75	1.1E+00	S80750.1	NT	tm39h11.x1 NCI_CGAP_X8411 Homo sapiens cDNA clone IMAGE:2160549 3'
							Acetabularia caliculus mitochondrial COX-like gene
							VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]

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8824	21518	34861	0.45	1.1E+00	A078946.1	EST_HUMAN	oz2405.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9337	20408		0.69	1.1E+00	BE394876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3817418 5'
9528	22181	35365	0.53	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smx gene)
9580	22233		1.2	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9872	22324	35520	1.14	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaeE, psaeF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
9732	22383	35535	1.37	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
9837	22488	35680	4.59	1.1E+00	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9898	22548	35742	18.34	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10398	23044	36260	1.1	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10504	23150	36375	0.73	1.1E+00	AB78021.1	EST_HUMAN	eu51c11.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518292 5' similar to gb:D10522
10547	23243	36478	2.25	1.1E+00	11067364	NT	Human mRNA for 80K-L protein, complete cds. (HUMAN);
10606	23300		3.1	1.1E+00	AF068942.1	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
11023	23695	36958	1.28	1.1E+00	11439506	NT	Klebsiellidium filitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11026	23698	36961	1.58	1.1E+00	L16877.1	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), mRNA
11042	17801		5.23	1.1E+00	8922973	NT	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
11048	23718	36988	3.68	1.1E+00	AF012862.1	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11048	23718	36989	3.68	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11328	24019	37323	4.58	1.1E+00	AB09699.1	EST_HUMAN	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11561	24160	37470	1.63	1.1E+00	D88501.1	NT	wf78e11.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11561	24160	37471	1.63	1.1E+00	D88501.1	NT	Human PBI gene, complete cds
12153	24638		3.66	1.1E+00	P07888	SWISSPROT	Human PBI gene, complete cds
12550	24697	31078	1.93	1.1E+00	AF216896.1	NT	LOW TEMPERATURE ESSENTIAL PROTEIN
12378	25225		2.09	1.1E+00	AF234169.1	NT	Taenidia solum immunogenic protein Te76 mRNA, partial cds
12388	25200		1.44	1.1E+00	8393196	NT	Dichostellium discoidium isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
97	12923		2.46	1.0E+00	U23808.1	NT	Rattus norvegicus C-reactive protein, member of the pentraxin family (Crp), mRNA
111	12932	25568	0.73	1.0E+00	D88425.1	NT	Xenopus laevis rhodopsin gene, complete cds
409	13194		2.25	1.0E+00	AB021684.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
562	13344	25971	1.2	1.0E+00	AJ251680.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
562	13438	26078	4.38	1.0E+00	AL163218.2	NT	Giardia lamblia mRNA for homeodomain transcription factor (so gene)
						NT	Homo sapiens chromosome 21 segment HS21C018

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
663	13439		0.95	1.0E+00	AF125084.1	NT	Aedes aegypti mucin-like protein MJC1 mRNA, complete cds
1365	15567		3.03	1.0E+00	X80418.1	NT	V. carteri Algal-CAM mRNA
1751	14493	27193	0.93	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2489	15206	27947	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2489	15206	27948	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2878	15645	28287	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2878	15645	28288	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2867	15733		1.17	1.0E+00	O14228	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08CIN CHROMOSOME I
3194	15957	28609	1.24	1.0E+00	AA628453.1	EST_HUMAN	af26p08.s1 Soares, total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA208.3 CE04204 contains element MER22 MER22 repetitive element;
3585	12923		1.24	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3689	16422	28063	1.04	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase
4050	16795	28424	0.76	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4242	16983		0.76	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4934	17680		0.93	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
4975	17698	30306	0.74	1.0E+00	AF092505.1	NT	Mus musculus dipeptidyl aminopeptidase-like protein 6 (Dpp6) gene, partial cds; and proximal Rump white inversion breakpoint
5200	18008	30629	3.53	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5759	18551	31472	4.97	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5759	18551	31473	4.97	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5967	18654	31595	1.53	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA 1 FCA contig fragment No. 6
6024	18804	31765	4.7	1.0E+00	P04501	SWISSPROT	FIBRIN PROTEIN
6030	18810	31770	1.49	1.0E+00	AW452782.1	EST_HUMAN	U1-H-B13-abx-d-09-0-UI.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088669 3'
6397	19166	32166	1.95	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6447	19215	32213	0.91	1.0E+00	AF104690.1	NT	Homo sapiens cell cycle protein (PA264) gene, exons 2 through 5
6534	19300		1.06	1.0E+00	P46508	SWISSPROT	SRB-1.1 PROTEIN
6679	18596	32634	1.33	1.0E+00	Y11204.1	NT	V. carteri gene encoding volvoxpsn

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7038	19730	32788	1.09	1.0E+00	S62770.1	NT	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7378	20058		9.29	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7611	20277	33385	1.56	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7626	20292	33401	5.26	1.0E+00	AA775191.1	EST_HUMAN	ac78608.s1 Stratiogene lung (8937210) Homo sapiens cDNA clone IMAGE:868781 3'
7861	20556	33681	1.36	1.0E+00	BE868287.1	EST_HUMAN	601443950.F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
7861	20556	33682	1.36	1.0E+00	BE868287.1	EST_HUMAN	601443950.F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8041	17680		1.19	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8248	20942	34079	2.02	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8248	20942	34080	2.02	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8376	21069		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8408	21101	34237	0.5	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UB-P-M)
8408	21101	34238	0.5	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UB-P-M)
8436	25122		2.34	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0228-181099-011-e06 HT0228 Homo sapiens cDNA
8476	21168	34312	0.88	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8825	21317	34459	1.27	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9171	21841	35006	2.43	1.0E+00	BE907592.1	EST_HUMAN	601497581.F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9381	22043	35215	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9381	22043	35216	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9510	22163	35345	1.83	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK C Homo sapiens cDNA clone GKCCYA11 5'
9516	22169	35351	1.43	1.0E+00	U44962.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9516	22169	35352	1.43	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds

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9763	22404	35609	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
9763	22404	35610	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10012	22660	35975	0.71	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10012	22660	35976	0.71	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10104	22752	35966	0.81	1.0E+00	A1077920.1	EST_HUMAN	oy15007.s1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1865901 3'
10225	22873	36085	4.36	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMAFWC04 5'
10375	23021	36237	18.16	1.0E+00	AA004982.1	EST_HUMAN	Z194602.1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10375	23021	36238	18.16	1.0E+00	AA004982.1	EST_HUMAN	Z194602.1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10407	23053	36270	1.1	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10893	23573	36823	4.57	1.0E+00	S90825.1	NT	PBR1=proline-rich protein (intron 3) [human, Genomic, 898 nt]
11025	23697	36960	1.49	1.0E+00	AA701494.1	EST_HUMAN	Z163b11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element;
11522	24122		1.59	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
11744	18008	30629	1.55	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
11838	24422	37763	12.29	1.0E+00	Q60019	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 8 (NADH DEHYDROGENASE 1, CHAIN 8) (NDH-1, CHAIN 8)
11868	24452	37784	1.38	1.0E+00	8626187	NT	Human adenovirus type 5, complete genome
12049	24568		3.01	1.0E+00	P15308	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12370	24772		2.32	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAGE resequences, MAGN Homo sapiens cDNA
2643	15363	28097	1.19	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3591	16345		0.97	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5547	18344	31253	10.08	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
5779	18570	31498	0.93	9.9E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9160	21830		1.37	9.9E-01	U65687.1	NT	Lycopodium obscurum putative M1 copy 1 nematode-resistance gene
9455	22005		2.18	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10614	23308	36547	2.37	9.9E-01	AJ005028.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk3
11592	24191	37508	2.3	9.9E-01	Y11972.1	NT	B. aphidicola 16S rDNA (host T. subseri)
11592	24191	37508	2.3	9.9E-01	Y11972.1	NT	B. aphidicola 16S rDNA (host T. subseri)
510	13294	25928	1.14	9.9E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2295	16020		1.21	9.9E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2804	15509		1.01	9.9E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3781	16533	29171	0.92	9.9E-01	O87551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEONUCLEASE IV)
7099	18788	32852	4.97	9.9E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983

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7099	19788	32853	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7545	20215	33316	1.15	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
7545	20215	33317	1.15	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8619	21311	34453	0.91	9.8E-01	P38852	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10336	22983			9.8E-01	AA825565.1	EST_HUMAN	cd55404.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
10916	23598	36842	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
10916	23598	36843	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11784	24355	37888	1.57	9.8E-01	A1680878.1	EST_HUMAN	b42a10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
12256	24702			9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cez2y/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7058	19749	32812	2.28	9.7E-01	U28716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8401	21094	34230	1.68	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8407	21100	34236	1.3	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
11123	23762		3.64	9.7E-01	BF511209.1	EST_HUMAN	UIH-B14-act-e-07-0-UI.s1 NCL_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3085140 3'
4425	17161	29791	1.5	9.6E-01	AW789674.1	EST_HUMAN	PM2-JM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5687	18462	31377	3.77	9.6E-01	Z70558.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5687	18462	31377	3.77	9.6E-01	Z70558.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6648	19410	32424	0.61	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
8291	20885		2.33	9.6E-01	X95275.1	NT	P. falciparum complete gene map of plasid-like DNA (IR-A)
8750	21442	34589	0.59	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
11503	24104	37416	3.47	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11503	24104	37417	3.47	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11952	24505		1.92	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12558	25301	30710	2.18	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2480	15198	27938	1.05	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
2673	15382	28122	0.97	9.5E-01	Q02894	SWISSPROT	ENDOGLUCANASE I (PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE I))
3782	16514	29150	2.04	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3782	16514	29151	2.04	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8899	21590	34730	0.69	9.5E-01	A1190162.1	EST_HUMAN	qd57d07.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1739581 3'
9003	21693	34843	1.05	9.5E-01	AW681102.1	EST_HUMAN	RC1-CT0295-241189-011-b02 CT0295 Homo sapiens cDNA

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11209	23872	37159	1.88	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11429	23196	36427	2.42	9.5E-01	AW283798.1	EST_HUMAN	U1H-B12-arp-f-03-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
11795	24385	37718	1.55	9.5E-01	T67204.1	EST_HUMAN	ya53404.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66631 3'
3196	15959		3.33	9.4E-01	AF165590.1	NT	Bartonia clarridgeae RNA polymerase beta subunit (pob) gene, partial cds
3212	15975		2.06	9.4E-01	AF080595.1	NT	Plimphella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8764	21456	34606	0.67	9.4E-01	M80724.1	NT	Human Fe-gamma-receptorIIA (FCGR2A) gene, exon 4
12202	24670		1.82	9.4E-01	BE781251.1	EST_HUMAN	601468703F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3886929 5'
12557	25219		1.79	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1726	14468		1.05	9.3E-01	AF242382.1	NT	Homo sapiens phytoyl-CoA hydroxylase (PHYH) gene, exon 5
2640	19351	28085	1.36	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271189-011-B01 BT0503 Homo sapiens cDNA
4015	16761	29388	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4015	16761	29389	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5505	18303	31204	1.56	9.3E-01	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5592	18388	31288	3.99	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7956	20661	33785	1.65	9.3E-01	AA847040.1	EST_HUMAN	ce09003.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
8713	21405		1.04	9.3E-01	AF061981.1	NT	Xenopus laevis CCOH zinc finger protein G3H-2 (G3H-2) mRNA, complete cds
8835	21527	34673	0.85	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12681	24970		3.12	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
12802	25049		1.48	9.3E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltracin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
3233	15995	28648	2.93	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3816184 3'
4822	17553		0.97	9.2E-01	BF129973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5631	18426		1.15	9.2E-01	7106410	NT	Mus musculus scutula carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
5898	18883	31631	7.36	9.2E-01	BF037588.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884661 5'
6537	19302	32306	0.61	9.2E-01	M84703.1	NT	N.crassa valyl-tRNA synthetase (cyl-20/un-3) gene
9560	22213	35399	0.92	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9648	22300	35496	1.07	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10165	22813	36031	3.16	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10315	22962	36178	1.9	9.2E-01	BF593251.1	EST_HUMAN	7658e06.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW.NUSM_TRYBB
10543	23239	38473	1.63	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11722	24316	37639	1.79	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1621	14368	27057	1.88	9.1E-01	T86875.1	EST_HUMAN	ye52P01.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
2120	14851		2.76	9.1E-01	8923058	NT	Alu repetitive element
3200	15963	28614	1.15	9.1E-01	T28418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3200	15963	28615	1.15	9.1E-01	T28418.1	EST_HUMAN	AB20038R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LAB200G8 5'
6075	18854	31821	1.28	9.1E-01	L36033.1	NT	AB20038R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LAB200G8 5'
6413	19181	32180	3.53	9.1E-01	Q61704	SWISSPROT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7475	20148	33241	17.62	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7637	20302	33410	2.34	9.1E-01	U72995.1	NT	0571g08.s1 NC1 CGAP_G081 Homo sapiens cDNA clone IMAGE:1338862 3'
10075	22723	35940	0.45	9.1E-01	P38432	SWISSPROT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
12291	25294		27.98	9.1E-01	AF050113.1	NT	P80-COILIN
4346	17085	29714	2.08	9.0E-01	AF098810.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
7291	18974	33052	0.72	9.0E-01	L42547.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
7321	20004		1.18	9.0E-01	D38621.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
9249	21928	35100	0.49	9.0E-01	AF086781.1	NT	Xenopus laevis gene for aldolase, complete cds
							Danio rerio semaphorin 21a mRNA, complete cds
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
5610	18406	31318	2.68	8.9E-01	AF026198.1	NT	Rabbit MHC fragment RLA-DF DNA
6154	18931		1.38	8.9E-01	X60886.1	NT	Citrona nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
8325	21018	34154	0.71	8.9E-01	AF256667.1	NT	Xylella fastidiosa, section 90 of 228 of the complete genome
11787	24377	37707	2.51	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 228 of the complete genome
12138	24627		2.86	8.9E-01	AE002186.2	NT	Chlamydomonas reinhardtii AR39, section 21 of 94 of the complete genome
12762	25343		2.51	8.9E-01	AF150836.1	EST_HUMAN	qb64d08.x1 Soares_fetal_heart_NHH18W Homo sapiens cDNA clone IMAGE:1704878 3'
4505	17240	29873	3.82	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5289	18094	30755	0.67	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
10131	22779	35892	0.83	8.8E-01	7656078	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11018	23690	36953	4.96	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
11968	25382		1.8	8.8E-01	D80911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576583-1719643
452	13238	25877	1.54	8.7E-01	AF106853.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2401	15122	27859	1.07	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2877	15644	28298	5.05	8.7E-01	AA595883.1	EST_HUMAN	m05f11.s1 NC1 CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
4946	17673		3.17	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
5102	17820		0.97	8.7E-01	AJ288085.1	NT	Homo sapiens partial LGALS9 gene for galectin-9, exon 3
7839	20634	33761	0.82	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
8828	21520	34685	0.69	8.7E-01	A1239456.1	EST_HUMAN	qh36e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
8828	21520	34686	0.69	8.7E-01	A1239456.1	EST_HUMAN	qh36e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9838	22280	35483	1.57	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PA01, section 524 of 629 of the complete genome
10202	22850	36065	0.81	8.7E-01	BF570169.1	EST_HUMAN	60218554111 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309806 3'
10202	22850	36066	0.81	8.7E-01	BF570169.1	EST_HUMAN	60218554111 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309806 3'
10735	23422	36685	5.25	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
11739	24332	37657	5.47	8.7E-01	BF107694.1	EST_HUMAN	601823884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11739	24332	37658	5.47	8.7E-01	BF107694.1	EST_HUMAN	601823884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
462	13247		1.75	8.6E-01	X17012.1	NT	Rat TGFII gene for Insulin-like growth factor II
838	13608	26279	3.45	8.6E-01	W69089.1	EST_HUMAN	z444603.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2268	14994	27733	0.96	8.6E-01	4603210	NT	Homo sapiens cytochrome P450, subfamily XXV1A (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3608	16361	29003	0.85	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
3782	16534	29172	1.55	8.6E-01	U49724.1	NT	Drosophila melanogaster medlin (Dmedlin) mRNA, complete cds
5808	18597	31524	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5808	18597	31525	10.88	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6809	19372	32385	2.08	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6809	19372	32386	2.08	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7427	20104		0.78	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
7828	20523		1.12	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
7941	20636	33763	0.55	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapse response mediator protein (CRMP) mRNA, complete cds
9585	22238		0.46	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12518	25144		1.35	8.6E-01	AL112162.1	NT	Baby's china strain T4 cDNA library under conditions of nitrogen deprivation
6626	19388	32401	0.95	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7425	20102	33189	2.51	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8317	21010	34147	0.78	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8317	21010	34148	0.78	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8402	21095	34231	0.67	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10248	22896	36105	1.17	8.5E-01	AB006799.1	NT	Cyandidium caldarium gene for SigC, complete cds
10248	22896	36106	1.17	8.5E-01	AB006799.1	NT	Cyandidium caldarium gene for SigC, complete cds
12278	25296		2.24	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
4702	17436	30067	0.73	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome
6408	25068	30910	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5406	25068	30911	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7708	20372	33485	0.63	8.4E-01	AF051142.1	NT	Maestria brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
9858	22508		2.68	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
724	13498	26181	2.8	8.3E-01	M63437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3091	15856	28497	2.99	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3780	16542	29177	0.79	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3983	16741	29375	3.35	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5187	17895	30511	2.41	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9568	22221		4.51	8.3E-01	AI791952.1	EST_HUMAN	mm01f12.y5 NCL CGAP_C09 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element;
10010	22658	35872	1.27	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10118	22786	35978	3.46	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10572	23287	36506	3.35	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10560	23284		2.03	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11274	23936	37227	2	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2045	14778	27506	2.3	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2083	14815		1.31	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2888	15395		1.09	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
6676	19593	32831	0.76	8.2E-01	AJ010142.1	NT	Anasita muscaria mRNA for SCIL25 protein
6797	19541	32569	3.49	8.2E-01	AW376433.1	EST_HUMAN	CMA-HT0243-081189-037-e01 HT0243 Homo sapiens cDNA
7169	26106	32926	4.74	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8343	21036	34173	0.69	8.2E-01	BE263145.1	EST_HUMAN	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3180412 5'
9924	22572	35770	0.65	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
9959	22607	35812	1.37	8.2E-01	AF052659.1	NT	Homo sapiens thiorodotin-related protein mRNA, complete cds
10123	22771	35985	0.59	8.2E-01	AF223688.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22771	35986	0.59	8.2E-01	AF223688.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1

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10283	22831	36145	3.65	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10283	22831	36146	3.65	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11841	24238	37862	4.65	8.2E-01	L10127.1	NT	Molluscum contagiosum Virus Type 1 ORF1 and ORF2 DNA
11735	24328	37652	6.38	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11740	24333	37659	6.02	8.2E-01	H87398.1	EST_HUMAN	yw14d02r1 Soares_placenta_866weeks_2NHP8608W Homo sapiens cDNA clone IMAGE:252185 5'
12288	24723	31054	2.37	8.2E-01	AJ001281.1	NT	similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2782	15467		1.08	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3451	16207	28857	3.08	8.1E-01	AF050086.1	NT	Mus musculus MHC class 1 region
3451	16207	28858	3.08	8.1E-01	AF050086.1	NT	Homo sapiens MHC class 1 region
4893	17592		0.74	8.1E-01	AF202634.1	NT	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbetz2) mRNA, complete cds
6223	18997	31973	0.64	8.1E-01	U16790.1	NT	Mus musculus putative collagen alpha-2(X) chain (COL11A2) gene, partial cds
6526	19282	32295	2.66	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
6526	19282	32296	2.66	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7229	19914	32987	0.78	8.1E-01	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7412	20089	33173	0.65	8.1E-01	Q47477	SWISSPROT	CYTOTOCHROME B
7811	20506	33628	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picoct) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
7811	20506	33628	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picoct) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8507	21199	34344	0.93	8.1E-01	AF001617.1	NT	Bacillus halodurans genomic DNA, section 11/14
8507	21199	34345	0.93	8.1E-01	AF001617.1	NT	Bacillus halodurans genomic DNA, section 11/14
8668	21360	34507	1.08	8.1E-01	AW242847.1	EST_HUMAN	xx01h03.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692489 3' similar to SW1LYAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ;contains MER22.b1 PTR5.repetitive element
10025	22673	35888	0.7	8.1E-01	P06425	SWISSPROT	PROBABLE E4 PROTEIN
10311	22958	36174	0.5	8.1E-01	N84541.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to EST(CLONE C-0PE11)
11464	24067	37374	2.63	8.1E-01	BE98858.1	EST_HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
11464	24067	37375	2.63	8.1E-01	BE98858.1	EST_HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
12022	24550	31110	1.67	8.1E-01	AE001711.1	NT	Thermoboga maritima section 23 of 136 of the complete genome
172	12985		3.49	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphatase acetyltransferase allele 15

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282	13089	25730	13.81	8.0E-01	AJ132772.1	NT	Bos taurus tub and rlf genes
1595	14341	27031	1.12	8.0E-01	8394087	NT	Rattus norvegicus protease (prosome, macropain) 28 subunit, alpha (Psrne1), mRNA
2028	14784		1.91	8.0E-01	BF530962.1	EST_HUMAN	602072473F1 NCL_OGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215091 5'
3075	15841	28484	1.2	8.0E-01	AF127897.1	NT	Salmonella enteritidis serovar Enteritidis O:4,12:H:7 gene, partial cds
3307	16087	28718	1.35	8.0E-01	AB006183.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3690	16443		1.52	8.0E-01	AL182758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 717
4496	17232	29882	6.05	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
7889	20584		2.25	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-H08 NN1012 Homo sapiens cDNA
8423	21116	34254	0.98	8.0E-01	Y11085.1	NT	Rice stripe virus RNA 3
10878	23556	36803	2.78	8.0E-01	Q92783	SWISSPROT	GREB-BINDING PROTEIN
441	13227	25870	1.16	7.9E-01	DT1476.1	NT	Lymantria dispar nuclear polydrosis virus gene for DNA polymerase, complete cds
688	13473		1.14	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1600	14346		22.69	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1652	14398		1.2	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2259	14986	27726	5.86	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2260	14987	27727	2.4	7.9E-01	AF130459.1	NT	Danio rerio Tnp4-associated protein Tap1A (tap1A) mRNA, complete cds
3506	16262	28918	3.01	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4268	17008		0.85	7.9E-01	BE283812.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4572	17307	29835	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4572	17307	29836	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
6252	19026	32000	0.67	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8008	20703	33831	2.79	7.9E-01	X90998.1	NT	P.sativum GR gene
9447	22124	35304	4.04	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
9949	22597	35801	4.47	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
9991	22639	35849	0.91	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'
10408	23054	36271	1.94	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-kefo-L-rhamnose reductase, complete cds
10516	23162	36389	0.52	7.9E-01	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10929	23609		2.74	7.9E-01	7862471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11173	23840	37123	2.02	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
856	13625		2.24	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2273	14989	27737	7.47	7.8E-01	AW959567.1	EST_HUMAN	EST371687 MAGC resequences, MAGF Homo sapiens cDNA
4653	17387	30020	0.73	7.8E-01	U67305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5978	18760	31724	2.28	7.8E-01	AF115886.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6124	18902	31871	0.88	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
8371	18140	32136	0.63	7.8E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8389	21082	34216	1.02	7.8E-01	BF108927.1	EST_HUMAN	718405.x1 Scores NSF_F8_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525178 3'
9133	21821	34987	1.3	7.8E-01	Y10169.1	NT	D discoideum racGAP gene
9231	21910	35083	0.51	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214KD (CAN) (NUP214), mRNA
10024	22872		0.97	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12271	25275		2.5	7.8E-01	L29280.1	NT	Arabidopsis thaliana 1-amin-1-cyclopropanecarboxylate synthase (ACS6) gene, complete cds
139	12854	25586	7.61	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
709	13483		2.28	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region; major histocompatibility protein class II alpha chain (I-Aalpha) and major histocompatibility protein class II beta chain (I-Ebeta) genes, complete cds;
2717	15424	28163	2.21	7.7E-01	O33915	SWISSPROT	butyrophilin-like (NG8), butyrophilin-1² CITRATE SYNTHASE
3351	16111		0.84	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA
3586	16340	28985	3.98	7.7E-01	AF118085.1	NT	Homo sapiens PRO1978 mRNA, complete cds
4385	17103	29738	3.38	7.7E-01	AF199498.1	NT	Coltuxix columbix japonica sub-species japonica beta-actin mRNA, partial cds
4365	17103	29739	3.38	7.7E-01	AF199498.1	NT	Coltuxix columbix japonica sub-species japonica beta-actin mRNA, partial cds
5473	18272	31165	1.45	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5473	18272	31166	1.45	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5868	18553	31594	0.85	7.7E-01	R08800.1	SWISSPROT	y24x02.s1 Scores fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:127755 3'
9744	22385	35600	0.51	7.7E-01	AB021134.1	EST_HUMAN	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12161	24844		4.65	7.7E-01	11497821	NT	Archaeoglobus fulgidus, complete genome
6008	18789	31751	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6008	18789	31752	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6425	18193	32189	0.81	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
8751	17920	30555	0.94	7.6E-01	A1253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
8751	17920	30585	0.94	7.6E-01	A1253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6951	19433	32449	0.89	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7964	20659	33784	1.38	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; PHLIP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8026	20721	33852	1.88	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8026	20721	33853	1.88	7.6E-01	6857752	NT	Mus musculus cyclochrome P450, 2b6, phenobarbital inducible, type a (Cyp2b6), mRNA
8866	21557	34703	0.74	7.6E-01	6753577	NT	Mus musculus advillin (Advil-pending), mRNA
9179	21849	35015	6.03	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9179	21849	35016	5.03	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11330	24021	37325	2.68	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11330	24021	37326	2.68	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11711	24306		3.64	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11931	24489		3.73	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0896 protein, partial cds
500	13284		1.44	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
570	13351	25979	1.23	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
3354	16114	28789	0.95	7.5E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'
7421	20098	33186	1.01	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
11177	23844	37130	1.5	7.5E-01	AB047819.1	NT	Homo sapiens GOMa/GCM1 gene for chorion-specific transcription factor GOMa, complete cds
12228	24982		4.8	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialoprotein precursor (DSPP) gene, complete cds
12742	25008	30975	1.46	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1108	13865	26522	1.78	7.4E-01	AI598146.1	EST_HUMAN	tn14b08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR, repetitive element
2342	15065	27802	0.96	7.4E-01	AB011108.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
4276	17015	29642	4.73	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7743	20439	33562	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
7743	20439	33563	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
8531	21223	34365	0.83	7.4E-01	BF348268.1	EST_HUMAN	602018456F1 NCI_CGAP_Bm27 Homo sapiens cDNA clone IMAGE:4164340 5'
8613	21305		0.76	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
8994	21684	34834	6.95	7.4E-01	BE747503.1	EST_HUMAN	601573028F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9054	21743	34901	1.14	7.4E-01	AA187886.1	EST_HUMAN	zp67h01.61 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO, MOUSE P42832 T-COMPLEX PROTEIN 1, THETA SUBUNIT
10302	22949	36164	0.76	7.4E-01	11424933	NT	Homo sapiens NY-RN-45 antigen (LOC51133), mRNA

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11665	24260	37582	1.65	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11665	24260	37583	1.65	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11900	24467		3.62	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12008	24642		1.78	7.4E-01	AI472641.1	EST_HUMAN	let13h01.x1 NCJ_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
2999	15765	28413	0.8	7.3E-01	P08710	SWISSPROT	HYPOTHETICAL PROTEIN HKLF1 (RL1) (TRL1)
4575	17310	28638	0.7	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4652	17388	30019	4.37	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5040	17759	30373	1.01	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
5511	19276	32276	5.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6511	19276	32277	5.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6994	25103	32735	0.67	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7359	20040	33118	0.68	7.3E-01	Z14133.1	NT	D.melanogaster Cdc mRNA for clathrin heavy chain
7445	20121	33210	7.84	7.3E-01	M26511.1	NT	V.algihydricus sucrose (scrB) gene, complete cds
7445	20121	33211	7.84	7.3E-01	M26511.1	NT	V.algihydricus sucrose (scrB) gene, complete cds
11407	24056	37361	3.83	7.3E-01	AA678019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431789 3'
11407	24056	37362	3.83	7.3E-01	AA678019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431789 3'
812	13583		3.89	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1950	14685	27398	2.32	7.2E-01	X70140.1	NT	N.tabacum Nelf-4A13 mRNA
2463	15181	27920	1.27	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3063	15829	28473	1.38	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3445	16201	28651	2.56	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-1 allele, complete cds
3501	16354	28994	1.06	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
4040	16785		0.7	7.2E-01	AF108083.1	NT	Homo sapiens A-2 gene, intron 18
4718	17450	30083	2.65	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5075	17794	30410	0.74	7.2E-01	P33068	SWISSPROT	NUCLEOSIDE TRIPHOSPHATASE I (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE I) (NPH I)
7112	19800	32864	0.88	7.2E-01	U69633.1	NT	Sclerium tuberosum ccd-stress inducible protein (C17) gene, complete cds
8353	21046	34183	1.11	7.2E-01	AF260061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
8882	21553		0.46	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10239	22887	36100	2.33	7.2E-01	BF670061.1	EST_HUMAN	602118381F1 NH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
10639	23330	36568	4.02	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
11104	23774	37049	1.27	7.2E-01	S76838.1	NT	Dbs=Dbp guanine nucleotide exchange factor homolog [mice, 32D murine hemopoietic cell line, mRNA, 3923 nt]

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12422	24798		2.9	7.2E-01	AF000063.1	NT	Aeropyrum pernix genomic DNA, section 67
676	13451	26094	1273	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RyR1), complete cds
3059	15825	28470	11.76	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4184	16925	29555	3.18	7.1E-01	7305360	NT	Mus musculus obogelin (Obog), mRNA
4184	16925	29556	3.18	7.1E-01	7305360	NT	Mus musculus obogelin (Obog), mRNA
5858	18645	31585	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
5858	18645	31586	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6950	19550	32580	7.68	7.1E-01	U36232.1	NT	Drosophila melanogaster G-pyruvyltetrahydropterin synthase (pr) gene, complete cds
8001	20785	33916	0.56	7.1E-01	H54244.1	EST_HUMAN	yp86d09.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:202961 3'
8635	21327	34469	0.93	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-409 BT0567 Homo sapiens cDNA
8635	21327	34470	0.93	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-409 BT0567 Homo sapiens cDNA
9755	22406	35613	1.43	7.1E-01	BE904405.1	EST_HUMAN	801496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10309	22956	36172	1.22	7.1E-01	M12961.1	NT	Human T-cell receptor gamma-chain J2 gene
12211	25205		2.21	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731109 3'
1207	13958	26624	0.99	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1207	13958	26625	0.99	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2450	15169	27907	1.13	7.0E-01	N62412.1	EST_HUMAN	yz79e07.s1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2450	15169	27908	1.13	7.0E-01	N62412.1	EST_HUMAN	yz79e07.s1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
4896	17719		1.78	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5962	19649		1.11	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8276	20970		11.76	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9216	21895	35084	0.57	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (P ⁺ TS) system, mtuA, mtuR, mtuF, and mtuD genes, complete cds
9216	21895	35065	0.57	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (P ⁺ TS) system, mtuA, mtuR, mtuF, and mtuD genes, complete cds
10526	23172	36400	0.49	7.0E-01	U34662.1	NT	Danio rerio complement factor B mRNA, complete cds
11064	23734	37006	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHIE04 5'
11064	23734	37007	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHIE04 5'
949	13715	26380	11.02	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds

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949	13715	26381	11.02	6.8E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1287	14037	26708	2.74	6.8E-01	AA593530.1	EST_HUMAN	nm28a09.s1 NCI_OGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3213	15676	28627	1.97	6.8E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5634	18488	31409	0.91	6.8E-01	AB035682.1	NT	Branchiostoma belcheri BbNA3 mRNA for neofolion actin, complete cds
5900	18685	31633	0.82	6.8E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6277	18050	32027	1.36	6.8E-01	BE286188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7687	20360	33474	0.65	6.8E-01	AF248883.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
7870	20574	33700	2.06	6.8E-01	AL181573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7878	20574	33701	2.06	6.8E-01	AL181573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9060	21758	35431	0.70	6.8E-01	AF118046.1	NT	Enammosa dispar calpon transporting ATPase (atpase) gene, partial cds
9594	22247	35432	0.59	6.8E-01	AF206318.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9594	22247	35432	0.59	6.8E-01	AF206318.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11223	23886	37172	2.38	6.8E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11223	23886	37173	2.38	6.8E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11878	25197		3.01	6.8E-01	Q98958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK
837	13704	26369	1.05	6.8E-01	AF017784.1	NT	HEAD PROTEIN 1) (MTH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
2680	15389		0.99	6.8E-01	D90817.1	NT	Giardia intestinalis carbanilate kinase gene, complete cds
						NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2832	14358	27045	1.49	6.8E-01	AA854475.1	EST_HUMAN	aj76a06.s1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1402258 3' similar to
4533	17268	29901	1.45	6.8E-01	J00762.1	NT	gbcX56411_mnt1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
9538	22191	35375	1.45	6.8E-01	AB037766.1	NT	Rat(hooded) prolactin gene : exon III and flanks
11027	23699	36962	1.92	6.8E-01	AJ276675.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11027	23699	36963	1.92	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11058	23728	37000	2.4	6.8E-01	AF038839.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11058	23728	37001	2.4	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
						NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
						NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29,
11607	24205	37527	1.36	6.8E-01	AF110520.1	NT	KIFC1, Fas-binding protein, BING1, tapasin, RagGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and
						NT	RPS18 genes, complete cds; Sacm21 gene, partial>
11607	24205	37528	1.36	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29,
						NT	KIFC1, Fas-binding protein, BING1, tapasin, RagGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and
						NT	RPS18 genes, complete cds; Sacm21 gene, partial>

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
291	13097	25739	44.11	6.7E-01	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
330	13131	25768	21.34	6.7E-01	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2143	14873	27606	1.73	6.7E-01	AA451894.1	EST_HUMAN	z12g12.s1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2163	15567	27628	2.51	6.7E-01	AF166073.1	NT	Drosophila melanogaster Ms85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2994	15760	28408	3.41	6.7E-01	6878580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4419	17155	29786	0.79	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5422	18221	30932	0.94	6.7E-01	J04836.1	NT	M. bakeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5422	18221	30933	0.94	6.7E-01	J04836.1	NT	M. bakeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6231	19005	31981	1.18	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6231	19005	31982	1.18	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
7215	19800		4.34	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7240	19925	33000	0.82	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10044	22692		0.68	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
10873	23553	36800	2.07	6.7E-01	BF364649.1	EST_HUMAN	CM3-HT0768-010600-197-c03 HT0768 Homo sapiens cDNA
11436	23203	36435	3.59	6.7E-01	O14357	SWISSPROT	N-ACETYL-GLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
11659	24255	37578	1.66	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2505	15222	27964	1.29	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2704	15411	28148	1.44	6.6E-01	AF196339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3650	16403	29043	4.57	6.6E-01	Y07869.1	NT	C. albicans random DNA marker, 282bp
4089	16832		0.85	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5125	17843	30461	1.13	6.6E-01	AL161672.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
6240	19014	31988	4.29	6.6E-01	6980577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7585	20253	33359	3.76	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'
8484	21158	34289	0.52	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9584	22217		2	6.6E-01	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C078
12470	24836	31033	1.48	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
610	13388	26019	18.23	6.5E-01	MT75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
610	13388	26020	18.23	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3426	16183	28833	4.25	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4249	16890	28615	4.23	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4277	17016	28643	0.78	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5003	17726	30329	2.6	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5357	25087	30843	1.77	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWISNF COMPLEX COMPONENT SNF5)
5627	19424	31337	0.62	6.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6625	18387	32400	1.5	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7568	20236	33340	0.84	6.5E-01	AJ798882.1	EST_HUMAN	wo46602.x1 NCI_OGAP_P128 Homo sapiens cDNA clone IMAGE:23218423'
9737	22388		0.8	6.5E-01	T78904.1	EST_HUMAN	y421b04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108847 3'
10233	22881	36084	1.96	6.5E-01	AF118676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10529	23226	36460	2.68	6.5E-01	H87583.1	EST_HUMAN	hw1706.r1 Soares placenta, 8 to 9 weeks 2N1b-P81c9W Homo sapiens cDNA clone IMAGE:252515 5'
10385	23280	36518	3.5	6.5E-01	AA601287.1	EST_HUMAN	no16c07.s1 NCI_OGAP_P1e1 Homo sapiens cDNA clone IMAGE:1100748 3'
10690	23381		3.93	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone IMAGE:1007810 5'
11599	24198	37518	2.42	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12267	24710		2.07	6.5E-01	BE465050.1	EST_HUMAN	hw74e10.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12904	25146		1.81	6.5E-01	Z74145.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097c
245	13054	25694	8.05	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
2593	18307	28043	1.16	6.4E-01	AF161184.1	NT	Pseudomonas fluorescens tylophane halogenase (pma) gene, complete cds
3449	16205	28855	2.16	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3842	16593	29230	1.06	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
8510	21202	34347	1.82	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
9889	22637	35848	8.6	6.4E-01	U82628.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10004	22852	35864	1.22	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5'
12382	24777		5.99	6.4E-01	AV769212.1	EST_HUMAN	AV769212 MDS Homo sapiens cDNA clone MDSGC09 5'
425	13211	25658	4.58	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
522	13306	25938	2.25	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2159	14889	27623	2.02	6.3E-01	U81136.1	NT	Stigella flexneri multi-antigen resistance locus
2583	15297	28035	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2583	15297	28036	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds

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5973	19755	31716	0.94	6.3E-01	BE093908.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6504	19269	32271	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (msg) gene, complete cds
6504	19269	32272	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (msg) gene, complete cds
8419	21112	34624	3.44	6.3E-01	BE02044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
8784	21476	34624	0.95	6.3E-01	S62927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9120	21808	34975	0.8	6.3E-01	BF216884.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102598 5'
9320	21987	35169	2.45	6.3E-01	9627521	NT	Varicella virus, complete genome
9320	21987	35160	2.45	6.3E-01	9627521	NT	Varicella virus, complete genome
9838	22489	36193	0.67	6.3E-01	AE002328.2	NT	Chlamydia muridarum, section S9 of 85 of the complete genome
10326	22973	36193	1.47	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10427	23073	36294	1.19	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10456	23102		0.45	6.3E-01	AW793395.1	EST_HUMAN	PMO-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
10993	23687	36924	2.21	6.3E-01	AA877715.1	EST_HUMAN	nr0906.s1 NCI_CGAP_Corf0 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002816 002816 HLARK ;
11308	23967	37268	9.25	6.3E-01	AI904160.1	EST_HUMAN	CM-BT043-090289-046 BT043 Homo sapiens cDNA
11402	24051	37355	1.68	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11581	24180	37495	1.84	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11988	25355	30607	4.37	6.3E-01	9810283	NT	Mus musculus keratin complex 2, gene 6g (Krl2-6g), mRNA
12078	24687		1.45	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
12283	26272		2.93	6.3E-01	X83828.1	NT	C. limicola pscD gene
5780	18571	31499	2.31	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7394	20073		3.44	6.2E-01	AF02253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7443	25114	33209	1.33	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magee9 gene, Caltradin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8200	20894	34031	4.52	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:213542 3'
8755	21447	34595	0.52	6.2E-01	AF034411.1	NT	Lycopodium obscurum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase/dehydratase/hikmate:NADP oxidoreductase gene, complete cds
9349	20420	33540	1.55	6.2E-01	BE562887.1	EST_HUMAN	601338146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3800010 5'
9410	22072		2.55	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
9978	22626	35834	6.2	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10121	22769	35982	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10121	22769	35983	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA

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10434	23080	36305	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10434	23080	36306	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2393	15114		4.38	6.1E-01	6978076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5449	18248	31137	1.15	6.1E-01	M58940.1	NT	Ceanothus elegans N2 CefMyoD (hnh-1) alternatively spliced genes, complete cds
6770	19514	32540	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6770	19514	32541	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6920	19656	32702	0.64	6.1E-01	AW105653.1	EST_HUMAN	xd50h03.x1 NCL CGAP_OY23 Homo sapiens cDNA clone IMAGE:2697237 3' similar to gb:X12671_mai HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7005	19697	32751	0.72	6.1E-01	Q63769	SWISSPROT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8132	20826	33962	3.27	6.1E-01	AF033535.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8694	21386	34526	1.09	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8694	21386	34529	1.09	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9315	21982	35153	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9315	21982	35154	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9742	22393	35597	0.93	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 529 of the complete genome
9946	22594	35787	1.06	6.1E-01	AF118117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11738	24331	37655	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11738	24331	37656	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12074	25159	30699	2.28	6.1E-01	AB041350.1	NT	Mus musculus Cdk4b5 mRNA for type IV collagen alpha 5 chain, complete cds
12694	24977		1.57	6.1E-01	X95287.1	NT	M.mazael orfA, orfB, and orfC of archaeal ABC-transporter system
482	13287	25903	1.24	6.0E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
548	13331		3.09	6.0E-01	5802899	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1341	14089	26765	1.91	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH103-53b attachment protein (G) gene, complete cds
3795	16547	29180	0.92	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4165	16905		1.09	6.0E-01	AF058885.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 28, 27, and 28
5199	18007	30628	2	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5353	18156	30839	2.86	6.0E-01	AW139713.1	EST_HUMAN	UH-HB1-aab-a-10-0-0-J1.61 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6445	19213	32210	2.78	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds

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6563	19328	32335	0.68	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7254	19938	33013	6.99	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8023	20718	33650	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8023	20718	33651	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9723	22374	35574	1.61	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10173	22821	36921	1.48	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PERO (PEROXIN-3)
10990	23664	36921	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
10990	23664	36922	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11540	24140	37449	3.77	6.0E-01	AI420623.1	EST_HUMAN	tf08107 x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2095621 3'
12354	24758	31060	2.25	6.0E-01	11421863	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12455	24824		2.6	6.0E-01	AA706087.1	EST_HUMAN	zfp905.s1 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:462778 3'
12639	25208	30815	3.04	6.0E-01	8055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12664	25142		2.06	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
980	13745	26407	1.38	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 19 of 183 of the complete genome
3264	16026	28675	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3264	16026	28676	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4196	16937		4.21	5.9E-01	AF182758.1	NT	Rattus norvegicus casein 2 mRNA, partial cds
6373	19142	32139	1.55	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7168	19853	32922	1.32	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7286	18679		0.61	5.9E-01	X68801.1	NT	G.gallus gene for skeletal alpha-actin, exon EF2
7898	20593	33726	0.46	5.9E-01	D60911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
8536	21228	34370	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9443	22120	35298	0.82	5.9E-01	AF083204.2	NT	Chlamydia trachomatis strain K/UW/31/Cx major outer membrane protein (omp1) gene, complete cds
9813	22464		0.74	5.9E-01	P06463	SWISSPROT	E8 PROTEIN
10088	22738	35951	1.15	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10569	23264	36502	2.5	5.9E-01	Q6X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10576	23271	36507	1.72	5.9E-01	AF197844.1	NT	Xeropus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
10861	23561	36808	2.91	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-003 DT0041 Homo sapiens cDNA
11149	23816	37099	1.95	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/EJ CD48 antigen (Cd48) gene, partial cds
11458	24062	37368	1.56	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11458	24082	37369	1.56	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN
12021	24549	31109	2	5.9E-01	L42320.1	NT	Cryptolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12552	24898		4.35	5.9E-01	AB017705.1	NT	Aspergillus oryzae Pyg gene for orodline-5'-phosphate decarboxylase, complete cds
12465	24832		5.72	5.9E-01	P34928	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1902	14839	27348	1.36	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
2569	16283	28021	1.01	5.8E-01	7305230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
4478	17213	29838	4.37	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
5290	18036		0.82	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5444	18243	31131	0.82	5.8E-01	O10689	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6091	18869	31836	1.09	5.8E-01	D78699.1	EST_HUMAN	HUM500E06B Human placenta poly(A) (T Fujiwara) Homo sapiens cDNA clone GEN-500E06 5'
6220	18994	31970	0.66	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
6715	19630		2.48	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7787	20482		2.61	5.8E-01	H41571.1	EST_HUMAN	Yn91803.g1 Soares adult brain N2b5K1855Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:S78187 M-PPHASE INDUCER PHOSPHATASE 2 (HUMAN);
7885	20880	33805	0.64	5.8E-01	AI280051.1	EST_HUMAN	qh5410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
7885	20880	33806	0.64	5.8E-01	AI280051.1	EST_HUMAN	qh5410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8090	20784	33914	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8090	20784	33915	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8789	21481	34628	8.97	5.8E-01	AI270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8871	21582	34707	0.99	5.8E-01	Q27368	SWISSPROT	TRANSSCRIPTION FACTOR E2F
8872	21563	34708	0.51	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
9496	22149		0.81	5.8E-01	BF031806.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
10911	23591	36837	7.58	5.8E-01	AI243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10962	23638		3.97	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11089	23759		1.99	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
1480	14227	26912	1.12	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1480	14227	26913	1.12	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
3038	15804		0.89	5.7E-01	8755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3217	15890	28631	1.82	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A)
3495	16251		2.82	5.7E-01	AB039503.1	NT	Populus euphratica peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6282	19036	32011	5.13	5.7E-01	BF035413.1	EST_HUMAN	601454982F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6611	19374	32388	0.81	5.7E-01	AA194201.1	EST_HUMAN	2788c06.1 Soares_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:865674 5'
6763	17932	30568	1.33	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7664	20328	33438	2.14	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5OR) (P5C REDUCTASE)
7870	20565		0.5	5.7E-01	AJ251835.1	NT	Mus musculus Krt1, Ltpe5, Mash2, Tape-1, Tsc4 and Tsc8 genes, alternative transcripts
8279	20973		0.47	5.7E-01	A065061.1	EST_HUMAN	HA0805 Human fetal liver cDNA library Homo sapiens cDNA
8689	22350	35544	1.19	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9699	22350	35545	1.19	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10475	23121	36351	0.72	5.7E-01	BF540962.1	EST_HUMAN	MR3-H10738-180700-003-e02 H10738 Homo sapiens cDNA
11883	24524		1.52	5.7E-01	BE715051.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066810 5'
12658	24958		3.01	5.7E-01	BE969722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839783 3'
3357	16117	28772	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3357	16117	28773	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3863	16813	28252	0.97	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4215	16956	28578	0.74	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8702	21394	34541	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
8702	21394	34542	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9275	22029	35199	1.08	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11884	24457		2.57	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3919457 5'
11897	24535	37272	1.63	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element
12352	16613	28252	1.69	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12379	24776		2.7	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12773	25027		4.26	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1189	13941	26606	0.85	5.5E-01	8393912	NT	Rattus norvegicus Proglut Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2705	15412	28149	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2705	15412	28150	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2919	15685	28330	1	5.5E-01	5802085	NT	Homo sapiens superkiller virulence activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3062	15928		1.55	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N258FIB55Y Homo sapiens cDNA clone IMAGE:178268 3'
3228	15991	28644	4.22	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3678	16431	29073	1.7	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
5082	17801	30419	1.78	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain Bcl A-DIB1 gene, partial cds
7187	19873		0.65	5.5E-01	AB015696.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8348	21041	34178	1.04	5.5E-01	AT91766.1	EST_HUMAN	orf2cd01.y6 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
9667	22319		0.7	5.5E-01	U88415.1	NT	Crimson-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds

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10276	22924	36136	0.86	5.5E-01	T06047.1	EST_HUMAN	EST02835 Fetal brain, Stragene (cat#336206) Homo sapiens cDNA clone HFBCQ35
11087	23757	37033	1.65	5.5E-01	BF129507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
140	12855	25597	4.91	5.4E-01	7657266	NT	Homo sapiens KIAA0928 protein Msd2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
140	12856	25598	4.91	5.4E-01	7657266	NT	Homo sapiens KIAA0928 protein Msd2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
571	13352	25980	1.16	6.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
571	13352	25981	1.16	6.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1248	13997	26664	3.41	5.4E-01	AF08087.1	EST_HUMAN	Q14-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2099	14830		3.43	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2252	14980	27719	1.91	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
5068	17785	30402	0.92	6.4E-01	M74439.1	NT	Rattus rattus UDP glucuronosyltransferase gene, complete cds
5571	18368	31278	0.74	5.4E-01	AB042327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6098	18976	31845	0.83	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIST1, complete cds
6828	19664	32710	0.87	5.4E-01	BE066592.2	EST_HUMAN	601860276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806090 3'
7235	19920	32883	0.81	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7235	19920	32894	0.81	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7237	19922	32897	1.48	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
9890	22540		2.09	5.4E-01	BF672638.1	EST_HUMAN	60207654F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
11016	23687	36948	2.87	5.4E-01	P36856	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11921	24218	37541	3.08	5.4E-01	Q60676	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11921	24218	37542	3.08	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11944	24489		3.6	5.4E-01	A1858398.1	EST_HUMAN	w87804.x1 NC1_CGAP_U01 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
503	13287	25921	1.54	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, heparinase (SKI2W), RD, complement factor B (B), and complement component C2 (C2) genes.>
2136	14866	27596	1.01	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2136	14866	27597	1.01	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2786	15491	28230	6.83	6.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA

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2786	15481	28231	6.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3237	15999	28849	2.74	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (SLC) gene, complete cds
4187	16928		1.58	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 8 of 51 of the complete genome
5371	18172	30860	1.98	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:740711 5'
5371	18172	30861	1.98	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:740711 5'
5468	18265	31156	0.84	5.3E-01	AA183672.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:668112 5'
5468	18265	31157	0.84	5.3E-01	AA183672.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:668112 5'
5559	18356	31266	1.82	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5559	18356	31267	1.82	5.3E-01	BE645620.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
8802	21494		1.8	5.3E-01	L01950.2	NT	7e73c12.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
8854	21545	34682	0.81	5.3E-01	BF433958.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
8854	21545	34683	0.81	5.3E-01	BF433958.1	EST_HUMAN	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast product
10111	22759	35971	0.82	5.3E-01	A1854210.1	EST_HUMAN	7e71c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29
11550	24149	37480	7.3	5.3E-01	BE568281.1	EST_HUMAN	7e71c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER28
11789	24379	37709	1.72	5.3E-01	Q05783	SWISSPROT	repetitive element;
11877	25206		4.03	5.3E-01	AA916053.1	EST_HUMAN	repetitive element;
797	13569	26229	18.35	5.2E-01	L20770.1	NT	W94b02.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to
1141	13896	26557	8.29	5.2E-01	Q8WV30	SWISSPROT	SW:COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;
1169	13923	26585	1.77	5.2E-01	AF224492.1	NT	601339837F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682169 5'
1878	14616	27605	2.35	5.2E-01	AL163285.2	NT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
2142	14872	27605	2.55	5.2E-01	AB018283.2	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
3117	15882	28521	1.23	5.2E-01	U65942.1	NT	cg30e05.s1 NCI CGAP_B77 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
3231	15994		1	5.2E-01	D73443.1	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN);
3400	16158		1.58	5.2E-01	AL116780.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
3437	16193	28843	2.27	5.2E-01	AA084165.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T CELLS 6 (T CELL TRANSCRIPTION FACTOR NFAT6) (NF-AT5)
							(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT6)
							Homo sapiens phospholipid scramblase 1 gene, complete cds
							Homo sapiens chromosome 21 segment HS21C085
							Homo sapiens mRNA for KIAA0740 protein, partial cds
							Chlamydomonas reinhardtii strain S283 POMIP91A and POMIP90A precursor, genes, complete cds
							Azotobacter vinelandii icd gene for isocitrate dehydrogenase, complete cds
							Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
							am77g05.s1 Stragene schizos brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'

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3623	16376		0.76	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
4568	17303	29930	0.82	5.2E-01	6752947	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
4953	17679		1.02	5.2E-01	7106444	NT	Mus musculus vanilloid receptor-like protein 1 (VHL), mRNA
5567	18964	31272	0.87	5.2E-01	AA284261.1	EST_HUMAN	zc44409.17 Soares_senscent fibroblasts NBH5F Homo sapiens cDNA clone IMAGE:325169 3'
9630	25126	35474	0.75	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9630	25126	35475	0.75	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9832	22463	35685	0.48	5.2E-01	AA194518.1	EST_HUMAN	zq0509.11 Stratagene muscle 837208 Homo sapiens cDNA clone IMAGE:628763 5'
9826	22574	35772	1.35	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12744	25010		7	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
603	13381	26013	1.84	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
633	13412	26047	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pt vt1) 16S rRNA gene
633	13412	26048	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pt vt1) 16S rRNA gene
1648	14394		1.09	5.1E-01	X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
2017	14752		1.29	5.1E-01	BF683085.1	EST_HUMAN	602139319F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4298117 5'
4057	16802	29433	3.96	5.1E-01	A189495.1	EST_HUMAN	w39b12.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4164	16904	29533	2.81	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5103	17821	30438	1.01	5.1E-01	U72663.1	NT	Human alpha 1a adrenergic receptor (alpha1a) gene, 5' flanking region
6128	18006	31874	0.67	5.1E-01	BE541068.1	EST_HUMAN	601063606F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3450000 5'
6183	18960		0.93	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAUF07 5'
6818	19479	32502	1.69	5.1E-01	R80873.1	EST_HUMAN	y94a03.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:146872 3'
8470	21162	34304	0.63	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8470	21162	34305	0.63	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9583	22236	35420	4.33	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9587	22240	35424	3.14	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp508I-cleaved sublibrary Homo sapiens cDNA not directional
10060	22708	35926	0.89	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12086	25137		4.26	5.1E-01	BF030207.1	EST_HUMAN	601566863F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3826767 5'
13226	24745		3.55	5.1E-01	BF439882.1	EST_HUMAN	nac51110.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element
2130	14861	27590	1.24	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation Increased 2-like 9 (PMS2L9), mRNA
2130	14861	27591	1.24	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation Increased 2-like 9 (PMS2L9), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2140	14870	27801	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene
2140	14870	27602	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene
3811	16563	29196	1.13	5.0E-01	L38483.1	NT	Rattus norvegicus lagged protein mRNA, complete cds
3854	16604	29241	2.75	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6547	19312		0.85	5.0E-01	BF576189.1	EST_HUMAN	602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271839 5'
7582	20232	33334	0.75	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7562	20232	33335	0.75	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8428	21121		1.92	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8569	21261	34398	0.71	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9358	20429	33547	2.74	5.0E-01	BF317212.1	EST_HUMAN	601903387F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
							GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9525	22178	35382	1.36	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9525	22178	35363	1.36	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10290	22938		1.12	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849438 5'
12026	24554		4	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12715	24989		1.86	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12726	24997		4.39	5.0E-01	O13861	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
772	13544	26205	2.43	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1656	14402	27090	1.54	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1899	14636	27345	1.15	4.8E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5321	18124	30783	0.89	4.9E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
5946	18728	31686	3.05	4.9E-01	AF020631.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5946	18728	31687	3.05	4.9E-01	AF020631.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7352	20033	33111	1.61	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7605	20271	33378	0.84	4.9E-01	Q10608	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7605	20271	33379	0.84	4.9E-01	Q10608	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
8888	21679		1.45	4.9E-01	BF209781.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9086	21775	34939	0.99	4.8E-01	AW339905.1	EST_HUMAN	h50cd02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:095714
9198	25431		1.98	4.8E-01	10946863	NT	095714 HERC2.1
10218	22864	36076	0.84	4.8E-01	AF063980.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10419	23065	35286	0.77	4.9E-01	X90000.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
11925	24486		1.72	4.8E-01	AF176912.1	NT	H sapiens DNA for BCL7A gene and BCL7AIGH locus fusion
12709	25392		6.73	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
4298	17037		0.77	4.8E-01	4504850	NT	h22a11.s1 NCI_CGAP_C010 Homo sapiens cDNA clone IMAGE:1144652 3'
5420	18219	30930	10.78	4.8E-01	J02987.1	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
6579	19342	32356	0.79	4.8E-01	U92882.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
8589	19352		3.76	4.8E-01	AA858978.1	EST_HUMAN	Mus musculus slow skeletal muscle tropoin T (Tnnt1) gene, complete cds
7218	19901		1.89	4.8E-01	5031650	NT	mus609.s1 NCI_CGAP_A161 Homo sapiens cDNA clone IMAGE:1217513
7585	20235	33339	0.78	4.8E-01	AL163208.2	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
7681	20325	33434	4.05	4.8E-01	AL161492.2	NT	Homo sapiens chromosome 21 segment HS21G009
7681	20325	33435	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7805	20500	33821	1.2	4.8E-01	AI820744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
9144	21875		0.92	4.8E-01	BE155148.1	EST_HUMAN	Y7710.Y5 Soares breast 2NBH8st Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER8 repetitive element
10029	23322		1.88	4.8E-01	X83502.1	NT	PM1-HT0350-201299-004-504 HT0350 Homo sapiens cDNA
12217	25165		3.04	4.8E-01	AF227565.1	NT	S. cerevisiae ORFs from chromosome X
12795	25216		1.68	4.8E-01	AJ132984.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
8422	19190	32186	8.41	4.7E-01	BF217173.1	EST_HUMAN	Chlamydomonas reinhardtii cop gene, exons 1-8
6941	19423	32438	0.94	4.7E-01	AI204374.1	EST_HUMAN	601883860F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7784	20460	33584	0.63	4.7E-01	T11414.1	EST_HUMAN	q72a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
7784	20460	33585	0.63	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8874	21664	34816	0.52	4.7E-01	6981501	NT	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
10751	23436		6.11	4.7E-01	AF102873.1	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11022	23694	36957	2.2	4.7E-01	U41069.1	NT	Influenza A virus isolate h5N1997 hemagglutinin (HA) gene, partial cds
11252	23914	37206	1.61	4.7E-01	BF528658.1	EST_HUMAN	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 18, and partial cds
11349	24039	37342	1.7	4.7E-01	AF869448.1	EST_HUMAN	60204389F1 NCI_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4181303 5'
12116	24809		1.52	4.7E-01	BE88763.1	EST_HUMAN	RO3-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12237	24889		1.51	4.7E-01	AW341581.1	EST_HUMAN	60151133F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
						EST_HUMAN	h411c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12813	25055		1.63	4.7E-01	AF000007.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position (7/7)
12817	25300		1.38	4.7E-01	6678902	NT	Mus musculus proteasome (prosome, macropain) 28S subunit, A TPase 3 (Psmc3), mRNA
3726	16479	29116	1.57	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3726	16479	29117	1.57	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5333	18136	30795	1	4.6E-01	BF131593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5'
5333	18136	30796	1	4.6E-01	BF131593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5'
5385	18185	30875	3.11	4.6E-01	Q80943	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5385	18185	30876	3.11	4.6E-01	Q80943	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5459	18258	31148	1.84	4.6E-01	BE734781.1	EST_HUMAN	601568759F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5472	18271	31163	2.17	4.6E-01	AI247679.1	EST_HUMAN	q59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.1
5472	18271	31164	2.17	4.6E-01	AI247679.1	EST_HUMAN	q59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.1
5480	18279	31175	1.8	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5560	18357		0.96	4.6E-01	AF212124.1	NT	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5645	18440		0.77	4.6E-01	BE817247.1	EST_HUMAN	PMD-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
5609	18598	31526	0.59	4.6E-01	D26215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
							Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
8163	18940	31911	1.21	4.6E-01	AE000894.1	NT	Emaricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
8669	19586	32620	3.2	4.6E-01	U62332.1	NT	Emaricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
8669	19586	32621	3.2	4.6E-01	U62332.1	NT	Emaricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7131	25105	32884	0.57	4.6E-01	L07320.1	NT	Murine cytomegalovirus e1 protein gene, complete cds
7629	20295	33403	0.91	4.6E-01	AA493577.1	EST_HUMAN	rh04h05.s1 NCI_CGAP_THTY Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element
							GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3; 8 KD PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 8 KD PROTEIN 2 (8K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NI>
7658	20322		0.59	4.6E-01	Q90068	SWISSPROT	602130953F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4287828 5'
8219	20913	34049	10.11	4.6E-01	BF697396.1	EST_HUMAN	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9201	21870	35035	1.11	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)

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9201	21870	35038	1.11	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9876	22526	35720	1.64	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
9876	22526	35721	1.64	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10912	23592		2.3	4.6E-01	P68163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
10922	23602	36850	10.22	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10922	23602	36851	10.22	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11450	23217	36449	5.32	4.6E-01	AF018368.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11450	23217	36450	5.32	4.6E-01	AF018368.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12163	24845		1.77	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03
1904	14841	27350	1.43	4.5E-01	AE001831.1	NT	Deihococcus radiodurans R1 section 88 of 228 of the complete chromosome 1
1904	14841	27351	1.43	4.5E-01	AE001831.1	NT	Deihococcus radiodurans R1 section 88 of 228 of the complete chromosome 1
2873	15840	28284	4.5	4.5E-01	AA677086.1	EST_HUMAN	455d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3312	16072	28722	4.58	4.5E-01	Q05783	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3372	16131	28787	1.07	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4007	16753	29431	0.85	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN
4055	16800	29431	0.88	4.5E-01	A1708908.1	EST_HUMAN	es96d09.x1 Barstead_aorta_HPLR86 Homo sapiens cDNA clone IMAGE:2353480 3'
4155	17887	30236	4.25	4.5E-01	AW873495.1	EST_HUMAN	h0d0g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4890	17617	30236	1.1	4.5E-01	BE983445.2	EST_HUMAN	601657225R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3986023 3'
5481	18260	31151	1.49	4.5E-01	AW908814.1	EST_HUMAN	QV2-PT0012-140100-031-009 PT0012 Homo sapiens cDNA
6510	19275		1.45	4.5E-01	Q00988	SWISSPROT	COAT PROTEIN
7312	19995	33073	1.27	4.5E-01	M37036.1	NT	Rat nuclear proteins B23.1 and B23.2
7509	20180	33273	2.54	4.5E-01	A1858849.1	EST_HUMAN	w32e02.x1 NCL_OGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
7621	20287	33398	0.85	4.5E-01	P50070	SWISSPROT	SWIISNF COMPLEX 170 KDA SUBUNIT. ;
8206	20900		0.86	4.5E-01	M32661.1	NT	DNA PRIMASE
8302	20996	34134	3.5	4.5E-01	A1648596.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds
							t55g11.x1 NCL_OGAP_Oy35 Homo sapiens cDNA clone IMAGE:2292844 3'
8457	21149	34292	0.83	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(B3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(B3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8680	21372		2.94	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA

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8897	21888	34728	0.88	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
9840	22491		1.02	4.5E-01	9830818	NT	Bombay mori nuclear polyhedrosis virus, complete genome
10392	23038	36254	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02631 Fetal brain, Striatogene (cat936206) Homo sapiens cDNA clone HFBCY17
10392	23038	36255	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02631 Fetal brain, Striatogene (cat936206) Homo sapiens cDNA clone HFBCY17
10772	23455	36689	2.15	4.5E-01	AW501271.1	EST_HUMAN	x014h01.x1 NCL CGAP_U18 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT8_MOUSE
11217	23880		1.52	4.5E-01	AV719382.1	EST_HUMAN	Q64262 VIRAL INTEGRATION SITE PROTEIN INT-6, [1] ;
11895	25384		3.52	4.5E-01	BE871481.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCE12 5'
12540	24980		1.58	4.5E-01	BF337531.1	EST_HUMAN	601449201 F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12811	24918		3.37	4.5E-01	11422069	NT	602035275 F1 NCL CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4183290 5'
2388	15109	27847	3.39	4.4E-01	P49765	SWISSPROT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
3310	16070	28719	1.29	4.4E-01	AF058790.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3310	16070	28720	1.29	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3313	16073	28723	2.92	4.4E-01	BF058726.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
4209	16650		1.88	4.4E-01	BE378707.1	EST_HUMAN	7891002.Y1 NCL CGAP_Br18 Homo sapiens cDNA clone IMAGE:3393795 5'
5334	18137	30798	1.2	4.4E-01	P04929	SWISSPROT	601237139 F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3809393 5'
5602	18397	31309	1.59	4.4E-01	S65019.1	NT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5619	18415	31328	2	4.4E-01	AV720408.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5864	18651	31591	1.46	4.4E-01	AI108413.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5864	18651	31592	1.46	4.4E-01	AI108413.1	EST_HUMAN	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
6146	18923	31894	1.78	4.4E-01	AW080795.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCSC12 5'
6236	19010		1.42	4.4E-01	AA776132.1	EST_HUMAN	q02h11.x1 NCL CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
7297	19980	33056	1.04	4.4E-01	AE000571.1	NT	UNKNOWN PROTEIN ;
7723	25119		0.8	4.4E-01	AE001188.1	NT	q02h11.x1 NCL CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
7740	20436		9.71	4.4E-01	Z11878.1	NT	UNKNOWN PROTEIN ;
8661	21353	34500	0.84	4.4E-01	AA056427.1	EST_HUMAN	xc27e08.x1 NCL CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O85154 O85154
9049	21738	34896	0.7	4.4E-01	AF112540.1	NT	ae85d11.x1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:970995 3' similar to gb:M16038
							TYROSINE-PROTEIN KINASE LYN (HUMAN);
							Helicobacter pylori 26695 section 49 of 134 of the complete genome
							Troponeura pallidum section 4 of 87 of the complete genome
							S. tuberosum mRNA for induced stolon tip protein (partial)
							369a03.s1 Striatogene colon (8837204) Homo sapiens cDNA clone IMAGE:509836 3'
							HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9082	21771	34834	0.57	4.4E-01	AW612578.1	EST_HUMAN	hh0508.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2964222 3' similar to SW.MSH6 HUMAN P62701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9190	21860	35025	1.24	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
9802	22512	35709	2.19	4.4E-01	AI288650.1	EST_HUMAN	gc39f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
9803	22513		1.88	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
9897	22645	35857	4.31	4.4E-01	P35580	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10273	22921	36132	1.33	4.4E-01	S78404.1	NT	beta-HKA=H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10273	22921	36133	1.33	4.4E-01	S78404.1	NT	beta-HKA=H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12148	24635	31095	3.44	4.4E-01		NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12578	24903	31000	3.35	4.4E-01		NT	Autographa californica nucleopolyhedrovirus, complete genome
12683	24971		1.91	4.4E-01	P64725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
12768	25152		1.43	4.4E-01	AW363338.1	EST_HUMAN	RC2-CT0320-281159-012-c07 CT0320 Homo sapiens cDNA
402	13187	25835	2.17	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
402	13187	25836	2.17	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2875	15642		1.84	4.3E-01	AW935269.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3056	15822	28486	0.75	4.3E-01	AW698477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4131	16873	29501	1.29	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4374	13187	25835	1.18	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4374	13187	25836	1.18	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4902	17629		1.19	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5280	18085	30742	0.8	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5280	18085	30743	0.8	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5788	18589	31515	1.59	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
5817	18606	31534	2.02	4.3E-01	AF178825.1	NT	Salmid scitrusus olfactory receptor (SSC188) gene, partial cds
6808	19371	32384	4.78	4.3E-01	AJ001678.1	NT	Colurnix colurnix japonica fnG gene
6899	19606	32846	0.6	4.3E-01	AF075628.1	NT	Equus caballus microsatellite LEX027
6787	19511		0.91	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7328	20011		1.88	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Brr87 Homo sapiens cDNA clone IMAGE:4158268 5'
7496	20168	33260	0.61	4.3E-01	U51002.1	NT	Mus musculus Dlx-2 gene, complete cds
8326	21019		2.72	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
9154	21885	35053	0.96	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9626	22278	35468	2.18	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
9626	22278	35469	2.18	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'

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10128	22776	35990	0.84	4.3E-01	AW170559.1	EST_HUMAN	xn63a03.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10409	23055	36272	0.5	4.3E-01	H65292.1	EST_HUMAN	TR:O00189 O00189 MU-ADAPTIN-RELATED PROTEIN 2 ;
10849	19006	32646	2.45	4.3E-01	AF075628.1	NT	y45505.s1 Soares_fetal_liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:208209 3'
11166	23833	37113	1.29	4.3E-01	AW963658.1	EST_HUMAN	Equus caballus microsatellite LEX027
11166	23833	37114	1.29	4.3E-01	AW963658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
11166	23833	37662	1.84	4.3E-01	AW963658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
11745	24336	37662	1.84	4.3E-01	AW963658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
12770	25025		2.18	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whH gene
1337	15666	26761	1.54	4.2E-01	Q39102	SWISSPROT	GELL DIVISION PROTEIN FISH HOMOLOG PRECURSOR
1941	14878		1.23	4.2E-01	AA761653.1	EST_HUMAN	nz24a09.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3596	16349	28990	4.4	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 228 of the complete genome
3628	16381	29021	1.41	4.2E-01	AI280338.1	EST_HUMAN	q194601.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3698	17886		0.85	4.2E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07879, Z40488
3964	18713	28352	0.97	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4849	17383	30015	4.88	4.2E-01	AA534093.1	EST_HUMAN	ij68h01.s1 NCL_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4731	17463	30100	3.46	4.2E-01	R13467.1	EST_HUMAN	y77e01.t1 Soares_infant_brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5626	18423	31336	0.82	4.2E-01	BF242055.1	EST_HUMAN	60187921F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5693	18487	31408	1.53	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-080400-029-g04 CT0254 Homo sapiens cDNA
6112	18889	31858	1.01	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6852	19552	32582	10.8	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6852	19552	32583	10.8	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6911	25101	32694	2.15	4.2E-01	S82504.1	NT	Brcal=breast cancer gene [rat, WF, spleen, Genomic, 419 nt, segment 2 of 2]
6963	19686	32734	7	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7891	20586	33715	2.21	4.2E-01	AW957448.1	EST_HUMAN	EST368413 MAGe resequences, MAGe Homo sapiens cDNA
7891	20586	33716	2.21	4.2E-01	AW957448.1	EST_HUMAN	EST368413 MAGe resequences, MAGe Homo sapiens cDNA
8106	20800	33932	0.61	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9870	22520		0.94	4.2E-01	AA705007.1	EST_HUMAN	z95f01.s1 Soares_fetal_liver_spleen_1N1LS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10081	22729	35944	0.45	4.2E-01	AF181854.1	NT	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10393	23039	36256	1.78	4.2E-01	AW863666.1	EST_HUMAN	MR3-SN0010-280300-103-R07 SN0010 Homo sapiens cDNA
10972	23648	36901	2.69	4.2E-01	AB073489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11370	23977	37277	2.11	4.2E-01	BE966485.2	EST_HUMAN	601860352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
1072	13630	26488	1.83	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210198-142 BT091 Homo sapiens cDNA

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1081	13839	28497	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1081	13839	28498	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2715	15422	28161	1.1	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2941	15708	28355	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2941	15708	28356	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3754	16506	29142	0.68	4.1E-01	AW961292.1	EST_HUMAN	EST373384 MAGG Homo sapiens cDNA
3754	16506	29143	0.68	4.1E-01	AW961292.1	EST_HUMAN	EST373384 MAGG Homo sapiens cDNA
4241	16982	29607	2.93	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 IsoG, IsoH, IsoI, IsoJ, IsoK, IsoL, IsoM, IsoN, IsoO, IsoP, IsoQ, IsoR, IsoS, IsoT, IsoU, IsoV, IsoW, IsoX, IsoY, IsoZ, IsoAA, IsoAB, IsoAC, IsoAD, IsoAE, IsoAF, IsoAG, IsoAH, IsoAI, IsoAJ, IsoAK, IsoAL, IsoAM, IsoAN, IsoAO, IsoAP, IsoAQ, IsoAR, IsoAS, IsoAT, IsoAU, IsoAV, IsoAW, IsoAX, IsoAY, IsoAZ, IsoBA, IsoBB, IsoBC, IsoBD, IsoBE, IsoBF, IsoBG, IsoBH, IsoBI, IsoBJ, IsoBK, IsoBL, IsoBM, IsoBN, IsoBO, IsoBP, IsoBQ, IsoBR, IsoBS, IsoBT, IsoBU, IsoBV, IsoBW, IsoBX, IsoBY, IsoBZ, IsoCA, IsoCB, IsoCC, IsoCD, IsoCE, IsoCF, IsoCG, IsoCH, IsoCI, IsoCJ, IsoCK, IsoCL, IsoCM, IsoCN, IsoCO, IsoCP, IsoCQ, IsoCR, IsoCS, IsoCT, IsoCU, IsoCV, IsoCW, IsoCX, IsoCY, IsoCZ, IsoDA, IsoDB, IsoDC, IsoDD, IsoDE, IsoDF, IsoDG, IsoDH, IsoDI, IsoDJ, IsoDK, IsoDL, IsoDM, IsoDN, IsoDO, IsoDP, IsoDQ, IsoDR, IsoDS, IsoDT, IsoDU, IsoDV, IsoDW, IsoDX, IsoDY, IsoDZ, IsoEA, IsoEB, IsoEC, IsoED, IsoEE, IsoEF, IsoEG, IsoEH, IsoEI, IsoEJ, IsoEK, IsoEL, IsoEM, IsoEN, IsoEO, IsoEP, IsoEQ, IsoER, IsoES, IsoET, IsoEU, IsoEV, IsoEW, IsoEX, IsoEY, IsoEZ, IsoFA, IsoFB, IsoFC, IsoFD, IsoFE, IsoFF, IsoFG, IsoFH, IsoFI, IsoFJ, IsoFK, IsoFL, IsoFM, IsoFN, IsoFO, IsoFP, IsoFQ, IsoFR, IsoFS, IsoFT, IsoFU, IsoFV, IsoFW, IsoFX, IsoFY, IsoFZ, IsoGA, IsoGB, IsoGC, IsoGD, IsoGE, IsoGF, IsoGG, IsoGH, IsoGI, IsoGJ, IsoGK, IsoGL, IsoGM, IsoGN, IsoGO, IsoGP, IsoGQ, IsoGR, IsoGS, IsoGT, IsoGU, IsoGV, IsoGW, IsoGX, IsoGY, IsoGZ, IsoHA, IsoHB, IsoHC, IsoHD, IsoHE, IsoHF, IsoHG, IsoHH, IsoHI, IsoHJ, IsoHK, IsoHL, IsoHM, IsoHN, IsoHO, IsoHP, IsoHQ, IsoHR, IsoHS, IsoHT, IsoHU, IsoHV, IsoHW, IsoHX, IsoHY, IsoHZ, IsoIA, IsoIB, IsoIC, IsoID, IsoIE, IsoIF, IsoIG, IsoIH, IsoII, IsoIJ, IsoIK, IsoIL, IsoIM, IsoIN, IsoIO, IsoIP, IsoIQ, IsoIR, IsoIS, IsoIT, IsoIU, IsoIV, IsoIW, IsoIX, IsoIY, IsoIZ, IsoJA, IsoJB, IsoJC, IsoJD, IsoJE, IsoJF, IsoJG, IsoJH, IsoJI, IsoJJ, IsoJK, IsoJL, IsoJM, IsoJN, IsoJO, IsoJP, IsoJQ, IsoJR, IsoJS, IsoJT, IsoJU, IsoJV, IsoJW, IsoJX, IsoJY, IsoJZ, IsoKA, IsoKB, IsoKC, IsoKD, IsoKE, IsoKF, IsoKG, IsoKH, IsoKI, IsoKJ, IsoKK, IsoKL, IsoKM, IsoKN, IsoKO, IsoKP, IsoKQ, IsoKR, IsoKS, IsoKT, IsoKU, IsoKV, IsoKW, IsoKX, IsoKY, IsoKZ, IsoLA, IsoLB, IsoLC, IsoLD, IsoLE, IsoLF, IsoLG, IsoLH, IsoLI, IsoLJ, IsoLK, IsoLL, IsoLM, IsoLN, IsoLO, IsoLP, IsoLQ, IsoLR, IsoLS, IsoLT, IsoLU, IsoLV, IsoLW, IsoLX, IsoLY, IsoLZ, IsoMA, IsoMB, IsoMC, IsoMD, IsoME, IsoMF, IsoMG, IsoMH, IsoMI, IsoMJ, IsoMK, IsoML, IsoMN, IsoMO, IsoMP, IsoMQ, IsoMR, IsoMS, IsoMT, IsoMU, IsoMV, IsoMW, IsoMX, IsoMY, IsoMZ, IsoNA, IsoNB, IsoNC, IsoND, IsoNE, IsoNF, IsoNG, IsoNH, IsoNI, IsoNJ, IsoNK, IsoNL, IsoNM, IsoNO, IsoNP, IsoNQ, IsoNR, IsoNS, IsoNT, IsoNU, IsoNV, IsoNW, IsoNX, IsoNY, IsoNZ, IsoOA, IsoOB, IsoOC, IsoOD, IsoOE, IsoOF, IsoOG, IsoOH, IsoOI, IsoOJ, IsoOK, IsoOL, IsoOM, IsoON, IsoOO, IsoOP, IsoOQ, IsoOR, IsoOS, IsoOT, IsoOU, IsoOV, IsoOW, IsoOX, IsoOY, IsoOZ, IsoPA, IsoPB, IsoPC, IsoPD, IsoPE, IsoPF, IsoPG, IsoPH, IsoPI, IsoPJ, IsoPK, IsoPL, IsoPM, IsoPN, IsoPO, IsoPP, IsoPQ, IsoPR, IsoPS, IsoPT, IsoPU, IsoPV, IsoPW, IsoPX, IsoPY, IsoPZ, IsoQA, IsoQB, IsoQC, IsoQD, IsoQE, IsoQF, IsoQG, IsoQH, IsoQI, IsoQJ, IsoQK, IsoQL, IsoQM, IsoQN, IsoQO, IsoQP, IsoQQ, IsoQR, IsoQS, IsoQT, IsoQU, IsoQV, IsoQW, IsoQX, IsoQY, IsoQZ, IsoRA, IsoRB, IsoRC, IsoRD, IsoRE, IsoRF, IsoRG, IsoRH, IsoRI, IsoRJ, IsoRK, IsoRL, IsoRM, IsoRN, IsoRO, IsoRP, IsoRQ, IsoRR, IsoRS, IsoRT, IsoRU, IsoRV, IsoRW, IsoRX, IsoRY, IsoRZ, IsoSA, IsoSB, IsoSC, IsoSD, IsoSE, IsoSF, IsoSG, IsoSH, IsoSI, IsoSJ, IsoSK, IsoSL, IsoSM, IsoSN, IsoSO, IsoSP, IsoSQ, IsoSR, IsoSS, IsoST, IsoSU, IsoSV, IsoSW, IsoSX, IsoSY, IsoSZ, IsoTA, IsoTB, IsoTC, IsoTD, IsoTE, IsoTF, IsoTG, IsoTH, IsoTI, IsoTJ, IsoTK, IsoTL, IsoTM, IsoTN, IsoTO, IsoTP, IsoTQ, IsoTR, IsoTS, IsoTT, IsoTU, IsoTV, IsoTW, IsoTX, IsoTY, IsoTZ, IsoUA, IsoUB, IsoUC, IsoUD, IsoUE, IsoUF, IsoUG, IsoUH, IsoUI, IsoUJ, IsoUK, IsoUL, IsoUM, IsoUN, IsoUO, IsoUP, IsoUQ, IsoUR, IsoUS, IsoUT, IsoUU, IsoUV, IsoUW, IsoUX, IsoUY, IsoUZ, IsoVA, IsoVB, IsoVC, IsoVD, IsoVE, IsoVF, IsoVG, IsoVH, IsoVI, IsoVJ, IsoVK, IsoVL, IsoVM, IsoVN, IsoVO, IsoVP, IsoVQ, IsoVR, IsoVS, IsoVT, IsoVU, IsoVV, IsoVW, IsoVX, IsoVY, IsoVZ, IsoWA, IsoWB, IsoWC, IsoWD, IsoWE, IsoWF, IsoWG, IsoWH, IsoWI, IsoWJ, IsoWK, IsoWL, IsoWM, IsoWN, IsoWO, IsoWP, IsoWQ, IsoWR, IsoWS, IsoWT, IsoWU, IsoWV, IsoWW, IsoWX, IsoWY, IsoWZ, IsoXA, IsoXB, IsoXC, IsoXD, IsoXE, IsoXF, IsoXG, IsoXH, IsoXI, IsoXJ, IsoXK, IsoXL, IsoXM, IsoXN, IsoXO, IsoXP, IsoXQ, IsoXR, IsoXS, IsoXT, IsoXU, IsoXV, IsoXW, IsoXX, IsoXY, IsoXZ, IsoYA, IsoYB, IsoYC, IsoYD, IsoYE, IsoYF, IsoYG, IsoYH, IsoYI, IsoYJ, IsoYK, IsoYL, IsoYM, IsoYN, IsoYO, IsoYP, IsoYQ, IsoYR, IsoYS, IsoYT, IsoYU, IsoYV, IsoYW, IsoYX, IsoYY, IsoYZ, IsoZA, IsoZB, IsoZC, IsoZD, IsoZE, IsoZF, IsoZG, IsoZH, IsoZI, IsoZJ, IsoZK, IsoZL, IsoZM, IsoZN, IsoZO, IsoZP, IsoZQ, IsoZR, IsoZS, IsoZT, IsoZU, IsoZV, IsoZW, IsoZX, IsoZY, IsoZZ

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2968	16734	28383	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2968	16734	28384	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3683	16436	29080	1.98	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (Y1C), Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3807	16559	29191	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3807	16559	29192	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4767	17499		7.97	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 6, CHLOROPLAST
5820	19609	31538	1.23	4.0E-01	AW970610.1	EST_HUMAN	EST382691 IMAGE resequencing; MAGK Homo sapiens cDNA
6345	19115	32104	0.94	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPROTEIN (P190) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
7728	20391	33504	0.68	4.0E-01	P27546	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7829	20524	33649	0.44	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
7910	20605	33738	1.04	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
8904	21595	34736	1.17	4.0E-01	AA323289.1	EST_HUMAN	EST26068 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
11560	24159		2.03	4.0E-01	BF030262.1	EST_HUMAN	601588283F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3828092 5'
11721	24315		2.83	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12162	25222		2.28	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12884	24972		2.2	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
1366	14104	26780	1.85	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2648	15358	28101	3.34	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1183 protein, partial cds
2709	15416	28153	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2709	15416	28154	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3093	19858	28499	4.73	3.9E-01	AJ225886.1	NT	Sinorhizobium meliloti egl, syrB2, cya3 genes and orf3
4059	16804	29435	1.05	3.9E-01	BF682611.1	EST_HUMAN	761d01.x1 NCI_CGAP_B116 Homo sapiens cDNA clone IMAGE:3339169 3'
4932	17660	30270	1.74	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3833689 5'
5843	18631	31566	3.91	3.9E-01	BF208038.1	EST_HUMAN	601862362F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:4082055 5'
7854	20649	33674	0.92	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
8760	21452	34600	0.81	3.9E-01	AW177011.1	EST_HUMAN	CMB-C10105-170899-004-b08 C10105 Homo sapiens cDNA
8769	21461		0.58	3.9E-01	BF348634.1	EST_HUMAN	602019944F1 NCI_CGAP_B167 Homo sapiens cDNA clone IMAGE:4155322 5'
9134	21822	34988	1.26	3.9E-01	AW195888.1	EST_HUMAN	xs6604.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O94821 O94821 KIAA0713 PROTEIN ;
9445	22122	35301	1.46	3.9E-01	AI937337.1	EST_HUMAN	wp76a02.x1 NCI_CGAP_B1m25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFx6_HUMAN P48382 BINDING REGULATORY FACTOR. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9778	22429	35635	3.03	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
9845	22496		0.58	3.9E-01	11465620	NT	Paraphyria purpurea mitochondrion, complete genome
10068	22714	35632	0.77	3.9E-01	D86722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10722	23410		1.98	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKC8QC11 5'
11753	24344	37674	1.47	3.9E-01	AV702623.1	EST_HUMAN	AV702623 ADB Homo sapiens cDNA clone ADBDBE06 5'
11948	25295		3.37	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12068	24581		2.08	3.9E-01	Q61970	SWISSPROT	HOMEOBOX PROTEIN HLX1
12559	24891		1.44	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
156	12971		8.33	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1863	14601		1.03	3.8E-01	AE008870.1	NT	Xylella fastidiosa, section 18 of 228 of the complete genome
2460	15178	27918	1.29	3.8E-01	U41846.1	NT	Ceanothus divaricatus bruggsae acetylcholinesterase (ace-1) gene, complete cds
2578	15290	28027	1.62	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2638	15601	28092	3.96	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3003	13769		1.14	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 86SE-MP1213)
3043	15809	28456	1.39	3.8E-01	AF043383.1	NT	Pleurocetes americanus antihopelidase N (ampN) gene, partial cds
3477	16233	28887	7.98	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3527	16283		0.79	3.8E-01	AI807219.1	EST_HUMAN	w38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3541	16283		1.22	3.8E-01	AI807219.1	EST_HUMAN	w38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3739	16492	29127	1.15	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3897	16647	29287	0.97	3.8E-01	8754095	NT	Mus musculus general transcription factor III (GTF2), mRNA
4043	16788	29416	0.74	3.8E-01	AJ271361.2	NT	Tadfig rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
5522	18320	31221	1.42	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6247	19021		0.74	3.8E-01	S46825.1	NT	piron protein [mink, Genomic, 2446 nt]
6528	19294	32298	5.5	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-602 BT0537 Homo sapiens cDNA
6682	19579	32614	4.58	3.8E-01	AI374601.1	EST_HUMAN	ta54f11.x1 Soares_total_fetus_Nb21F8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element
6840	19502	32527	1.25	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7416	20093		4.42	3.8E-01	X61597.1	NT	M.musculus gene for kallikrein-binding protein
8198	20890	34028	0.86	3.8E-01	M81395.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8455	21147	34289	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8523	21215	34358	1.02	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8716	21408	34551	1.28	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9461	22011		3.55	3.8E-01	T96413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element;

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10695	23386		1.67	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBC07 5'
11521	24121		3.18	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11693	24288	37610	2.27	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
11693	24288	37611	2.27	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
12149	24836		4.78	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12270	25316		2.08	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12394	24778		3.39	3.8E-01	BE828256.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
12723	24994		1.54	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
12771	26291		1.74	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
12788	25040	30968	1.51	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2486	15203	27944	12.24	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3483	16209	28860	9.64	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4204	16945	29572	7.39	3.7E-01	AF218707.1	EST_HUMAN	ck39c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510788 3'
4286	17025	29651	1.3	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4357	17095	29730	2.55	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MCS8 section 50 of 206 of the complete genome
5676	18470	31386	1.15	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
5860	18647	31588	0.9	3.7E-01	AL183278.2	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6417	19185	32183	0.66	3.7E-01	IM10806.1	NT	Mus sandoola haptoglobin mRNA, complete cds
6436	19204		0.72	3.7E-01	L10353.1	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7043	19734	32794	3.23	3.7E-01	11625843	NT	yes50a07.f3 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:68324 5'
7685	20349	33463	0.6	3.7E-01	T68802.1	EST_HUMAN	hd45d05.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2912457 3' similar to contains Alu repetitive element; contains L1.12 L1 repetitive element
7719	20383	33497	0.56	3.7E-01	AW511326.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8227	20921	34059	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8227	20921	34060	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8253	20957	34066	0.65	3.7E-01	AA902812.1	EST_HUMAN	ck43b11.s1 NCIL CGAP_L1e2 Homo sapiens cDNA clone IMAGE:1516701 3'
9101	21789		1.31	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10069	22717		0.8	3.7E-01	K00691.1	NT	mouse Ig gamma1 alpha membrane exon 5 region
10110	22758	35970	4.12	3.7E-01	AB384411.1	EST_HUMAN	q146b07.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
10764	23448	36690	1.98	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
10957	23633	36882	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
10957	23633	36883	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11443	23210	36441	2.75	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EO 2.7.7.31)
11676	24271	37593	1.43	3.7E-01	D78348.1	EST_HUMAN	HUM230A06B Human aorta polyA* (Tfujwara) Homo sapiens cDNA clone GEN-230A06 5'

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11771	24362		2.87	3.7E-01	6877676	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11869	24943		2.11	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12033	24558		3.09	3.7E-01	AJ243325.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12488	24847		1.9	3.7E-01	AL121154.1	EST_HUMAN	DKFZp782K075.1 782 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782K075 5'
12548	24886	30895	4.03	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
254	13082	25701	2.17	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
875	13740		8.22	3.6E-01	U89241.1	NT	Human mlb gene, partial cds
1281	14040	26713	3.83	3.6E-01	T80255.1	EST_HUMAN	yc03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1281	14040	26714	3.83	3.6E-01	T80255.1	EST_HUMAN	yc03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1908	14946	27356	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419 3'
1909	14946	27357	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419 3'
1944	14979	27393	5.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2047	14780		1.39	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2267	14993		1.05	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2389	15110		2.69	3.6E-01	X78725.1	NT	P. irregularis (P3804) gene for actin
2479	15197	27936	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2479	15197	27937	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2491	15208	27950	1.43	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN-L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2636	15348	28090	1.44	3.6E-01	P24206	SWISSPROT	
2900	17884		7.16	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3462	16218	28871	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3462	16218	28872	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4375	17112	29745	1.3	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4948	17675	30285	2.38	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCL_CGAP_L024 Homo sapiens cDNA clone IMAGE:2872566 3'
5298	18103	30762	0.82	3.6E-01	AJ006565.1	NT	Homo sapiens lipo gene intron 5
							FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (PHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
5995	18776	31738	0.85	3.6E-01	P16431	SWISSPROT	
6396	19155	32154	1.74	3.6E-01	Y10198.1	NT	Homo sapiens PHEX gene
7048	19739		3.2	3.6E-01	R94090.1	EST_HUMAN	yk74a06.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:275987 5'
							w172c10.x1 Soares thymus NHFTth Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
7183	19869	32943	1.9	3.6E-01	AW027174.1	EST_HUMAN	O15117 FYN BINDING PROTEIN, [1]:
8123	20817	33953	0.58	3.6E-01	P98167	SWISSPROT	SCO-SPONDIN

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8177	20871	34005	11.45	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8900	21591	34731	2.74	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8900	21591	34732	2.74	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9091	21780	34944	1.17	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9299	21966	35139	1.04	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9299	21966	35140	1.04	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9369	21944		0.57	3.6E-01	X62825.1	NT	C. perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
9763	22414	35621	14.67	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9893	22543	35735	0.51	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
9893	22543	35736	0.51	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10864	23544	36781	3.31	3.6E-01	BE902390.1	EST_HUMAN	601876418F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3958997 5'
11052	23722	36993	4.12	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11421	23188	36419	3.4	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11903	25415		1.83	3.6E-01	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
11978	24522		1.4	3.6E-01	D90901.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
11987	24528		3.89	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12135	24624		4	3.6E-01	U66888.1	NT	Mus musculus Enr1 mRNA, complete cds
12493	24850		2.12	3.6E-01	11432598	NT	Homo sapiens myeloidlymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
12746	25363		2.23	3.6E-01	AW190229.1	EST_HUMAN	x150e11.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
204	13017	25657	2.05	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
708	13482	26131	1.59	3.5E-01	7708196	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	13482	26132	1.59	3.5E-01	7708196	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
762	13535	26194	4.25	3.5E-01	BF129786.1	EST_HUMAN	601811060R1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4053951 3'
1615	14362	27053	1.1	3.5E-01	BF310688.1	EST_HUMAN	601894653F2 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4124244 5'
1636	14382	27069	1.96	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2281	15006	27747	1.35	3.5E-01	P06796	SWISSPROT	HOMEOBOX PROTEIN HDX-A4 (HOX-1.4) (MH-3)
2612	15600	28066	1.76	3.5E-01	AA223252.1	EST_HUMAN	zr08a08.s1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3785	16537		0.85	3.5E-01	AA642138.1	EST_HUMAN	nr60403.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4231	16972	26596	1.67	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb-5b) gene, complete cds
4443	17179	29805	0.94	3.5E-01	BE146585.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
4827	17362	29895	1.02	3.5E-01	Y18477.1	NT	Mus musculus Abx12B gene 5' flanking region
4880	17607	30230	4.58	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5251	18057	30685	0.76	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5251	18057	30688	0.76	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5462	18261	31152	1.13	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6143	18921		0.96	3.5E-01	AW883916.1	EST_HUMAN	PM4-SN0012-030400-001-at11 SN0012 Homo sapiens cDNA
6314	19085	32070	0.8	3.5E-01	AA431833.1	EST_HUMAN	zw79003.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR-G1068935
6359	19129	32124	0.66	3.5E-01	U37150.1	NT	G1068835 F10P2.1;
6566	19331	32338	1.08	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6956	19438		4.24	3.5E-01	X98505.1	NT	GLUCOSE 6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7441	20118	33207	0.55	3.5E-01	P47281	SWISSPROT	S. cerevisiae mRNA for CD31 protein (PECAM-1)
7441	20118	33208	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
7970	20665		2.19	3.5E-01	11448042	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
7973	20668	33790	0.71	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8366	21059		0.63	3.5E-01	AF051561.1	NT	RC4-E10024-260600-014-d07 ET0024 Homo sapiens cDNA
8825	21517	34682	1.17	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Ncc1) mRNA, complete cds
9636	22288	35481	1.52	3.5E-01	Q02294	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9786	22437	35644	5.64	3.5E-01	Z26825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL L
9867	22517	35713	0.96	3.5E-01	BE174794.1	EST_HUMAN	TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
10635	23327	36564	2.76	3.5E-01	X61084.1	NT	Xlaeis gene for albumin including HP1 enhancer
10946	23625	36875	2.39	3.5E-01	AJ243178.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10946	23625	36876	2.39	3.5E-01	AJ243178.1	NT	G griseus rhodopsin gene for opsin protein
11505	24106	37419	1.34	3.5E-01	U07000.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11585	24184	37499	1.64	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11619	24216		1.71	3.5E-01	M82885.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11684	24279	37601	1.51	3.5E-01	L05145.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
11776	24367		1.36	3.5E-01	A1064773.1	EST_HUMAN	Y200h12.11 Soares, multiple sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:290375 5'
12063	24578		1.47	3.5E-01	X64595.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
12214	24676		2.32	3.5E-01	AE001774.1	NT	Human alpha1 gene for F(0)ATP synthase alpha-subunit
						NT	Thermoplasma maritima section 86 of 136 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12402	24787		1.4	3.5E-01	AE001691.1	NT	Thermotoga maritima section 3 of 136 of the complete genome
12793	25269	30723	3.33	3.5E-01	H80814.1	EST_HUMAN	y844f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
12793	25269	30724	3.33	3.5E-01	H80814.1	EST_HUMAN	y844f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
691	13466		1.85	3.4E-01	AJ242958.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
955	13720	26386	7.61	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, cds genes, orf222 and partial InaA gene
1303	14052	28725	1.72	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2400	15121	27858	2.62	3.4E-01	D60909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3001	15767	28415	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3001	15767	28416	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3146	15910	28555	1.08	3.4E-01	D60909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3159	15922	28568	6.23	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3338	16096	28749	0.9	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3522	16278	28933	3.48	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3770	16522		1.69	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCL CGAP_OV18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
4029	16774		2.38	3.4E-01	AA584198.1	EST_HUMAN	Q8LJ16 DJ18C9.1
4460	17186	29823	0.82	3.4E-01	AF166341.1	NT	no11b10.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4599	17334	29863	1.54	3.4E-01	BE068912.1	EST_HUMAN	Homo sapiens Integrin alpha 6 (ITGA6) gene, exons 12 through 23
4898	17625		3.23	3.4E-01	AJ240973.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5143	17862		0.98	3.4E-01	U79746.1	NT	q95c05.x1 NCL CGAP_K43 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
5599	18394	31304	2.62	3.4E-01	AL161594.2	NT	Homo sapiens serotonin transporter (hSERT) gene, promoter region, exons 1B and 2, and partial cds
5721	18513		6.09	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5917	18702		1.99	3.4E-01	L02871.1	NT	zn12a11.s1 Stratagene HNT neuron (#637233) Homo sapiens cDNA clone IMAGE:547221 3'
5940	18722	31681	0.89	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6017	18798	31759	2.43	3.4E-01	AW204505.1	EST_HUMAN	6015/181171 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:383828 3'
6141	18919	31889	1.81	3.4E-01	AL120544.1	EST_HUMAN	UH-BIT-ae-e-12-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6644	19406		1.56	3.4E-01	N85225.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
						EST_HUMAN	zb55e12.s1 Soares fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:307342 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6848	19548	32578	1.02	3.4E-01	AH468082.1	EST_HUMAN	hm63q05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
6959	19441	32456	0.59	3.4E-01	BF678702.1	EST_HUMAN	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248365 5'
7806	20501		0.49	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8135	20829	33984	0.6	3.4E-01	Y14830.1	NT	Homo sapiens TCRAV28 gene, allele A4, partial
8188	20882		0.47	3.4E-01	BF449010.1	EST_HUMAN	7n84a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8UJ15
8386	21079		1.51	3.4E-01	AA337083.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' and
8461	21153	34296	0.72	3.4E-01	L04890.1	NT	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
8751	21443	34590	1.7	3.4E-01		9833824	Bovine enterovirus strain K2577, complete genome
9112	21800	34964	4.42	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9112	21800	34965	4.42	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9321	21988		0.51	3.4E-01	AB017510.1	NT	Ephydalia fluviatilis mRNA for PLC-gammaS, complete cds
9346	20417	33536	4.67	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9346	20417	33537	4.67	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9397	22059	35229	0.5	3.4E-01	AF193857.1	NT	Dichystallum discoidale putative CMF receptor CMFR1 mRNA, complete cds
9595	22248	35433	1.01	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scot-1) mRNA, complete cds
9789	22440	35648	1.86	3.4E-01	AJ25084.1	NT	Homo sapiens FAA gene, exon 18, 17 and 18
10378	23022		0.62	3.4E-01	AE000496.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
10940	23620		4.72	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1028212 (section 87 of 148) of the complete genome
10984	23659	36912	2.6	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11032	23703	36971	2.17	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11253	23915	37207	1.61	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11253	23915	37208	1.61	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11483	24084	37398	1.88	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds
11513	24113	37423	3.65	3.4E-01	AL161615.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11788	24378	37706	1.72	3.4E-01	BF061948.1	EST_HUMAN	7n69412.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480848 3'
11861	24445	37786	1.58	3.4E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11881	24455		1.85	3.4E-01	U93804.1	NT	Citrus variegation virus putative replicase gene, partial cds
12197	24666		11.43	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
12224	25192		1.61	3.4E-01	BE218652.1	EST_HUMAN	hw42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13 PTR5 repetitive element;

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12280	26292		2.28	3.4E-01	8838361	NT	Beta vulgaris mitochondrion, complete genome
12391	24781	31036	2.2	3.4E-01	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
12688	24974		1.82	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B) G11, helixase (SK2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
13	12840	25453	10.77	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
103	12840	25453	4.4	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
435	13221	25867	0.9	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
618	13397	26032	2.01	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1178	13931	26597	2.85	3.3E-01	Q12448	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1284	14034	26705	3.76	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1336	14085	26760	1.2	3.3E-01	U43628.1	NT	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster
1601	14347	27036	1.47	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1731	14473		1.02	3.3E-01	AA332734.1	EST_HUMAN	ES136722 Embryo, 8 week Homo sapiens cDNA 5' end
2022	14757		1.01	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2404	15125		4.62	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'- decarboxylase) (UMPS) mRNA
2949	15715	28368	1.87	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3051	15817	28462	1.48	3.3E-01	AJ007832.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3486	16243	28899	1.07	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3789	16541	29176	2.1	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3799	16551	29183	0.97	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3832	16682	29323	1.03	3.3E-01	4757739	NT	Homo sapiens A kinase (PKA) anchor protein 5 (AKAP5), mRNA
3947	16697	29336	1.47	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3983	16731	29365	1.79	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4334	17073		1.6	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4641	17375		1.23	3.3E-01	AJ539114.1	EST_HUMAN	tp78b12.x1 NC1 CGAP U8 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4768	17517	30139	1.22	3.3E-01	D84003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
5146	17865		0.96	3.3E-01	AW937982.1	EST_HUMAN	QV0-DT0047-170200-123-h08 DT0047 Homo sapiens cDNA
5241	18047	30675	2.61	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5241	18047	30676	2.61	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein

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5700	18494	31417	0.74	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
5856	18643	31582	1.9	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5856	18643	31583	1.9	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5947	18729	31688	1.18	3.3E-01	P05691	SWISSPROT	GIRCUKSPOROZOITE PROTEIN (CS)
6095	18612	32651	0.71	3.3E-01	AB034233.1	NT	Flexibacter fibrilis gyrB gene for DNA gyrase B subunit, partial cds
6095	18612	32652	0.71	3.3E-01	AB034233.1	NT	Flexibacter fibrilis gyrB gene for DNA gyrase B subunit, partial cds
6789	19533	32560	4.82	3.3E-01	AI628131.1	EST_HUMAN	tyb4h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6789	19533	32561	4.82	3.3E-01	AI628131.1	EST_HUMAN	tyb4h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7682	20346	33458	1.68	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8460	21152	34295	18.62	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8659	21351	34497	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8659	21351	34498	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9012	21702	34852	0.81	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9278	22032	35203	0.81	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9278	22032	35204	0.81	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9411	22073	35244	2.62	3.3E-01	N69866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:287649 3'
9452	22002	35174	2.77	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
9891	22541	36554	2.27	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG1-C) gene, exons 1-3, complete cds
10622	23315	36554	3.13	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10622	23315	36555	3.13	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10951	23628	36555	1.7	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Brr84 Homo sapiens cDNA clone IMAGE:4213585 5'
11196	23861	37147	11.61	3.3E-01	BE218351.1	EST_HUMAN	h51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11317	24008	37313	3.23	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11719	24313		3.06	3.3E-01	AA806621.1	EST_HUMAN	cb71g02.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
11741	12840	25453	1.87	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
11977	24521	37266	1.71	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12676	24967		3.34	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
444	13230		2.33	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
701	13476		1.43	3.2E-01	AL161861.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1139	13894	26555	27.53	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1259	14008	26677	1.36	3.2E-01	Z50202.1	NT	P. vulgaris arcS-1 gene
1369	14117	26792	5.42	3.2E-01	Q48824	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1767	14508	27210	1.26	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1777	14519	27222	4.7	3.2E-01	AW957194.1	EST_HUMAN	EST368284 MAGC resequences, MAGD Homo sapiens cDNA
1777	14519	27223	4.7	3.2E-01	AW957194.1	EST_HUMAN	EST368284 MAGC resequences, MAGD Homo sapiens cDNA
1835	14574	27286	1.23	3.2E-01	AL111655.1	NT	Baby's chineea strain T4 cDNA library under conditions of nitrogen deprivation
2157	14887	27621	2.52	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2543	18257		2.01	3.2E-01	7710079	NT	Mus musculus Pbx1/nr1011 homeobox (Pbx1), mRNA
2713	15420	28159	1.08	3.2E-01	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3594	16347		0.77	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4305	17044	29669	0.81	3.2E-01	4759195	NT	Homo sapiens symplekin (SYM) mRNA
4363	17101	29736	1.52	3.2E-01	IM18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4484	17200	29826	1.21	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04G IN CHROMOSOME 1 PRECURSOR
4688	17422		6.7	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4826	17557	30179	1.17	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
4965	17690	30299	0.74	3.2E-01	BE782748.1	EST_HUMAN	601485591F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3888799 5'
5190	17988	30621	3.26	3.2E-01	BE173954.1	EST_HUMAN	CMO-HT0569-060300-289-f10 HT0569 Homo sapiens cDNA
5868	18655	31596	1.07	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:ferredoxin oxidoreductase and flanking genes
							Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6211	18986	31963	0.9	3.2E-01	AF016494.1	NT	
6501	19268	32268	0.64	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FHITA Homo sapiens cDNA clone FHITAABH01 5'
6634	18396		1.09	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
7765	20451	33575	0.51	3.2E-01	AJ27661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8072	20766	33895	1.48	3.2E-01	ME0266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8164	20858	33980	0.45	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12W or1
8265	20959	34088	14.41	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8268	20962	34103	13.76	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8361	21054		1.38	3.2E-01	AL161874.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8398	21091	34228	1.24	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075827 5'
8398	21091	34227	1.24	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075827 5'
8471	21163	34306	2.65	3.2E-01	AE002015.1	NT	Dielococcus radiodurans R1 section 162 of 229 of the complete chromosome 1
8571	21283	34401	0.84	3.2E-01	U81028.1	NT	Oryzobolus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8571	21263	34402	0.84	3.2E-01	U51026.1	NT	Oryzobolus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8965	21658	34807	0.51	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8976	21668		2.18	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9048	21737	34894	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9048	21737	34895	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9894	22544	35737	3.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid op32-2, erpC and erpD genes, complete cds; and unknown genes
10099	22747	35982	0.45	3.2E-01	BE326230.1	EST_HUMAN	h66905.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181589 3'
10210	22858		3.41	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
10566	23261	36498	3.94	3.2E-01	U06813.1	EST_HUMAN	EST047022 Fetal brain, Strabagene (cat836206) Homo sapiens cDNA clone HFB2221
12010	25317		3.91	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12392	25374		1.44	3.2E-01	BE86846.1	EST_HUMAN	601607820F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909532 5'
12524	24871		4.21	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12655	24955		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
12712	25354	30606	1.75	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2677	15386	28128	2.89	3.1E-01	R18051.1	EST_HUMAN	y60h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN):
2702	15532	28145	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2702	15532	28146	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2862	18630		1.29	3.1E-01	AW629036.1	EST_HUMAN	h4408.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3170	15933		3.35	3.1E-01	AB029059.1	NT	Mus musculus gene for Ser/Thr kinase KIAMRE exon 6
3887	16637	29276	0.8	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4908	17636	30250	0.73	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5390	18190	30882	9.73	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5513	18311	31212	0.73	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN H1236
5514	18312	31213	0.67	3.1E-01	Z74883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5524	18322		0.88	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5685	18478	31396	2.11	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6191	25087	31942	0.59	3.1E-01	R94322.1	EST_HUMAN	h41f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:198367 5'

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6374	19143	32140	1.34	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6439	19207	32203	1.01	3.1E-01	AI2644458.1	EST_HUMAN	q339d01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874689 3'
6593	19346	32360	3.91	3.1E-01	X71887.1	NT	H. sapiens gene for Immunoglobulin kappa light chain variable region A9 and A9
6873	25061	30545	2.41	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7579	20248	33354	0.77	3.1E-01	4883390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8546	21238	34381	1.71	3.1E-01	R45318.1	EST_HUMAN	y946f01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
8802	22453	35655	0.54	3.1E-01	6679322	NT	Mus musculus phosphatidylinositol 4-phosphate 5-kinase, type 1 gamma (Pip5K1c), mRNA
9897	22615	35818	1.05	3.1E-01	BF686639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281811 5'
9897	22615	35819	1.05	3.1E-01	BF686639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281811 5'
10029	22677	35893	1.74	3.1E-01	AI244001.1	EST_HUMAN	q61611.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGUTARYL-COA LYASE PRECURSOR (HUMAN);
10201	22849		0.63	3.1E-01	T55325.1	EST_HUMAN	y447h08.s1 Stratagene fetal spleen (4937205) Homo sapiens cDNA clone IMAGE:74967 3' similar to similar to gb:J01036_m02 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10741	23428	36672	1.26	3.1E-01	BF218117.1	EST_HUMAN	601893592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
11524	24124	37430	2.56	3.1E-01	7682291	NT	Homo sapiens KIAA0784 gene product (KIAA0784), mRNA
12133	24623		1.48	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12165	24647		3.03	3.1E-01	AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12304	24729		2.62	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12660	24960		3.46	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor 1GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
12699	25347		1.35	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Pglypr-pending), mRNA
70	15512	25533	2.01	3.0E-01	6795083	NT	Mus musculus protein kinase C, epsilon (PKce), mRNA
247	13056	25696	14.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1202	13954	26618	2.51	3.0E-01	AW300400.1	EST_HUMAN	xs6308.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1497	14244	26930	5.57	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding arial naturretic peptide
2132	14862	27592	1.2	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3206	15969		1.18	3.0E-01	AB030491.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3846	16597	29234	1.46	3.0E-01	AW817785.1	EST_HUMAN	PM1-S10262-261199-001-g01 S10262 Homo sapiens cDNA
4477	17212	29837	1.95	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding arial naturretic peptide
5267	18073	30702	7.22	3.0E-01	BE741629.1	EST_HUMAN	601504960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5349	18152	30833	0.77	3.0E-01	AF229247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds

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5417	18216	30924	3.94	3.0E-01	BE683575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5417	18216	30925	3.94	3.0E-01	BE683575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5453	18252	31142	4.77	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6732	18566	32598	3.08	3.0E-01	D16313.1	NT	Mouse cyclotaxin 15 genes, complete cds
6762	17831	30567	0.61	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
6827	19488	32510	0.85	3.0E-01	AF228247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds
7021	18713	32770	0.71	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7227	18912	32885	2.77	3.0E-01	10947007	NT	Mus musculus midbrain (Mdn-pending), mRNA
7400	20078	33159	1.37	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
7827	20522	33648	1.3	3.0E-01	AE001755.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
8271	20965		2.97	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3b), mRNA
8374	21067	34207	1.32	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
8728	21420	34564	0.51	3.0E-01	AF141876.1	NT	Streptomyces sulfonolactis isopenicillin N synthase (pcbC) gene, partial cds
8770	21462		0.8	3.0E-01	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9118	21806	34972	0.81	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dimnB) gene, complete cds; putative
9856	22506		43.84	3.0E-01	BE001128.1	EST_HUMAN	anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9868	22518	35714	1.25	3.0E-01	BF574612.1	EST_HUMAN	RC2-BN0074-240400-110-M2 BN0074 Homo sapiens cDNA
10042	22690	35908	0.49	3.0E-01	AF152598.3	NT	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10042	22690	35909	0.49	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetomcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10294	22941	36155	0.84	3.0E-01	AW118111.1	EST_HUMAN	Actinobacillus actinomycetomcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10296	22943	36157	1.88	3.0E-01	AB030231.1	NT	Xe03d10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2686035 3'
10316	22963	36179	0.73	3.0E-01	BF683841.1	EST_HUMAN	Aspergillus oryzae bipA gene for ER chaperone BIP, complete cds
10316	22963	36180	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4301087 5'
11772	24363	37694	1.95	3.0E-01	H51028.1	EST_HUMAN	602140133F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4301087 5'
11772	24363	37695	1.95	3.0E-01	H51028.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:184107 5'
12416	25302		2.52	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12693	25345		5.51	3.0E-01	6877768	NT	Mus musculus ribose 5-phosphate isomerase A (Ria), mRNA
2018	14753	27481	1.43	2.9E-01	AE000736.1	NT	Aquifex acidicus section 68 of 109 of the complete genome
2245	14973	27710	1.16	2.9E-01	AF222718.1	NT	Chrysodidymus synurobletus mitochondrion, complete genome
3246	16008	28658	2.73	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA

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3246	16003	28659	2.73	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3877	16627	26265	0.72	2.9E-01	AI610836.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2189412 3' similar to gb:D15050 NIL-2-A
4052	16797	29427	0.73	2.9E-01	AB016426.1	NT	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element ;
4064	16809		0.77	2.9E-01	AW002802.1	EST_HUMAN	Cavia porcellus mRNA for glutathione s-transferase, complete cds
4452	17188	29813	1.1	2.9E-01	AA284468.1	EST_HUMAN	wr02f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480385 3'
5177	17986		1.66	2.9E-01	R37485.1	EST_HUMAN	zs57d12.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701681 5' similar to contains Alu repetitive element
5310	19507	32532	0.79	2.9E-01	AF321001.1	NT	yf77e12.e1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5877	18471	31387	5.19	2.9E-01	X66098.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthase 2 mRNA, complete cds
5877	18471	31388	5.19	2.9E-01	X66098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase
5889	18482	31401	6.4	2.9E-01	6678662	NT	system polypeptides P16,18,28,30 and levanase
5885	18747	31708	1.47	2.9E-01	AA418145.1	EST_HUMAN	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase
6187	18984	31937	1.08	2.9E-01	AI797128.1	EST_HUMAN	system polypeptides P16,18,28,30 and levanase
6233	19007	31984	2.4	2.9E-01	U03420.1	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
6365	19135	32130	0.58	2.9E-01	R69194.1	EST_HUMAN	ze97b12.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6365	19135	32131	0.58	2.9E-01	R69194.1	EST_HUMAN	we27c06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1, L1 L1 repetitive element ;
6621	19383		0.56	2.9E-01	Z50156.1	NT	Bos taurus myosin I mRNA, complete cds
6890	17966	30523	1.52	2.9E-01	AF142329.1	NT	y38d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6996	19688	32737	2.95	2.9E-01	Q04399	SWISSPROT	y38d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
							D. discoideum gene for 34 kD actin binding protein
							Mus musculus Filh protein (Filh) gene, complete cds; and Lgfh protein (Lgfh) gene, partial cds
							PUTATIVE MULTICOPPER OXIDASE YDR606C
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bng1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1,3-galactosyl tr>
7059	19750	32813	2.06	2.9E-01	AF100956.1	NT	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7820	20516	33640	1.67	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7820	20515	33641	1.67	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8049	20743	33875	0.48	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8049	20743	33876	0.48	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8062	20756		0.94	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
8237	20931		0.49	2.9E-01	AF197456.1	NT	Buchnera aphidicola-plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3- isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8493	21185	34328	0.84	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901.3'
8823	21615	34660	1.02	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
8931	21622	34785	0.65	2.9E-01	M22452.1	NT	Baloon lymphocyte homing/adhesion receptor mRNA, complete cds
9145	21878	35040	0.78	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
9145	21878	35041	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
10810	23493	36728	1.93	2.9E-01	AF128943.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11114	23784	37089	1.75	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11114	23784	37090	1.75	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11575	24174	37489	1.59	2.9E-01	AA935373.1	EST_HUMAN	ny35h02.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:123779 similar to contains LTR8.12 LTR8 repetitive element
11579	24178	37493	3.55	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 5/6
11600	24199	37519	1.62	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11600	24199	37520	1.62	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12452	24821	31024	4.05	2.9E-01	AF092453.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12741	25007	30973	1.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
12741	25007	30974	1.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
555	13338		1.7	2.8E-01	U67138.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
560	13342		1.01	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1061	13819	26481	3.69	2.8E-01	AF168050.1	NT	Guinea guinea oocyte maturation factor Mos (c-mos) gene, partial cds
1254	14003	26671	1.62	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1254	14003	26672	1.62	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1268	14017	26684	1.34	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1651	14397	27087	1.11	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
1720	14463	27163	2.04	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT03864-120200-065-505 CT03864 Homo sapiens cDNA
2006	14742	27467	2.35	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586i2321_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586i2321
2127	14858	27588	1.41	2.8E-01	AW511195.1	EST_HUMAN	h444b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2475	15193	27933	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2475	15193	27934	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2549	15264		1.66	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2870	15380	28118	0.97	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2970	15736		1.29	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2971	15737	28386	2.04	2.8E-01	Z14037.1	NT	B. laurus microsatellite (ETH121)
2971	15737	28387	2.04	2.8E-01	Z14037.1	NT	B. laurus microsatellite (ETH121)
3373	16132	28788	1.13	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-694000 nt. position (477)

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3978	16726	29360	1.69	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 68 of 70) of the complete genome
4174	16914		1.95	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MIER22 repetitive element;
4422	17158	29789	0.99	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4427	17163	29783	2.31	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4772	17504	30126	1.19	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4777	17509	30131	2.87	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4808	17539	30162	1.23	2.8E-01	BF528188.1	EST_HUMAN	602042801F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4180129 5'
4828	17660	30182	1.91	2.8E-01	AI272669.1	EST_HUMAN	q150c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
5228	25084	30660	24.65	2.8E-01	AA349987.1	EST_HUMAN	EST157072 Infant brain Homo sapiens cDNA 5' end
5519	18317	31218	3.07	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5727	18519		0.95	2.8E-01	AW992583.1	EST_HUMAN	GM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
5848	18635		0.63	2.8E-01	AA404576.1	EST_HUMAN	z141f01.11 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element
6083	25418		0.65	2.8E-01	MA36698.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6123	18901	31869	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6123	18901	31870	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6632	19394	32409	8.34	2.8E-01	BF511215.1	EST_HUMAN	UI-HB14-act-f-04-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7341	20022		1.17	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7382	20062	33140	0.58	2.8E-01	X69980.1	NT	L. esculentum yst2 mRNA for GTP-binding protein
7991	20886	33811	1.28	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
7991	20886	33812	1.28	2.8E-01	A1346126.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8108	20802	33935	1.92	2.8E-01	U17251.1	NT	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8412	21105	34244	0.51	2.8E-01	AA911826.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8488	21180		7.34	2.8E-01	BF347847.1	EST_HUMAN	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5'
9366	21941	35115	0.92	2.8E-01	U17251.1	NT	qp48h01.x1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M87789 IG
9611	22264		0.88	2.8E-01	L13654.1	NT	GAMMA-1 CHAIN C REGION (HUMAN);
9788	22439	35646	0.66	2.8E-01	AF132728.1	NT	60202987F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4158525 5'
							Neurospora crassa negative regulator sulfur controller-2 (scn-2) gene, complete cds
							Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
							Escherichia coli translocated intrin receptor Tir (tir) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9788	22439	35647	0.66	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9850	22500	35700	0.52	2.8E-01	AF294393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b;
9950	22908	35813	3.35	2.8E-01	7706163	NT	nuclear gene for mitochondrial product
10211	22859		1.47	2.8E-01	9626154	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10251	22899	36109	0.6	2.8E-01	BE959727.2	EST_HUMAN	Fujinami sarcoma virus, complete genome
10644	23335	36573	2.42	2.8E-01	BF241082.1	EST_HUMAN	601654822R1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:3839765 3'
10644	23335	36574	2.42	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4109350 5'
10671	23382	36603	3.83	2.8E-01	BF605970.1	EST_HUMAN	601880794F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4109350 5'
10794	23477	36719	1.33	2.8E-01	AF051682.1	NT	601882148F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4076028 5'
11247	23909		4.51	2.8E-01	BF674023.1	EST_HUMAN	Drosophila melanogaster fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11593	24192	37510	17.65	2.8E-01	AL139074.2	NT	602137418F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4273853 5'
12406	24789		15.41	2.8E-01	DB3329.1	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
12509	24861	31013	4.22	2.8E-01	BE178699.1	EST_HUMAN	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12532	24877	31019	1.77	2.8E-01	BE900116.1	EST_HUMAN	PM4-HT0608-030400-001-a07 HT0608 Homo sapiens cDNA
12885	25306		2.52	2.8E-01		NT	601673020F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3955996 5'
12806	25401		1.49	2.8E-01	AW026400.1	EST_HUMAN	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
464	13249	25690	3.97	2.7E-01	Y17324.1	NT	wu98g05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2627928 3'
598	13377	26007	3.25	2.7E-01	AA450091.1	EST_HUMAN	Rattus norvegicus CDK104 mRNA
1238	13987	26654	2.13	2.7E-01	AB004906.1	NT	z339b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1671	14384		1.58	2.7E-01	X79815.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1722	14465	27164	3.5	2.7E-01	W58067.1	EST_HUMAN	G.lambila SR2 gene
1769	14511	27212	2.58	2.7E-01	P03341	SWISSPROT	z422h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
2131	15586		2.25	2.7E-01	AF047575.1	NT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2367	15089	27826	10.01	2.7E-01	Y13688.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2457	15175	27914	4.07	2.7E-01	A1310858.1	EST_HUMAN	Feline immunodeficiency virus env gene, isolate ITT0089PU (M88), partial
2899	15668	28314	1.2	2.7E-01	AF251276.1	NT	ta43c11.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element
2983	15749		2.53	2.7E-01	BF088284.1	EST_HUMAN	Mus musculus serine protease inhibitor 14 (Spr14) mRNA, complete cds
3283	16044	28693	0.68	2.7E-01	8393820	NT	GM1-HT0875-060900-385-a05 HT0875 Homo sapiens cDNA
3692	16740	28374	1.97	2.7E-01	A1928015.1	EST_HUMAN	Rattus norvegicus Insulin receptor (Insr), mRNA

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4002	16749	29380	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4002	16749	29381	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4008	16754	29384	2.12	2.7E-01	U77569.1	NT	Homo sapiens Digeorge syndrome critical region, telomeric end
4980	17703		2.85	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5011	17733	30339	2.53	2.7E-01	AA100856.1	EST_HUMAN	Zf90a01.1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gb:X65488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5011	17733	30340	2.53	2.7E-01	AA100856.1	EST_HUMAN	Zf90a01.1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gb:X65488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5185	17963	30509	2.39	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4)
5402	18202		0.85	2.7E-01	AB033171.1	NT	Astrocera myrtilphalma mitochondrial cyb gene for cytochrome b, partial cds
6249	19023	31985	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6249	19023	31996	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6515	19280	32282	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6515	19280	32283	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6681	19598	32637	2.23	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6916	19653	32699	0.58	2.7E-01	U15967.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
6952	19434		0.79	2.7E-01	A1540070.1	EST_HUMAN	h08h08.x1 NCL_OGAP_CLL1 Homo sapiens cDNA clone IMAGE:2076103 3'
7256	19940	33015	0.74	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
7461	20134	33225	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7461	20134	33226	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7686	20266	33363	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7586	20256	33364	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7638	20303	33411	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7638	20303	33412	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7694	20358	33472	0.71	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
7763	20458	33583	0.68	2.7E-01	AA013147.1	EST_HUMAN	ze35b1.1.s1 Soares retina N2b4-IR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element

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7925	20620		0.53	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8086	20780	33909	0.51	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:235113'
8190	20894	34022	0.8	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8657	21349	34494	0.59	2.7E-01	Q14764	SWISSPROT	MAJOR VAILT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8925	21616	34760	0.46	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9232	21911	35084	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9232	21911	35085	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9235	21914		2	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
9700	22351	35546	0.61	2.7E-01	D89660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9981	22629	35838	0.74	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10018	22666	35882	3.09	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-A1c isoform a (NF-A1c) mRNA, complete cds
10149	22797	36012	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, Intron 9
10149	22797	36013	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, Intron 9
10714	23403	36642	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10714	23403	36643	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10724	23412	36653	3.13	2.7E-01	AJ133289.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
11820	24406		1.5	2.7E-01	O14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C
12482	25180		1.49	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12665	24963		2.83	2.7E-01	AF217491.1	NT	Homo sapiens fragile T6D oxido reductase (FOR) gene, exon 6
12811	26054	30929	1.95	2.7E-01	AV742419.1	EST_HUMAN	AV742419 CB Homo sapiens cDNA clone CBMAXF02 5'
457	15542	25983	2.03	2.6E-01	P78411	SWISSPROT	IFROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
468	13254		1.38	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1372	14120	26795	1.65	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912345 5'
1417	14165	26948	1.14	2.6E-01	AB013280.1	NT	Glycine max pseudogene for Bd 30K
1889	14626	27335	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1889	14626	27336	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC 14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2086	14818		10.48	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2148	14878	27613	3.7	2.6E-01	MT1844.1	NT	
2476	15194		1.62	2.6E-01	Y12986.1	NT	B.martinius rbel gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2548	15263		8.87	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
3568	16323	28871	8.99	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3634	16387	29028	2.02	2.6E-01	AF228118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4079	16823	29449	0.96	2.6E-01	AW050510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4134	16876	29506	16.7	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-Q40400-132-803 BT0630 Homo sapiens cDNA
4324	17063	29691	1.2	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N87-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4459	17195	29821	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4459	17195	29822	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4511	17246	29881	1.46	2.6E-01	AA457617.1	EST_HUMAN	aa89407.11 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:338477 5'
4601	17336	29965	1.77	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lrca3-1) mRNA, complete cds
4697	17401	30035	1.18	2.6E-01	AF142703.1	NT	Ophrestia radiosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4910	17638	30252	0.95	2.6E-01	AF153350.1	NT	Mus musculus metalloproteinase disintegrin (Adam28) mRNA, complete cds
4914	17642	30257	3.6	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:152288 5'
5257	18063		1.06	2.6E-01	AB035972.1	NT	Paramecium caudatum gene for PAP, complete cds
5484	18283		0.68	2.6E-01	AB02398.1	EST_HUMAN	td16a03.x1 NCI CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element ;
5688	18481	31400	0.73	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor GHM enhancer 3 genes, partial cds; and unknown gp
5960	25417		2.35	2.6E-01	AE001811.1	NT	Thermococcus maritima section 123 of 136 of the complete genome
6108	18885	31854	2.26	2.6E-01	AF582557.1	EST_HUMAN	ts02e12.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
6108	18885	31855	2.26	2.6E-01	AF582557.1	EST_HUMAN	ts02e12.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
6328	19098	32086	0.91	2.6E-01	AL162767.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
6570	19334	32344	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836156 5'
6570	19334	32345	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836156 5'
6938	19673	32719	0.9	2.6E-01	AF194380.1	EST_HUMAN	wd48604.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);

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7289	19972	33050	0.62	2.6E-01	BE148961.1	EST_HUMAN	CMO-HT0245-031199-085-104 HT0245 Homo sapiens cDNA
7329	25110		0.79	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
7363	20044		0.69	2.6E-01	AA196149.1	EST_HUMAN	zp92a01.r1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:827672 5'
7639	20304	33413	1.9	2.6E-01	R10365.1	EST_HUMAN	yf37a03.s1 Scores fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:129004 3' similar to
7687	20351	33465	0.66	2.6E-01	Q09855	SWISSPROT	gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7748	20444	33566	1.3	2.6E-01	R02411.1	EST_HUMAN	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C28E8.01 IN CHROMOSOME I
7804	20499	33620	1.15	2.6E-01	BE144331.1	EST_HUMAN	yf82a07.r1 Scores fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:124212 5'
8040	20735	33867	0.64	2.6E-01	X82841.1	NT	MF0-HT0188-181199-003-d12 HT0188 Homo sapiens cDNA
8040	20736	33868	0.64	2.6E-01	X82841.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8232	20928	34064	3.05	2.6E-01	BF343588.1	EST_HUMAN	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8309	21003	34140	2.13	2.6E-01	Q10199	SWISSPROT	602014422F1 NCI CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150396 5'
8594	21286	34424	4.32	2.6E-01	BE830339.1	EST_HUMAN	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8594	21286	34425	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9367	21942	35116	0.96	2.6E-01	X17604.1	NT	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9639	22291		0.62	2.6E-01	AF057121.1	NT	S. occidentalis INV gene for Invertase (EC 3.2.1.26)
9768	22419	35626	1.19	2.6E-01	P87368	SWISSPROT	Lunba canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9768	22419	35627	1.19	2.6E-01	P87368	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
9930	22578		0.48	2.6E-01	U67581.1	NT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
10090	22738		0.74	2.6E-01	Q28295	SWISSPROT	Methanococcus jannaschii section 123 of 160 of the complete genome
10408	23052		0.9	2.6E-01	Y10196.1	NT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10467	23113		0.45	2.6E-01	AB015355.1	NT	Homo sapiens PHEX gene
11400	24006	37310	1.78	2.6E-01	P48280	SWISSPROT	Homo sapiens NRAMP2 gene for natural resistance-associated macrophage protein 2, complete cds
11511	24111		68.41	2.6E-01	X51755.1	NT	CELL DIVISION PROTEIN FTSW HOMOLOG
11996	24534		1.71	2.6E-01	10190655	NT	Human lambda-immunoglobulin constant region complex (germline)
12177	25309		3.1	2.6E-01	BE883491.1	EST_HUMAN	Mus musculus Jerky (Jrk), mRNA
12242	24693	31077	2.81	2.6E-01	AF316896.1	NT	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12665	24895		1.56	2.6E-01	D88425.1	NT	Homo sapiens NefK-ATPase gamma subunit (FYD2) gene, complete cds, alternatively spliced
12725	24996		2.19	2.6E-01	P47285	SWISSPROT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
234	13045	25684	2.55	2.5E-01	4502298	NT	HYPOTHETICAL PROTEIN MG039 Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
235	13045	26684	2.39	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
248	13057		3.32	2.5E-01	M26501.1	NT	Starfish (P. ochreaceus) cytoplasmic actin gene, complete cds
813	13584	26250	1.35	2.5E-01	U09984.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1038	13788		1.2	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1099	13857	26517	6.42	2.5E-01	T89837.1	EST_HUMAN	ye11g07.11 Stratiotes lung (#837210) Homo sapiens cDNA clone IMAGE:117488 5'
1509	14255	26841	0.9	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1721	14464		4.79	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCNA4) mRNA
1876	15581	27323	1.58	2.5E-01	BE686604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1878	15581	27324	1.58	2.5E-01	BE686604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2407	15128		16	2.5E-01	AE000675.1	NT	Aquifex acidicus section 7 of 109 of the complete genome
2500	15217		1.09	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
3370	16129		0.84	2.5E-01	BF688193.1	EST_HUMAN	602125525F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4282279 5'
3407	16165		3.04	2.5E-01	AW973471.1	EST_HUMAN	EST385464 MAGE resequences, MAGM Homo sapiens cDNA
3524	16280	26935	1.25	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3537	16293	28942	7.54	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3828	16579	29211	1.53	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3828	16579	29212	1.53	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4283	17022		0.97	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4700	17434		1.25	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (Mih)
4706	17438	30070	3.98	2.5E-01	AF007768.1	NT	Charistoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4732	17484	30101	2.01	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4751	17483		3.7	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4781	17513	30135	1.09	2.5E-01	BE898785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'
4987	17710	30315	0.71	2.5E-01	AW879588.1	EST_HUMAN	he62h11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041997 3' similar to WP:Y71P9A_294.D CE22858 ;
5243	18049	30678	13.48	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2830 nt]
5870	18657	31598	0.73	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5871	18658		0.98	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6529	19295	32299	0.95	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
6945	19427	32442	0.79	2.5E-01	8394138	NT	Rattus norvegicus rab3 (RABIN3), mRNA

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7252	19936	33011	0.88	2.5E-01	U13992.1	NT	Feline calicivirus CFI68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7278	19962		1.29	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7494	20167	33259	0.83	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7536	20206	33303	3.6	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7744	20440	33564	2.47	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7754	20450	33574	0.8	2.5E-01	BE908712.1	EST_HUMAN	60165391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8125	20819	33955	1.87	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
8266	20990	34128	0.7	2.5E-01	P04492	SWISSPROT	ETB PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8334	21226	34368	3.67	2.5E-01	H53236.1	EST_HUMAN	yq8407.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:202501 5'
8774	21466	34613	0.79	2.5E-01	M88626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9416	22094	35265	15.72	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9416	22094	35266	15.72	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9472	22081	35253	2.06	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9472	22081	35254	2.08	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9998	22646	35658	1.39	2.5E-01	AW581897.1	EST_HUMAN	RC3-ST0186-130700-015-a07 ST0186 Homo sapiens cDNA
10441	23087	36315	2.13	2.5E-01	AW152248.1	EST_HUMAN	xy40c10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element;
10444	23090	36319	1.21	2.5E-01	X58491.1	NT	Human mRNA for KIAA0124 gene, partial cds
11013	23685	36945	3.43	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
11647	24244		1.61	2.5E-01	AF027153.1	NT	Homo sapiens sodium/hydro-lyso-lipid cotransporter (SLC5A3) gene, complete cds
11803	24993	37727	1.29	2.5E-01	U46315.1	NT	Litomosoides sigmodontis microfilarial sheath protein SHP1a precursor (shp1a) gene, complete cds
11932	24490	37808	5.12	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
11960	25388		6.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12365	24768		1.37	2.5E-01	AF000003.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position (3/7)
12412	25233	30821	1.37	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUG mRNA, complete cds
540	13323	25955	1.69	2.4E-01	AA936316.1	EST_HUMAN	on70d04.r1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
828	13598	26269	3.34	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1281	14031	26700	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1281	14031	26701	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1363	14111	26785	1.03	2.4E-01	Y17263.1	NT	Homo sapiens FLJ-1 gene, partial
1843	14581		32.88	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1893	14630	27340	1.33	2.4E-01	AF251708.1	NT	Zaccys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2134	14884	27594	1.1	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2165	14894		1.44	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2258	14985	27725	2.28	2.4E-01	AE000680.1	NT	Aquifex aerolicus section 12 of 109 of the complete genome
2382	15104	27843	1.38	2.4E-01	BF002171.1	EST_HUMAN	7n23404.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2539	15254	27894	2.46	2.4E-01	Z36534.1	NT	O42588 26S PROTEASE REGULATORY SUBUNIT 6A ;
2765	15470	28213	2.18	2.4E-01	X71783.1	NT	D.discoideum (Ax3-K) ponA gene
2789	15494	28234	2.84	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
						NT	Bovine adenovirus 3 complete genome
3129	15694		2.94	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3145	15909	28554	1.48	2.4E-01	X74209.1	NT	H.sapiens AGT gene, PstI fragment of Intron 4
3743	16496	29131	0.73	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4010	18756		0.74	2.4E-01	D29960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4883	17610		1.09	2.4E-01	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
4989	17712	30317	0.98	2.4E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5375	18175	30865	0.98	2.4E-01	A1925707.1	EST_HUMAN	wc33405.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5375	18175	30866	0.98	2.4E-01	A1925707.1	EST_HUMAN	wc33405.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5397	18197	30891	0.8	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5569	18366	31275	8.16	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5597	18392		0.77	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5799	25076		0.99	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)
						EST_HUMAN	T15404.x1 NCL CGAP_B16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
						EST_HUMAN	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element
5805	18595	31520	2.22	2.4E-01	BF592336.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
5895	18680	31627	3	2.4E-01	AF035546.1	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
5999	18780	31741	2.53	2.4E-01	7661807	NT	Homo sapiens cDNA clone cDADE11 5'
6050	18830	31793	0.67	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cDADE11 5'
6441	19209	32206	2.23	2.4E-01	A1698989.1	EST_HUMAN	wc62-11.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03484
7243	19228	33004	9.5	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7404	20081	33163	0.55	2.4E-01	N48732.1	EST_HUMAN	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7625	20291	33400	0.91	2.4E-01	AF229044.1	NT	Y55c11.1 Soares multiple sclerosis 2NbrHNSP Homo sapiens cDNA clone IMAGE:277460 5'
8247	20941	34078	1.61	2.4E-01	AJ012585.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
						NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8497	21189	34332	1.02	2.4E-01	BF242794.1	EST_HUMAN	601877678F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
8552	21244		0.47	2.4E-01	BF878275.1	EST_HUMAN	602080188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9030	21720	34874	0.49	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9030	21720	34875	0.49	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9463	22013	35181	7.01	2.4E-01	AI693515.1	EST_HUMAN	wd43602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22.b1 TAR1 repetitive element;
9603	22256	35441	0.88	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
9603	22256	35442	0.88	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10337	22984	36202	1.68	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
10667	23359	36598	4.6	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
10739	23426	36671	1.39	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11158	23825		2.09	2.4E-01	Z21647.1	NT	P. asiatica mosaic virus genomic RNA
11840	24424	37765	1.32	2.4E-01	BE617638.1	EST_HUMAN	601441421T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845836 3'
11891	24461	37801	1.75	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12019	25160		2.34	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12080	24588		2.74	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
12287	25162		1.87	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12400	25201		2.06	2.4E-01	BF184542.1	EST_HUMAN	601842848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4063739 5'
12720	24992		3.66	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
380	13167	25810	1.06	2.3E-01	S75898.1	NT	aromatase [Poephila guttata-zabza finches, ovary, mRNA, 3188 nt]
622	13401		5	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
652	13430	26069	33.31	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
913	13680	26341	4.19	2.3E-01	BE311883.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1558	14305		1.12	2.3E-01	U22837.2	NT	Yersinia pestis HmsH (HmsH), HmsF (HmsF), HmsR (HmsR), and HmsS (HmsS) genes, complete cds
1599	14345	27035	1.23	2.3E-01	AJ245480.1	NT	Brassica napus sig gene for S-b locus glycoprotein, cultivar T2
1628	14374	27063	2.74	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2038	14772		1.51	2.3E-01	AJ235553.1	NT	Homo sapiens partial Intron 3 of the wild type AF-4/FEL gene
2447	15166	27903	2.66	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2657	15367	28105	1.59	2.3E-01	MT1319.1	NT	Human erythropoietin gene, complete cds
2827	14114	26789	3.38	2.3E-01	AB015033.1	NT	Mariellabla agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2963	15729	28379	1.36	2.3E-01	AA601379.1	EST_HUMAN	repetitive element contains element TH-R repetitive element;
3082	15847		7.07	2.3E-01	R21732.1	EST_HUMAN	yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
3363	16122	28780	1.14	2.3E-01	H68836.1	EST_HUMAN	jr97h10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3821	16573	29205	1.01	2.3E-01	S82821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3914	16684		5.22	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4316	17055	29680	1.1	2.3E-01	R82252.1	EST_HUMAN	jj1701.1 Soares placenta Nu2HP Homo sapiens cDNA clone IMAGE:149017 5'
4368	17106		1.98	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4417	17163	29784	1.03	2.3E-01	D80898.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4454	17190	29816	2.51	2.3E-01	AF082535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4517	17252	29887	6.19	2.3E-01	5031884	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4988	17111	30316	0.84	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5221	18028	30654	2.53	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5343	18146	30825	2.06	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NC1 CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476898 3' similar to SW:GAG SMSAV
5443	18242	31130	4.58	2.3E-01	X96687.1	NT	P03330 GAG POLYPROTEIN (CONTAINS: CORE PROTEIN P16; INNER COAT PROTEIN P12; CORE
5563	18360		0.94	2.3E-01	L39112.1	NT	SHELL PROTEIN P30; NUCLEOPROTEIN P10);
5665	18460	31374	0.76	2.3E-01	S60371.1	NT	C.familialis rom1 gene
5851	18638	31575	1.59	2.3E-01	A1708840.1	EST_HUMAN	Vitisformae cornum small subunit ribosomal RNA gene
5851	18638	31576	1.59	2.3E-01	A1708840.1	EST_HUMAN	23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
6558	19323	32330	0.93	2.3E-01	AF198089.1	NT	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
6778	19522	32549	4.33	2.3E-01	A1718148.1	EST_HUMAN	CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7011	19703	32759	1.08	2.3E-01	AF000227.1	NT	CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7188	19874	32947	0.9	2.3E-01	AF175389.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for
7315	19898	33077	3.14	2.3E-01	AF175389.1	EST_HUMAN	mitochondrial product
7318	20001	33079	0.64	2.3E-01	AF175389.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu
7318	20001	33080	0.64	2.3E-01	AF175389.1	EST_HUMAN	repetitive element
7508	20179		2.94	2.3E-01	6754778	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7513	20184	33278	1.38	2.3E-01	BE888071.1	EST_HUMAN	Secale cereale omega secalin gene, complete cds
7652	20316		2.73	2.3E-01	N80983.1	EST_HUMAN	Glycine max resistance protein LM17 precursor RNA, partial cds
7750	20446	33569	0.71	2.3E-01	AL181568.2	NT	AV719881 GLC Homo sapiens cDNA clone GLCDB08 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7892	20587	33717	2.16	2.3E-01	M88931.1	NT	Oxyfliche nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8391	21084	34217	0.47	2.3E-01	U57099.1	NT	Mus musculus prosaposin (psap)SGP-1) gene, complete cds
8671	21363	34510	0.56	2.3E-01	AW090541.1	EST_HUMAN	xc90606.x1 NCJ CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591554 3'
8786	21478	34627	0.45	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGE resequences, MACH Homo sapiens cDNA
9039	21729	34883	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST184061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9039	21729	34884	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST184061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9480	22133	35313	0.82	2.3E-01	6679318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
9609	22262	35448	0.82	2.3E-01	U77974.1	NT	Tribolium castaneum transcription factor homolog (Tc-ew) gene, complete cds
9628	22281	35471	0.5	2.3E-01	BE277890.1	EST_HUMAN	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
9682	22334	35529	0.59	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGE resequences, MACH Homo sapiens cDNA
9731	22382	35584	1.02	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
9767	22418	35625	0.56	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281299-001-f04 DT0036 Homo sapiens cDNA
9834	22485	35686	2.45	2.3E-01	BE173060.1	EST_HUMAN	MFO-HT0558-240400-014-g11 HT0559 Homo sapiens cDNA
9892	22542	35734	2.75	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10340	22987	36205	0.84	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22998		5.11	2.3E-01	BF133577.1	EST_HUMAN	601646155R2 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:4102092 3'
10937	23617	36867	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10937	23617	36868	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11144	23811	37092	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11144	23811	37093	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11324	24015	37318	3.03	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
11815	24403		1.75	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
11855	24439		1.33	2.3E-01	6008010	NT	Homo sapiens integrin, alpha 3 (enigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, mRNA
12004	24539		4.47	2.3E-01	U46426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12083	24593		4.88	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCOE44 5'
12120	24612		1.52	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
12173	25318	30711	2.88	2.3E-01	AW303623.1	EST_HUMAN	xx21d07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q8Z175
12206	25366	30613	8.63	2.3E-01	BE882464.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5,b2 TAR1 repetitive element;
12255	24701		2.51	2.3E-01	BF683319.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
							602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'

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12303	24728		2.35	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12398	24784		1.76	2.3E-01	U49945.1	NT	Pleurodeles walli distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12403	24728		1.55	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12647	24952		2	2.3E-01	BF475611.1	EST_HUMAN	hac38h12.x1 Lupskl_sclatic_nerve Homo sapiens cDNA clone IMAGE:3395960 3' similar to contains element MER38 repetitive element;
88	12914	25552	1.63	2.2E-01	AI052190.1	EST_HUMAN	cc14a10.x1 Soares_fetal_liver_INFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR-Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
1557	14304	26993	1.64	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
2082	14814	27547	2.52	2.2E-01	M34840.1	NT	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2402	15123	27860	6.3	2.2E-01	BF877538.1	EST_HUMAN	602085608F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249889 5'
2594	15308	28044	2.02	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3886190 5'
2594	15308	28045	2.02	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3886190 5'
2684	15651	28204	4.36	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-at12 HT0353 Homo sapiens cDNA
2884	15651	28295	4.36	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-at12 HT0353 Homo sapiens cDNA
2921	15687		1.57	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3387	16146		1.97	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3794	16546		1.12	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4105	16848		0.72	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4194	16935	29562	6.45	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4232	16973	29597	2.11	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4232	16973	29598	2.11	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4323	17082	29689	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4323	17082	29690	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4775	17507		1.36	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4779	17511	30133	2.1	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Stratiagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:848968 5'
4982	17705		1.1	2.2E-01	L13298.1	NT	Mus musculus vinculin gene, exon 3
5082	17781		0.93	2.2E-01	S57565.1	NT	histamine H2-receptor (H2R, Genomic, 1928 nt)
5140	17858	30474	2.64	2.2E-01	5835974	NT	Vidua chalybeata mitochondrion, complete genome
5659	18454	31368	2.07	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5669	18464		4.5	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
5910	18694	31646	0.56	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
5910	18694	31647	0.56	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6606	18369	32381	0.73	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
6928	19682	32708	10.21	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7028	19721	32777	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerate kinase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7029	19721	32778	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerate kinase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7191	19877	32950	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7191	19877	32951	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7388	20068	33144	0.63	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7628	20294	33402	0.66	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
7819	20614	33808	2.04	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
7987	20682	33808	1.01	2.2E-01	Z49633.1	NT	E. coli sepA and sepB genes
8449	21141	34279	0.54	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
8784	21486	34632	3.53	2.2E-01	AE001713.1	NT	Thermodesulfobacterium section 25 of 138 of the complete genome
8920	21611	34853	4.35	2.2E-01	AW85039.1	EST_HUMAN	PM8-CT0263-241289-009-507 CT0263 Homo sapiens cDNA
9013	21703	34952	1.45	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9098	21786	34952	1.04	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
9189	21859	35024	1.36	2.2E-01	W02988.1	EST_HUMAN	z94f08.t1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:291591 5'
9207	22086	35268	13.43	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9252	21931	35104	0.69	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (klp3)
9283	22017	35185	0.81	2.2E-01	M89643.1	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9276	22030	35200	3.95	2.2E-01	M89643.1	NT	Brachydanio rerio appendin beta and gamma chains (Epd) gene, complete cds
9521	22174	35358	0.58	2.2E-01	Q90980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
9715	22366	35564	3.4	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;
9853	22503	35703	1.85	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10076	22724	35941	0.95	2.2E-01	9625671	NT	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10232	22880	36092	0.6	2.2E-01	T59472.1	EST_HUMAN	Human herpesvirus 5, complete genome
10232	22880	36093	0.5	2.2E-01	T59472.1	EST_HUMAN	y63dd08.t1 Stratagene ovary (#637217) Homo sapiens cDNA clone IMAGE:76855 5'
							Pseudomonas aeruginosa quinolone protein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinone synthesis A (pqoA) genes, complete cds; and pyrroloquinone
10288	22816	36126	0.58	2.2E-01	AF068264.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10341	22888		0.61	2.2E-01	AF071001.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10387	23033	36247	0.6	2.2E-01	AE001592.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10387	23033	36248	0.6	2.2E-01	AE001592.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10520	23166	36394	0.48	2.2E-01	AF049720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 11 and AS
11070	23740	37014	1.56	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11164	23831	37110	1.46	2.2E-01	AB021083.1	NT	TT virus ORF1 gene, isolate TS4-II, partial cds
11399	24005	37309	4.83	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11438	23205	36437	5.22	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
11935	24493		1.66	2.2E-01	BE870959.1	EST_HUMAN	601446957F1NH_MGC_66 Homo sapiens cDNA clone IMAGE:3850670 5'
12040	25380		2.21	2.2E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
12123	24815		2.19	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12225	17904	30591	3.87	2.2E-01	AW361098.1	EST_HUMAN	RC1-C70249-14199-021-g04 C70249 Homo sapiens cDNA
12226	24881		1.6	2.2E-01	AW681922.1	EST_HUMAN	h17b02.x1 NCL_OGAP_GLI1 Homo sapiens cDNA clone IMAGE:2972523 3'
12731	25371		2.58	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAHB02 5'
950	13716	26382	2.12	2.1E-01	AA568289.1	EST_HUMAN	nm31e11.s1 NCL_OGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
953	13718	26384	0.77	2.1E-01	AL181504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1102	13659		2.75	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1176	13929	26593	1.15	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1176	13929	26594	1.15	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1906	14643	27353	2.07	2.1E-01	AA906824.1	EST_HUMAN	ok73e02.s1 NCL_OGAP_GC4 Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02765
2152	14882	27616	4.2	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2485	15596	27942	1	2.1E-01	H73968.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2485	15596	27943	1	2.1E-01	H73968.1	EST_HUMAN	yu04f07.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:232837 3'
2556	16270	28005	0.91	2.1E-01	AF022814.1	NT	yu04f07.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:232837 3'
2925	15691	28335	2.3	2.1E-01	6912445	NT	Fugu rubripes transcription factor (SLP-1) and heme-oxygenase genes, complete cds
3786	16538		6.08	2.1E-01	8838361	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
4032	16777	29408	1.1	2.1E-01	P11675	SWISSPROT	Beta vulgaris mitochondrion, complete genome
4032	16777	29409	1.1	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4343	17082	29904	1.77	2.1E-01	AB033041.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4537	17272	29904	1.23	2.1E-01	AB010273.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
5013	17734	30341	1.4	2.1E-01	Q01338	SWISSPROT	Homo sapiens pahpa47 gene, complete cds
							ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)

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5090	17609	30425	1.09	2.1E-01	AE001526.1	NT	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
5218	18026	30650	6.24	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4293001 5'
6787	19531	32559	1.4	2.1E-01	AJ223392.1	NT	Drosophila melanogaster 16S rRNA gene, partial cds
6798	19459	32481	1.92	2.1E-01	U04942.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7306	19889	33065	0.65	2.1E-01	Q01958	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7306	19889	33066	0.65	2.1E-01	Q01958	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7317	20000		2.38	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7606	20272	33380	1.94	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
7651	20315	33425	1.22	2.1E-01	AF068897.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7651	20315	33426	1.22	2.1E-01	AF068897.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7671	20666		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b3), mRNA
8400	21093	34229	4.44	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemoglobin processing protein (hmcC), putative ABC transporter (hmcB), putative haemoglobin structural protein (hmcA), and haemoglobin immunity protein (hmcE) genes, complete cds
8696	21388	34531	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
8696	21388	34532	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
8857	21548		0.45	2.1E-01	AB022524.1	NT	Homo sapiens APC1 gene, exon 9
8935	21626	34768	5.58	2.1E-01	Z85788.1	NT	Saccharomyces cerevisiae chromosome II reading frame ORF YBL025W
9404	22066	35237	0.57	2.1E-01	N42538.1	EST_HUMAN	Y11010.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270954 5'
9404	22066	35238	0.57	2.1E-01	N42538.1	EST_HUMAN	Y11010.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270954 5'
9413	22091	35262	2.31	2.1E-01	X97376.1	NT	A.thaliana mRNA for ARA1BP1b protein
9518	22171	35354	1.13	2.1E-01	AB038529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8
10227	22875	36098	1.47	2.1E-01	Z87087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10258	22906	36116	2.5	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10264	22912	36122	0.97	2.1E-01	BF574254.1	EST_HUMAN	802131427F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4270831 5'
11554	24153		2.19	2.1E-01	11038647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11572	24171	37487	1.59	2.1E-01	BE180422.1	EST_HUMAN	RC9-HT0822-040500-013-b11 HT0822 Homo sapiens cDNA
11870	24944		1.38	2.1E-01	X57624.1	NT	Drosophila melanogaster ALA-E8 DNA, repeat region
12377	24775		2.07	2.1E-01	AF217490.1	NT	Homo sapiens fragile 18D alpha reductase (FOR) gene, exons 8, 9, and partial cds
12578	25287		1.47	2.1E-01	L32588.1	NT	Human granulosa gene
12635	24936		1.42	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3915675 5'

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12758	25019	30960	1.79	2.1E-01	BE672330.1	EST_HUMAN	7a59d02.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:3223034 3'
195	13008	26550	2.43	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avana, complete cds
521	13305		3.11	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
683	13458	26103	1.24	2.0E-01	M77085.1	NT	O.cuniculus germline IgH heavy chain V-H pseudogene, alleotype VHa2
782	13564	26225	2.19	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
991	13753	26414	1.09	2.0E-01	D80905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1103	13860	26519	2.47	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1232	13981	26651	1.77	2.0E-01	AJ132695.5	NT	Homo sapiens rec1 gene
1285	14035	26706	1.63	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-281289-002-c06 HT0422 Homo sapiens cDNA
1443	14190		1.52	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1470	14217	26804	14.63	2.0E-01	AB007874.1	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1544	14280	26977	1.97	2.0E-01	AB007874.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1550	14296	26983	1.01	2.0E-01	AF260700.1	NT	Homo sapiens sodium/folate symporter mRNA, partial cds
1692	14436	27132	1.4	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1712	14455		1.67	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1752	14494		4.33	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1853	14620	27328	1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1883	14620	27330	1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2347	15070		1.63	2.0E-01	X82877.1	NT	H.s.sapiens Nat-D-glucose cotransport regulator gene
							xp15002.x1 NCL_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3555	16310		0.71	2.0E-01	AW238005.1	EST_HUMAN	MER21 repetitive element
3693	16447	28087	0.89	2.0E-01	P34641	SWISSPROT	CED-11 PROTEIN
3822	16574	28206	1.12	2.0E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3936	16886	28327	0.76	2.0E-01	Z46906.1	NT	Sus scrofa
4528	17263		8.49	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
4979	17702	30309	5.26	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
							HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP
5009	16237	28893	0.8	2.0E-01	P46607	SWISSPROT	PROTEIN ATHB-10)
5359	18161	30845	2.63	2.0E-01	X56600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5655	18450	31363	1.94	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5750	18542	31464	0.76	2.0E-01	X91856.1	NT	F.rubripes DNA encoding for valyl-RNA synthetase
5989	18751	31712	6.3	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Halp (HAL5) mRNA, complete cds
6081	18860		0.73	2.0E-01	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
6192	18968	31943	0.79	2.0E-01	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR

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6335	19105	32094	3.2	2.0E-01	X61033.1	NT	Mauritius mu class glutathione transferase gene
6435	19203	32200	4.02	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141089-001-g06 CT0247 Homo sapiens cDNA
7194	19880	32854	1.28	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (PfkC) gene, exons 3 through 7
7345	20026	33102	0.68	2.0E-01	P54422	SWISSPROT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
7875	20339	33452	0.84	2.0E-01	V00726.1	NT	Mouse germ line gene coding for beta-globin (Y2)
7853	20548		5.8	2.0E-01	AF028026.1	NT	Andes virus strain O23133 glycoprotein G1 and G2 precursor, gene, partial cds
8100	20794	33925	2.95	2.0E-01	X61151.1	NT	M.musculus sep2 gene exon 14
8624	21316		0.99	2.0E-01	BE552247.1	EST_HUMAN	G01344648F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3877794 5'
9251	21930	35103	0.82	2.0E-01	U82511.1	NT	Dicystostelium discoideum random slug cDNA19 protein (res19) mRNA, partial cds
9290	21957	35129	0.68	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9456	22006		4.97	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9646	22298	35493	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9646	22298	35494	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9791	22442		2.11	2.0E-01	AF146692.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9941	22589	35792	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
9941	22589	35793	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10067	22715	35933	0.68	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10067	22715	35934	0.68	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10114	22762		0.68	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (heppel)
10305	22952	36167	2.78	2.0E-01	X87121.1	NT	R.norvegicus mRNA for NTR2 receptor
10744	23431	36674	1.56	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
10744	23431	36675	1.56	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11609	24207	37530	1.4	2.0E-01		NT	Chlorella vulgaris chloroplast, complete genome
11609	24207	37531	1.4	2.0E-01		NT	Chlorella vulgaris chloroplast, complete genome
12358	24762		1.51	2.0E-01	AF206837.2	NT	Pimphales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12545	25210		1.39	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12556	25139	30894	1.38	2.0E-01	AW975297.1	EST_HUMAN	EST1387405 MAGE resequences, MAGN Homo sapiens cDNA
12594	24950	30985	3.58	2.0E-01	A023592.1	EST_HUMAN	ov80a10.31 Sceres testis NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12618	24924		2.88	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
12753	25014	30978	1.87	2.0E-01		NT	Mus musculus fructosamine 3 kinase (Fn3K) mRNA
108	12928		3.9	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arlt1) mRNA
342	13143	25781	6.86	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
641	13420	26058	1.43	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
641	13420	26058	1.43	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
648	13427	26066	5.97	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-001 BT0502 Homo sapiens cDNA
649	13427	26066	8.46	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-001 BT0502 Homo sapiens cDNA
665	13730			1.73	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (IL2rg), mRNA
1092	13840	26499	13.43	1.9E-01	AA358813.1	EST_HUMAN	EST167784 Fetal lung II Homo sapiens cDNA 5' end
1349	14097	26772	1.76	1.9E-01	AF081282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1414	14162		2.51	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rpb-2) gene, complete cds
2380	15102	27841	3.61	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2923	15689	28333	3.43	1.9E-01	U66066.1	NT	Signodan hispidus p53 gene, partial cds
2939	15704		5.68	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3002	15768	28417	0.95	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3390	16149	28803	4.28	1.9E-01	D13197.1	NT	Mouse gene for Immunoglobulin diversity region D1
3473	16228	28883	4.44	1.9E-01	R16467.1	EST_HUMAN	Y42710.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128547 5'
3818	18568	29189	1.33	1.9E-01	P39768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3973	18722	29356	3.15	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4063	18908	29438	1.28	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-011 CT0315 Homo sapiens cDNA
4206	16947	29573	1.09	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-004 FN0010 Homo sapiens cDNA
4950	17877		1.05	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5517	18315		4.88	1.9E-01	AW130149.1	EST_HUMAN	x29a07.x1 NCL_CGAP_UH Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5558	18355	31265	7.87	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5749	18541	31463	0.7	1.9E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5795	18586		2.56	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6235	19009	31985	0.75	1.9E-01	A1762391.1	EST_HUMAN	w154402.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2394099 3'
6294	19067	32050	1.03	1.9E-01	AW148452.1	EST_HUMAN	x14c08.x1 NCL_CGAP_Kd8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
6876	17652	30548	1.69	1.9E-01	R43212.1	EST_HUMAN	Yg08a12.s1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MIER13 repetitive element;
6900	19638	32682	0.69	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
6900	19638	32683	0.69	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7160	19847	32917	0.62	1.9E-01	U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7391	20070	33149	1.38	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7436	20113	33201	3.11	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
7885	20580	33709	1.46	1.9E-01	AL161567.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8686	21278	34417	10.77	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1186 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8844	21536	34681	1.24	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
8844	21536	34682	1.24	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9775	22426	35632	0.81	1.9E-01	AA912486.1	EST_HUMAN	cb96g10.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element;
10142	22790	36005	0.85	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10142	22790	36008	0.85	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10540	23237	36470	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10540	23237	36471	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10655	23346	36583	2.09	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10986	23661	36915	1.34	1.9E-01	AA912480.1	EST_HUMAN	cb9602.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537487 3' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element ;
10986	23661	36916	1.34	1.9E-01	AA912480.1	EST_HUMAN	cb9602.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537487 3' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element ;
11487	24088	37399	1.53	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel I mRNA, complete cds
11726	24320	37645	2.77	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11752	24343	37673	1.6	1.9E-01	L07344.1	NT	Influenza A/Guangdong/243772 nucleoprotein (seg 5) gene, 5' end
11847	24431	37772	1.3	1.9E-01	AF287263.1	NT	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
12399	24785		1.67	1.9E-01	AF055600.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
30	12858	25475	2.61	1.8E-01	U73200.1	NT	Mus musculus p118Rip mRNA, complete cds
253	15539	25700	0.9	1.8E-01	AB022090.1	NT	Mus musculus Ccig gene for chaperonin containing TCP-1 gamma subunit, partial cds
361	13159	25802	1.76	1.8E-01	4502632	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	13503	26158	1.01	1.8E-01	AB021480.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
961	13726	26390	0.94	1.8E-01	A1912212.1	EST_HUMAN	wd7102.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337061 3'
1059	13826	26485	1.63	1.8E-01	AF000580.1	NT	Dicotyledon discoidium plasmid Ddp6, complete genome
1266	14015	26683	8.26	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1492	14239	26925	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1492	14239	26926	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1839	14577		1.2	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1859	14597		1.58	1.8E-01	A1733708.1	EST_HUMAN	q922d10.x5 NCL_CGAP_Kd3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:076938 OT5936 GAMMA BUTYROBETAINE HYDROXYLASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1908	14645	27355	1.75	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2697	15406		2.36	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2898	15665		1.89	1.8E-01	AF184588.1	NT	Junctidum scale LEAFY protein (LEAFY2) gene, partial cds
2904	15670	28319	1.28	1.8E-01	AW182300.1	EST_HUMAN	X41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3121	15886	28526	1.76	1.8E-01	AW985178.1	EST_HUMAN	QV0-BN0041-070300-147-g04 BN0041 Homo sapiens cDNA
3610	16363	29005	0.88	1.8E-01	H03369.1	EST_HUMAN	Y45e01.s1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3610	16363	29008	0.88	1.8E-01	H03369.1	EST_HUMAN	Y45e01.s1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4299	17038		1.43	1.8E-01	D37854.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4519	17254	29888	5.94	1.8E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4721	17453	30087	2.9	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4754	17488	30114	0.94	1.8E-01	X92179.1	NT	S. tuberosum mRNA for alcohol dehydrogenase
4884	17707	30311	2.03	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151298-112-g06 ST0203 Homo sapiens cDNA
4999	17722	30325	1.06	1.8E-01	AI792382.1	EST_HUMAN	en28g07.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5035	17754	30367	4.68	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholeate cotransporting polypeptide mRNA, partial cds
5718	18510	31431	0.82	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5835	18624	31558	0.68	1.8E-01	N28629.1	EST_HUMAN	Yx38n08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:264063 5'
6037	18817	31777	1.18	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6419	19187	32185	1.15	1.8E-01	Q9QY14	SWISSPROT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6463	19230		2.06	1.8E-01	N94853.1	EST_HUMAN	FORKHEAD BOX PROTEIN E3
6906	19644	32889	1.18	1.8E-01	AB018561.1	NT	Yy62n02.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:278163 5'
6906	19844	32890	1.18	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7346	20027	33103	0.7	1.8E-01	AP001511.1	NT	Citullus lanatus mRNA for wsus, complete cds
9242	21921	35091	1.23	1.8E-01	M73258.1	NT	Bacillus halodurans genomic DNA, section 5/14
9274	22028	35198	1.22	1.8E-01	9626232	NT	Human cellular DNA/human papillomavirus proviral DNA
9391	22053		0.5	1.8E-01	AA463751.1	EST_HUMAN	Bacteriophage Ite, complete genome
9473	22126	35305	0.94	1.8E-01	P15272	SWISSPROT	nh02a05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1 repetitive element
							AMP NUCLEOSIDASE

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9473	22126	35306	0.94	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9514	22167	35349	0.91	1.8E-01	M26019.1	NT	S.commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9514	22167	35349	0.91	1.8E-01	M26019.1	NT	S.commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9679	22331	35526	0.75	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9683	22335	35530	0.77	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 80 of 150 of the complete genome
10033	22681						Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10266	22914	36124	0.78	1.8E-01	AF200252.1	NT	
10333	23230	36465	1.48	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
			3.08	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10577	23272	36508	7.28	1.8E-01	U38908.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysin genes, complete cds
10637	19644	32689	2.61	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wus, complete cds
10637	19644	32690	2.61	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wus, complete cds
10638	23329	36567	5.69	1.8E-01	AF019107.1	NT	Dicystostellum discoideum unknown (DG1041) gene, complete cds
10942	23621	36870	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11439	23206	36438	4.04	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
11787	24358	37691	3.45	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Txra2), mRNA
11967	24514		1.59	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12025	24593	31111	2.04	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12476	24839		3.26	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12585	24908		1.91	1.8E-01	R24494.1	EST_HUMAN	yh48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12628	24931		2.3	1.8E-01	Y11114.1	NT	E.dispar mRNA for hexokinase (hbk1)
12745	25324		1.61	1.8E-01	X16635.1	NT	Rattus norvegicus CaBP9k gene
563	13345	25972	1.57	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
787	13559	26221	2.32	1.7E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
941	13708		2.21	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1036	13796	26455	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolyhedrovirus, complete genome
1036	13796	26456	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolyhedrovirus, complete genome
1974	14710		2.6	1.7E-01	AF255061.1	NT	Homo sapiens BNIIP3H (BNIIP3H) gene, complete cds; nuclear gene for mitochondrial product
2863	15631	28275	2.28	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds

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2863	15631	28276	2.29	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds
2927	15683	28338	1.55	1.7E-01	AA336909.1	EST_HUMAN	EST141651 Endometrial tumor Homo sapiens cDNA 5' end
2995	15761	28409	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra cbc-1 gene, exons 1-3
2995	15761	28410	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra cbc-1 gene, exons 1-3
3103	15868	28508	1.24	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3439	16195	28845	1.74	1.7E-01	AJ266505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3595	16348	28989	1.04	1.7E-01	AJ224877.1	NT	Homo sapiens hap1 gene, complete CDS
3616	16369		0.92	1.7E-01	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3918	16688	29309	4.84	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4522	17257		1.69	1.7E-01	X52838.1	NT	Schistosoma gregaria alpha repetitive DNA
4787	17518	30140	1.08	1.7E-01	AJ247835.1	EST_HUMAN	qh57609.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element
5054	17773		1.11	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (se) gene, complete cds
5122	17840	30456	0.75	1.7E-01	D37951.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5323	18126	30785	2	1.7E-01	AA470886.1	EST_HUMAN	ne13402.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5323	18126	30786	2	1.7E-01	AA470886.1	EST_HUMAN	ne13402.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5506	18304	31205	0.62	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6237	19011	31988	13.23	1.7E-01	H72118.1	EST_HUMAN	ys02606.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6293	19066	32048	0.97	1.7E-01	AJ370876.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6293	19066	32049	0.97	1.7E-01	AJ370876.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6753	17922	30557	0.65	1.7E-01	BE300286.1	EST_HUMAN	60084406771 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860248 3'
6780	18524		2.28	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
6902	19640		0.83	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7120	19808	32874	1.1	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sekel-VT2 prophage inserted region
7197	19893	32957	8.8	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7380	20060	33139	1.37	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HPLF0 PROTEIN)
7386	25112	33153	0.71	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
7760	20456	33590	1.32	1.7E-01	AF000573.1	NT	Homo sapiens homogametic 1,2-dioxygenase gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7863	20558	33884	0.62	1.7E-01	AF150899.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8175	20869	34001	6.19	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8175	20869	34002	6.19	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8598	21290	34431	0.47	1.7E-01	AW992873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8628	21320	34462	2.08	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
8743	21435	34580	0.75	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
8743	21435	34581	0.75	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9066	21755	34916	0.48	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9066	21755	34917	0.48	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9480	22143	35323	7.85	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9597	22250	35435	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST389584 IMAGE resequences, MAGO Homo sapiens cDNA
9597	22250	35436	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST389584 IMAGE resequences, MAGO Homo sapiens cDNA
9615	22268	35455	3.14	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9708	22359	35555	0.63	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10133	22781		2.4	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10293	22940	36154	1.4	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10295	22942	36156	1.72	1.7E-01	AA627872.1	EST_HUMAN	nc60607.s1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081
10501	23147		0.45	1.7E-01	AL161542.2	NT	TRANSFORMING PROTEIN RHOC (HUMAN);
10579	23274	36511	8.78	1.7E-01	BE390835.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42
10709	23398	36637	2.65	1.7E-01	AA814817.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
11055	23725	36995	9.13	1.7E-01		NT	of43a03.s1 NCI_CGAP_CNST Homo sapiens cDNA clone IMAGE:1428924 3'
11055	23725	36996	9.13	1.7E-01	7106300	NT	Mus musculus adenomatous polyposis coli binding protein Eb1 (Eb1), mRNA
11146	23813	37098	1.62	1.7E-01	Y08391.1	NT	Mus musculus adenomatous polyposis coli binding protein Eb1 (Eb1), mRNA
11348	24038	37341	1.69	1.7E-01	AA883375.1	EST_HUMAN	S. pombe pop1+ gene
11712	24307		1.83	1.7E-01	P16272	SWISSPROT	al45f09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480287 3'
11746	24337	37663	1.62	1.7E-01	P55899	SWISSPROT	AMP NUCLEOSIDASE
11746	24337	37664	1.62	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FORN) (NEONATAL FC RECEPTOR)
11874	24453	37789	2.62	1.7E-01	11418157	NT	IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN
12000	25320		1.95	1.7E-01	AL163278.2	NT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FORN) (NEONATAL FC RECEPTOR)
							IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN
							Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
							Homo sapiens chromosome 21 segment HS21C078

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1268	25167		1.65	1.7E-01	AB24404.1	EST_HUMAN	68905.x1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12552	24889	30996	10.27	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
122	12940	25582	2.38	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
684	15518	26081	1.51	1.6E-01	R31497.1	EST_HUMAN	Y17512.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1493	14240	26927	1.16	1.6E-01	AA548863.1	EST_HUMAN	nt28d12.st NCL CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014839 3'
1512	14258	26944	3.92	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1917	14654	27364	1.86	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1977	14713		1.51	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2363	15593	27844	1.35	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2497	15214	27957	1.4	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2894	15661	28307	10.17	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2894	15661	28308	10.17	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3624	16377	29018	1.21	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3624	16377	29019	1.21	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3682	16730		2.49	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 83 of the complete chromosome
4294	17033	29661	9.42	1.6E-01	AF176680.1	NT	Homo sapiens apelin gene, complete cds
4423	17159		3.07	1.6E-01	AW968601.1	EST_HUMAN	EST380677 IMAGE resequences, MAGJ Homo sapiens cDNA
4431	17167		4.35	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cdc8), mRNA
4669	17596	30219	0.7	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
4892	17619	30237	1.38	1.6E-01	AA098343.1	EST_HUMAN	284109.x1 Stralagene cdon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:221955
4911	17639	30253	1.54	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
4911	17639	30254	1.54	1.6E-01	AJ006356.1	NT	Lycopodium obscurum Real fragment 2, satellite region
5303	18108	30768	0.99	1.6E-01	L40608.1	NT	Lycopodium obscurum Real fragment 2, satellite region
5435	18234	30947	2.95	1.6E-01	AW197496.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5435	18234	30948	2.95	1.6E-01	AW197496.1	EST_HUMAN	XM43101.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:075984 075984
5447	18246	31134	2.15	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
5938	18720	31679	0.83	1.6E-01	BE925803.1	EST_HUMAN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6162	18939	31909	0.71	1.6E-01	BF183584.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6162	18939	31910	0.71	1.6E-01	BF183584.1	EST_HUMAN	601809725R1 NIH MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'

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6334	19104	32092	2.37	1.0E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6334	19104	32093	2.37	1.0E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6685	19802	32841	0.55	1.0E-01	AA398047.1	EST_HUMAN	288404.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:729511 5'
6867	17044	30639	5.32	1.0E-01	AW281215.1	EST_HUMAN	UI-H-B12-egl-B-08-O-UI.st NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7676	20340	33453	1.66	1.0E-01	AW246359.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7703	20366		0.74	1.0E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'
7768	20464	33589	1.81	1.0E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7924	20619		0.51	1.0E-01	BE244087.1	EST_HUMAN	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8018	20713	33844	0.87	1.0E-01	U38243.1	NT	Bacteroides vulgatus beta-lactamase (cfxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
8530	21222	34364	0.88	1.0E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2987771 to 3213410
8725	21417	34561	0.63	1.0E-01	R13673.1	EST_HUMAN	y60008.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
8831	21523		0.59	1.0E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
8870	21561	34708	1.72	1.0E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9009	21699		0.83	1.0E-01	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9551	22204		2.09	1.0E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA
9554	22207	35391	1.7	1.0E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9589	22242		0.97	1.0E-01	BE155684.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
10553	23249	36486	3.3	1.0E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111189-028-G01 CT0220 Homo sapiens cDNA
10918	23598	36845	1.59	1.0E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10918	23598	36846	1.59	1.0E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10923	23603	36852	1.55	1.0E-01	BE259649.1	EST_HUMAN	601145783.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11059	23729		4.28	1.0E-01	AF106084.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11388	23994	37286	7.28	1.0E-01	6071552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
11706	24301		1.26	1.0E-01	BF527237.1	EST_HUMAN	602039495.F2 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4177073 5'
11886	25331		1.64	1.0E-01	6079466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
12002	24538	37273	5.28	1.0E-01	AV719685.1	EST_HUMAN	AV719685 GLC Homo sapiens cDNA clone GLCEMF07 5'
12292	24721	31052	1.72	1.0E-01	L14833.1	NT	Rat convertase PC5 mRNA, 5' end
12321	24740		1.5	1.0E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_L1LT0074 Homo sapiens cDNA
12418	25149		287.76	1.0E-01	AB045310.1	NT	Cucumis sativus KS mRNA for anti-kaurine synthase, complete cds
12574	24901		2.4	1.0E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds

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12681	24961		1.72	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12687	24973	30992	1.7	1.6E-01	9508522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
12798	25048		1.52	1.6E-01	BF672698.1	EST_HUMAN	602152004F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4293145 5'
241	13050	25689	1.4	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA
241	13050	25690	1.4	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA
573	15517		9.31	1.5E-01	AV711688.1	EST_HUMAN	AV711688 DCA Homo sapiens cDNA clone DCAADH08 5'
766	13539	26198	1.09	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1070	13828	26487	1.01	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1075	13833	26491	2.75	1.5E-01	AJ251895.1	NT	Homo sapiens partial SLG22A2 gene for organic cation transporter (OCT2), exon 1
1091	13849		1.42	1.5E-01	L36125.1	EST_HUMAN	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1194	13948	26610	0.82	1.5E-01	AW195518.1	NT	xi39d11.x1 NCI_CGAP_Ki611 Homo sapiens cDNA clone IMAGE:2696085 3'
1252	14001	26668	2.96	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1252	14001	26669	2.96	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1465	14212	26901	1.86	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (MekK1) mRNA, complete cds
1901	14638	27347	1	1.5E-01	AW444451.1	EST_HUMAN	UJ-H-B13-akb-b-09-0-UJ s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2716	15423	28162	1.98	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4247537 5'
2914	15680		1.15	1.5E-01	AW572516.1	EST_HUMAN	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3048	15814	28459	0.74	1.5E-01	O78687	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3347	16106	28761	5.06	1.5E-01	AA935049.1	EST_HUMAN	0668405.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3361	16120	28777	0.82	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
3361	16120	28778	0.82	1.5E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3738	16491	29126	2.11	1.5E-01	U08984.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3752	16504	29140	0.74	1.5E-01	7108358	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3848	16599	29236	2.55	1.5E-01	AW665883.1	EST_HUMAN	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
4028	16773	29405	1.1	1.5E-01	AW366659.1	EST_HUMAN	h10f06.x1 Soares_NFL_T_08C_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
4161	16801	29630	8.35	1.5E-01	AL163284.2	NT	RC2-HT0149-191099-012-c08 HT0149 Homo sapiens cDNA
4676	17410	30046	1.57	1.5E-01	BF687665.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4703	15423	28162	1.92	1.5E-01	BF695391.1	EST_HUMAN	602083269F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4068223 5'
5132	17650	30467	1.55	1.5E-01	Z72808.1	NT	602083269F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4247537 5'
							S.cerevisiae chromosome VII reading frame ORF YGL086w

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5146	17864	30480	1.05	1.5E-01	AF056313.1	NT	Morone saxatilis gonadotropin-releasing hormone type II gene, complete cds
5176	17984	30499	2.16	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5203	18011	30632	1.15	1.5E-01	AF256852.1	NT	Canian crocodilus MHC class II beta chain (helibeta) gene, complete cds
5245	18051		6.92	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5451	18250	31139	5.08	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5492	18291	31188	8.42	1.5E-01	U85016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5492	18291	31189	8.42	1.5E-01	U85016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5915	18700	31653	3.09	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5915	18700	31654	3.09	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5932	18734	31693	1.93	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6102	18880	31847	3.1	1.5E-01	BE727658.1	EST_HUMAN	601584322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6152	18929		1.77	1.5E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6231	19025	31959	2.09	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds, and neuraminidase gene, partial cds
6409	25089	32176	2.21	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6437	19205	32201	4.99	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6448	19216	32214	1.95	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6493	19259	32260	2.35	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6585	19348	32361	1.25	1.5E-01	AA714760.1	EST_HUMAN	nm30d10.s1 NCI CGAP GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6612	19375	32389	1.66	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6882	17968	30554	6.82	1.5E-01	AW970295.1	EST_HUMAN	EST382378 IMAGE resequences, MAGK Homo sapiens cDNA
6918	25102		0.79	1.5E-01	AA811545.1	EST_HUMAN	cb7302.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element
7115	19803		2.07	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7280	19973	33051	2.96	1.5E-01	AF973167.1	EST_HUMAN	wf52c08.xt NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3'
7490	20162	33254	2.04	1.5E-01	AF290073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7490	20162	33255	2.04	1.5E-01	AF290073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7499	20171	33262	2.04	1.5E-01	AW500611.1	EST_HUMAN	ULHF-BN0-akk-d05-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7499	20171	33263	2.04	1.5E-01	AW500611.1	EST_HUMAN	ULHF-BN0-akk-d05-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7640	20305	33414	0.81	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds
7957	20652	33775	0.96	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8118	20812	33947	1.13	1.5E-01	AA970317.1	EST_HUMAN	cc85g12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M28062
8211	20905		0.95	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8299	20993		11.54	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8332	21025	34162	1.8	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-528H09 5'
8491	21183	34325	1.65	1.5E-01	D84476.1	NT	Pangasinanodon gigas growth hormone (GH) mRNA, complete cds
8512	21204		0.71	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8737	21429	34575	1.16	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9002	21692	34842	2.88	1.5E-01	N74226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9092	21781	34945	1	1.5E-01	BF586465.1	EST_HUMAN	za58e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866 3' similar to
9100	21788		2.3	1.5E-01	AV754819.1	EST_HUMAN	PIR:S44443 S44443 RAD23 protein homolog 2 - human ;
9305	21972		0.74	1.5E-01	AU130007.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9353	20424	33543	7.32	1.5E-01	U00455.1	NT	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
							AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
							Acipenser transmontanus vitellogenin mRNA, partial cds
9717	22968	35566	0.53	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase 5-delta - 4-delta isomerase gene, complete cds
9821	22472	35674	7.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
9821	22472	35675	7.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10103	22751	35965	2.92	1.5E-01	X98852.1	NT	P. lentusculus mRNA for integrin beta subunit
10207	22855	36070	2.16	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_P722 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
							GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10207	22855	36071	2.16	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_P722 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10285	22833	36148	2.01	1.5E-01	U40932.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10438	23084	36311	1.43	1.5E-01	AJ011964.1	NT	Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds
10438	23084	36312	1.43	1.5E-01	AJ011964.1	NT	Glaviceps purpurea ps1 gene
10595	23289	36526	1.62	1.5E-01	BE088492.1	EST_HUMAN	Glaviceps purpurea ps1 gene
10595	23289	36527	1.62	1.5E-01	BE088492.1	EST_HUMAN	GM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10726	23414	36654	7.31	1.5E-01	AL163280.2	NT	GM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10726	23414	36655	7.31	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10896	23576		1.7	1.5E-01	AB042975.1	NT	Homo sapiens chromosome 21 segment HS21C080
11012	23684	36944	1.6	1.5E-01	AW841915.1	EST_HUMAN	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
							IL5-CN0024-030300-025-D04 GN0024 Homo sapiens cDNA
11057	23727	36999	1.95	1.5E-01	AA425488.1	EST_HUMAN	zw46d02.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773091 5' similar to
							contains element MER22 repetitive element;

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11119	19973	33051	1.56	1.5E-01	AI973157.1	EST_HUMAN	wf5208.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
11625	24222		1.56	1.5E-01	AI189704.1	EST_HUMAN	q672e01.x1 Soares_Fetal_Lung_NHL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to
11959	25202		11.07	1.5E-01	BF700582.1	EST_HUMAN	gb1M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12320	24739		1.37	1.5E-01	AF030358.2	NT	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12324	24743		1.77	1.5E-01	AJ238332.1	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
							Mus musculus mRNA for death inducer-obliterat-1 (Dlc-1)
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12369	24771		5.35	1.5E-01	AB026988.1	NT	
12385	25220		9.97	1.5E-01	RB3077.1	EST_HUMAN	y878d04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
12472	25241		2.53	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA004 5'
12573	25150	30897	9.2	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 1/6
12783	25036	30965	1.89	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
292	13088		1.72	1.4E-01	AF009683.1	NT	Homo sapiens T cell receptor beta locus, TORBV85SP to TORBV21S2A2 region
890	13659		3.62	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-methyltransferase, complete cds)
1236	13985		2.48	1.4E-01	T91864.1	EST_HUMAN	y54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1742	14484		1.5	1.4E-01	6878980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1745	14487	27186	1.71	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1898	14635		0.96	1.4E-01	AW135741.1	EST_HUMAN	UI-H-B11-acf-a-09-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1978	14714		9.33	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2478	15198	27835	1.38	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPA1)
2795	15500	28241	4.23	1.4E-01	AI833486.1	EST_HUMAN	wm74d01.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3879	16629	29267	0.96	1.4E-01	R59232.1	EST_HUMAN	y977d03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41467 5'
3879	16629	29268	0.96	1.4E-01	R59232.1	EST_HUMAN	y977d03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41467 5'
4153	16895	29524	8.69	1.4E-01	AI699094.1	EST_HUMAN	b56c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4153	16895	29525	8.69	1.4E-01	AI699094.1	EST_HUMAN	b56c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4212	16953	29577	3.73	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
5014	17735	30342	0.94	1.4E-01	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5223	18030	30656	5.48	1.4E-01	T90677.1	EST_HUMAN	y15c11.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:117812 3'
5246	18052	30679	4.6	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5246	18052	30680	4.6	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6205	18980	31959	3	1.4E-01	BE326891.1	EST_HUMAN	h67d02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135338 3'
6391	19160	32160	5.6	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6391	19160	32161	5.6	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6477	19244	32244	3.14	1.4E-01	AW082766.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'

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6490	19257		1.64	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6509	19274	32275	2.45	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA
7026	19718		0.65	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hary2) Homo sapiens cDNA clone DKFZp761A0910 5'
7284	19967		1.51	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-aat-c-09-Q-JLs1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7521	20192	33283	1.19	1.4E-01	UB5645.1	NT	Oryctolagus cuniculus fructose 1,6 biphosphatase aldolase (AldB) gene, complete cds
7653	20317	33427	0.98	1.4E-01	A1305192.1	EST_HUMAN	ql90b12.x1 Soares NIH-MPc S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8373	21066		1.23	1.4E-01	AV69047.1	EST_HUMAN	AV658047 GLC Homo sapiens cDNA clone GLCFSH08 3'
8683	21376		0.57	1.4E-01	AI436083.1	EST_HUMAN	th92b12.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:002710 O02710 GAG POLYPROTEIN. ;
8811	21503	34650	4.18	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8892	21583	34722	0.59	1.4E-01	AW023636.1	EST_HUMAN	df68b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9021	21711	34864	0.97	1.4E-01	R62746.1	EST_HUMAN	y10105.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9021	21711	34865	0.97	1.4E-01	R62746.1	EST_HUMAN	y10105.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9085	21774	34938	0.81	1.4E-01	BF310559.1	EST_HUMAN	601895465F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4124824 5'
9175	21845	35011	1.24	1.4E-01	W03411.1	EST_HUMAN	z094a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
9246	21925	35095	0.46	1.4E-01	X73293.1	NT	M. vanilleii genes rpoH, rpoB and rpoA
9246	21925	35096	0.46	1.4E-01	X73293.1	NT	M. vanilleii genes rpoH, rpoB and rpoA
9258	21937	35111	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9258	21937	35112	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9350	20421	33541	1.96	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase la (IAL), and zinc finger protein (DNZ1) genes, complete cds
9704	22355	35551	0.97	1.4E-01	X66092.1	NT	C. parvifrons ORF for putative membrane transport protein
9887	22537	35732	1.26	1.4E-01	AF023813.1	NT	Macromitrium levalium small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
9888	22638	35846	0.58	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
9888	22636	35847	0.56	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22805	36022	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-a08 ST0218 Homo sapiens cDNA
10157	22805	36023	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-a08 ST0218 Homo sapiens cDNA
10360	23007		0.57	1.4E-01	T84293.1	EST_HUMAN	y474d03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111365 5'
10499	23145	36372	0.62	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21); from 2599451 to 2812870
10607	23301		1.64	1.4E-01	AA811480.1	EST_HUMAN	ae99a03.s1 NCI CGAP_GCBT Homo sapiens cDNA clone IMAGE:1320364 3'
10746	23433	36676	3.24	1.4E-01	R53400.1	EST_HUMAN	y170c05.r1 Soares breast 2NBHBS1 Homo sapiens cDNA clone IMAGE:154088 5'
10964	23631	36879	1.31	1.4E-01	AW104882.1	EST_HUMAN	xt73e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11036	23707	36976	1.3	1.4E-01	T96102.1	EST_HUMAN	ye17g10.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5'
11036	23707	36976	1.3	1.4E-01	T96102.1	EST_HUMAN	ye17g10.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5'
11038	23709	36979	2.35	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-6) (CD49E)
11262	23924	37216	1.66	1.4E-01	X68092.1	NT	C. perfringens ORF for putative membrane transport protein
11301	19967		1.41	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-aat-c-09-0-U1.s1 NCL CGAP Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11446	23213	36445	2.37	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11512	24112		1.82	1.4E-01	X62102.1	NT	M. musculus p16K gene for 16 kDa protein
11743	24335	37661	1.83	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; pPILP (Tpilp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pht27) gene, complete cds; and HBAR (Hbar) gene, complete cds
11827	24411	37747	1.31	1.4E-01	AW684572.1	EST_HUMAN	h14h08.x1 NCL CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2872319 3'
11827	24411	37748	1.31	1.4E-01	AW684572.1	EST_HUMAN	h14h08.x1 NCL CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2872319 3'
12213	25172	30904	1.98	1.4E-01	AB000890.1	NT	Ephydrata fluviatilis mRNA for aldolase, partial cds
12261	24706	31049	2.03	1.4E-01	X74773.1	NT	P. salina plasmid gene secY
12275	24714		2.2	1.4E-01	11988117	NT	Rattus norvegicus desmin (Des), mRNA
12318	25383		2.84	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3634329 5'
12413	24794		1.35	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
12425	24801		2.97	1.4E-01	D84004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002865
12500	25407		3.15	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12708	25221		8.26	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
12779	25033		2.37	1.4E-01	AW377998.1	EST_HUMAN	MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
314	13118	25756	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
314	13118	25757	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
518	13300	26932	2.8	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
621	13400	26035	1.05	1.3E-01	AJ277608.1	NT	Human calcitriol receptor (HJNLV/Girlington/93/JUK RNA for capsid protein (ORF2), strain HJNLV/Girlington/93/JUK
621	13400	26036	1.05	1.3E-01	AJ277608.1	NT	Human calcitriol receptor (HJNLV/Girlington/93/JUK RNA for capsid protein (ORF2), strain HJNLV/Girlington/93/JUK
824	13594	26264	0.92	1.3E-01	X63330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
874	13643	26313	1.8	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1005	13765	26425	1.31	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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1105	13862		2.8	1.3E-01	AL115285.1	NT	Bovine chitorea strain T4 cDNA library under conditions of nitrogen deprivation
1193	13945	26609	1.13	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1425	14172		1.18	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein GMS mRNA, complete cds
1850	14588	27303	0.97	1.3E-01	6880957	NT	Mus musculus procollagen, type XI, alpha 1 (Caf11a1), mRNA
1952	14687	27400	2.18	1.3E-01	AL117078.1	NT	Bovine chitorea strain T4 cDNA library under conditions of nitrogen deprivation
2167	14696		1.22	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA9 and pucC genes and ORF151
2288	15013		1.2	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2379	15101		3.34	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2592	15308	28042	4.76	1.3E-01	M86018.1	NT	Carassius auratus keratin type I mRNA, complete cds
3065	15831	28474	1.01	1.3E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3443	16199	28849	0.98	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3669	16718		1.43	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4117	16859		1.27	1.3E-01	AF020713.1	NT	Bacteriophage SPB-c2 complete genome
4137	16879		4.24	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-038-a03 DT0018 Homo sapiens cDNA
4145	16887	29518	2.03	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4163	16903	29532	18.52	1.3E-01	AW273741.1	EST_HUMAN	xv23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4257	16998	29627	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4257	16998	29628	0.99	1.3E-01	AV752278.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4279	17018		12.76	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4445	17181	29806	0.77	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4497	17233	29863	2.68	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2980063 5'
4963	17688		0.74	1.3E-01	BF091980.1	EST_HUMAN	RC4-TN0077-180900-012-c05 TN0077 Homo sapiens cDNA clone h607508.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5242	18048	30877	0.83	1.3E-01	AW46988.1	EST_HUMAN	L1 repetitive element;
5278	18083	30739	2.23	1.3E-01	AW804417.1	EST_HUMAN	QVQ-UM0083-100400-189-a08 UM0083 Homo sapiens cDNA
5414	18213		0.77	1.3E-01	AF107793.1	NT	Emeticella nidulans DNA-dependent RNA polymerase II RPB2 gene, partial cds
5497	18295		0.75	1.3E-01	AF056980.1	NT	Hepatitis C Virus 68 CL10 genome polyprotein gene, partial cds
5638	18433	31346	0.97	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
5896	18681	31828	0.57	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4177283 5'
5896	18681	31629	0.57	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4177283 5'
6392	19161	32162	15.12	1.3E-01	AE031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6474	19241	32241	1.95	1.3E-01	X88891.1	NT	C. jacchus intron 4 of visual pigment gene (red allele)
6691	19608		0.75	1.3E-01	W26387.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6914	19851		0.99	1.3E-01	BF629560.1	EST_HUMAN	602044345F1 NCI CGAP_Bmt7 Homo sapiens cDNA clone IMAGE:4181866 5'
7162	19849		1.96	1.3E-01	H48664.1	EST_HUMAN	y33402r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:207075 5'
7859	20554		0.88	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
7873	20568	33694	1.34	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
7902	20597	33727	1.17	1.3E-01	BF680522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298074 3'
8136	20830		0.51	1.3E-01	BE562528.1	EST_HUMAN	601335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688934 5'
8172	20868	33998	0.84	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8243	20837		4.47	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8285	20979		4.44	1.3E-01	8823919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8426	21119	34258	1.02	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298074 3'
8847	21538	34683	0.58	1.3E-01	R11172.1	EST_HUMAN	y339g11.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP-RL2B RAT P29316 60S RIBOSOMAL PROTEIN
8847	21538	34684	0.58	1.3E-01	R11172.1	EST_HUMAN	y339g11.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP-RL2B RAT P29316 60S RIBOSOMAL PROTEIN
9119	21807	34973	0.61	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9119	21807	34974	0.61	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9372	21947	35120	3.71	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
9671	22923		0.56	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
9951	22598		0.99	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
10030	22878	35894	0.85	1.3E-01	AW851599.1	EST_HUMAN	MR2-CT0222-201089-001-e01 CT0222 Homo sapiens cDNA
10291	25128	36151	1.1	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10423	23069	36290	0.84	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10471	23117	36347	0.52	1.3E-01	AW247836.1	EST_HUMAN	2820837.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820837 3'
10528	23225		2.93	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
10775	23458	36701	1.56	1.3E-01	H01883.1	EST_HUMAN	y332d09.r1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:150449 5'
11039	23710	36880	1.33	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11216	23879		3.28	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Ctf2), mRNA
11304	23963	37263	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11304	23963	37264	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11589	24188	37504	4.26	1.3E-01	BE278449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11723	24317	37640	1.94	1.3E-01	BE618384.1	EST_HUMAN	601473369F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
11755	24346	37678	1.44	1.3E-01	BF683555.1	EST_HUMAN	602139760F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300863 5'
12114	24607	31088	1.37	1.3E-01	BE618346.1	EST_HUMAN	601482741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3666003 5'

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12247	24695		4.43	1.3E-01	AJ242790.1	NT	Gallus gallus scyl1 gene for lymphocytin, exons 1-3
12274	24713		1.51	1.3E-01	Z13994.1	NT	R. norvegicus crp2 gene for cystatin related protein 2
12606	24915		1.43	1.3E-01	AB026829.1	NT	Ephydraia fluviatilis mRNA for SALK-6, complete cds
12636	24936		2.26	1.3E-01	AW001114.1	EST_HUMAN	wu24409.x1 Soares, Dieckgraefe, colon, NHCD Homo sapiens cDNA clone IMAGE:2520877 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN. ;
374	13199	25844	8.42	1.2E-01	AI421744.1	EST_HUMAN	h59502.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_ma1 ANNEXIN V (HUMAN);
415	12826		1.05	1.2E-01	U66812.1	NT	Dicystotellum discoideum ORF DG1016 gene, partial cds
534	13317		4.33	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1355	14103	26778	3.22	1.2E-01	AU149148.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1355	14103	26779	3.22	1.2E-01	AU149148.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1362	14110		4.36	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaA.B11 5'
1496	14243		1.23	1.2E-01	AA897474.1	EST_HUMAN	ak4809.s1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480584 3' similar to TR:Q16671 Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1627	14373	27082	1.26	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1646	14392	27082	2.81	1.2E-01	AI285402.1	EST_HUMAN	q66909.x1 NCI_CGAP_Ecd2 Homo sapiens cDNA clone IMAGE:1960553 3'
1762	14504		20.17	1.2E-01	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
1913	14650		1.03	1.2E-01	AW448388.1	EST_HUMAN	U1-H-B18-akt-e-10-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2181	14910	27642	1.75	1.2E-01	BF248490.1	EST_HUMAN	601821567F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4046224 5'
2284	15009	27748	1.2	1.2E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2597	15311	28047	1.49	1.2E-01	AW066556.1	EST_HUMAN	QV3-BN0046-220300-128-f10 BN0046 Homo sapiens cDNA
							is18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1]; contains element PTR5 repetitive element ;
2731	15438	28176	1.12	1.2E-01	AI623388.1	EST_HUMAN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2847	15615	28262	1.3	1.2E-01	U18018.1	NT	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2903	15669	28318	2.5	1.2E-01	AI720470.1	EST_HUMAN	Human creatine kinase-B mRNA, complete cds
2935	15701	28350	2.92	1.2E-01	M16364.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3004	15770	28418	0.97	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3224	15987	28641	1.59	1.2E-01	AW370668.1	EST_HUMAN	QV1-BT0259-261089-021-d05 BT0259 Homo sapiens cDNA
3252	16014		1.12	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3472	16228		0.8	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3511	16267	28921	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3511	16267	28922	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3592	16228		1.46	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
4160	16900	29528	1.97	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4160	16900	29529	1.97	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4672	17406	30041	1.1	1.2E-01	Z48183.1	NT	L. esculentum mRNA for glycylase-1
						NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
4739	17471		0.92	1.2E-01	AF221633.1	NT	my63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282850 3'
5170	17979	30492	0.81	1.2E-01	AA744369.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5217	18026	30649	1	1.2E-01	AF223391.1	NT	z008d02.r1 Scores_peratyrroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5227	18034	30659	2.59	1.2E-01	W33035.1	EST_HUMAN	Homo sapiens gene encoding plakophilin (exons 1-13)
5284	18089	30749	2.3	1.2E-01	Z98266.1	NT	M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
5418	18217	30828	0.68	1.2E-01	Z48234.1	NT	601493181FT NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3895613 6'
6107	18884	31853	1.93	1.2E-01	BE620845.1	EST_HUMAN	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6153	18930	31898	1.36	1.2E-01	P10842	SWISSPROT	IL0-CT0031-221098-113-404 CT0031 Homo sapiens cDNA
6206	18981	31960	2.35	1.2E-01	AW845276.1	EST_HUMAN	Mouse galactosyltransferase mRNA, complete cds
6270	19043	32020	1.54	1.2E-01	M26925.1	NT	mx85c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289024 3'
6337	19107	32097	0.57	1.2E-01	AA747535.1	EST_HUMAN	602023112F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158386 5'
6550	19315	32321	1.14	1.2E-01	BF347985.1	EST_HUMAN	JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
6700	19616	32668	0.56	1.2E-01	AF295739.1	NT	PM3-BN0137-290300-002-09 BN0137 Homo sapiens cDNA
7793	20488		1.4	1.2E-01	BE007072.1	EST_HUMAN	wc89g03.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
7862	20557	33683	4.36	1.2E-01	A1913753.1	EST_HUMAN	Q99736 MICROSOMAL GLUTATHIONE S-TRANSFERASE II ;
7906	20601	33731	0.57	1.2E-01	Q02369	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (G-B22)
8208	20902	34037	0.73	1.2E-01	A1832681.1	EST_HUMAN	a171b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
						EST_HUMAN	xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8285	20989		10.29	1.2E-01	AW083652.1	EST_HUMAN	
8315	21008		3.34	1.2E-01	AF063772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8354	21047	34184	0.99	1.2E-01	J03968.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8354	21047	34185	0.98	1.2E-01	J03966.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8499	21191		1.09	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
8589	21281		1.49	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome

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8023	21315		0.62	1.2E-01	X16191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9471	22080	35252	2.93	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
9906	22555	35750	1.59	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
10611	23305	36543	1.38	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
10801	23484		2.17	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10989	23672		3.18	1.2E-01	BE962324.2	EST_HUMAN	601955578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11094	23764		1.58	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11220	23883	37168	2.61	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNA1 (DNAI1) gene, exon 17
11283	23944	37238	1.65	1.2E-01	R40249.1	EST_HUMAN	y80c02 s1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:28880 3'
11492	24093		1.67	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11892	24462		2.53	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFB12 3'
12230	24683		3.52	1.2E-01	AL27136.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
12305	25351	30605	2.87	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW138) (CD136 ANTIGEN)
12417	24796		3.16	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12418	13317		3.19	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12525	24872		2.11	1.2E-01	X53981.1	NT	R.nervosus NF68 gene for 88kDa neurofilament
12586	25364	30611	1.44	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
12610	24917	31007	5.86	1.2E-01	AL299903.1	EST_HUMAN	gn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12632	24932		2.83	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12638	25289		7.95	1.2E-01	Q66433	SWISSPROT	CYCLIN T
12663	24962	30689	1.39	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 83 of the complete chromosome
12800	16228		1.81	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
12812	25372	30614	1.38	1.2E-01	9845282	NT	Mus musculus protein (16kDa) similar to human SYK interacting protein (p16K), mRNA
551	13334	25964	0.8	1.1E-01	AL561003.1	EST_HUMAN	h18d08.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2167883 3'
601	13379	26010	1.65	1.1E-01	AA599006.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb-X06983_rna1
1032	13792	26452	2.03	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1063	13921		1.3	1.1E-01	AL161560.2	NT	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1138	15661	26552	4.62	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1227	13977	26648	3.01	1.1E-01	D64004.1	NT	EST384142 MAGL Homo sapiens cDNA
1511	14257	26943	2.52	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002865
2312	15037		1.85	1.1E-01	6755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
							Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2540	15530		1	1.1E-01	6979876	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2572	15286		1.17	1.1E-01	AW821908.1	EST_HUMAN	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
3030	15786	28442	0.82	1.1E-01	F03265.1	EST_HUMAN	HSC1R022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3336	16098		1.78	1.1E-01	8753231	NT	Mus musculus calcium channel, voltage-dependent, I type, alpha 1G subunit (Ca α 1g), mRNA
3415	16173	28822	2.11	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3444	16200	28850	1.21	1.1E-01	X62135.1	NT	C. reithardti nuclear gene on linkage group XIX
3570	16325	28972	0.77	1.1E-01	Y07695.1	NT	A. limnerus gene for transposase
3688	16441		0.74	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3696	16450	29089	1.47	1.1E-01	X52708.1	NT	G. gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4050	16833	29456	1.28	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4090	16833	29457	1.28	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4226	16967		8.78	1.1E-01	AF157066.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4254	16995	29624	0.77	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4594	17328	29958	0.96	1.1E-01	S44957.1	NT	Tapa-1=Integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4780	17512	30134	1.2	1.1E-01	Y07695.1	NT	A. limnerus gene for transposase
4957	16839		0.85	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
5077	17796	30412	1	1.1E-01	P70281	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 3 (SCP-3 PROTEIN)
5584	18381		1.4	1.1E-01	AA747216.1	EST_HUMAN	rx76a03.s1 NC1_CGAP_Evrl Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5653	18448	31361	1.23	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5687	18480	31399	0.58	1.1E-01	AL110985.1	NT	Bairya's chinea strain T4 cDNA library under conditions of nitrogen deprivation
5745	18537	31459	1.81	1.1E-01	X68851.1	NT	S. pombe sls8 gene encoding protein kinase
5781	18572	31500	5.31	1.1E-01	MB6533.1	NT	Providencia rettgeri penicillin G amidase gene
5938	18718	31678	1.67	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
5955	18737	31696	1.75	1.1E-01	BE769152.1	EST_HUMAN	PM3-F70024-130800-004412 FT0024 Homo sapiens cDNA
5975	18757	31719	9.4	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280599-011-e01 CT0254 Homo sapiens cDNA
6330	19100	32088	0.67	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6338	19108	32098	1.25	1.1E-01	AF035746.1	EST_HUMAN	AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL 43
6381	19150	32149	0.72	1.1E-01	AI216307.1	EST_HUMAN	qg78d08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6512	19277	32278	3.71	1.1E-01	O68635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6604	18367		3.03	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds

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6697	19814	32855	2.81	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6948	19430	32445	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
6948	19430	32446	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7087	25423		0.89	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:4050653 5'
7203	25107	32984	0.84	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (87)
7435	20112	33199	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4302019 5'
7435	20112	33200	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4302019 5'
7555	20225	33329	1.93	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7595	20283	33371					ah31506.s1 Soares_parityoid_tumor_Nb-IPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
7898	20563	33690	3.35	1.1E-01	AA788784.1	EST_HUMAN	CHROMOGHRANIN A PRECURSOR (HUMAN);
8107	20801	33833	0.5	1.1E-01	U67492.1	NT	Methanococcus jannaschii section 34 of 150 of the complete genome
8107	20801	33834	1.7	1.1E-01	AA483574.1	EST_HUMAN	nt04910.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8153	20847	33979	1.15	1.1E-01	X91233.1	NT	nt04910.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8193	20887		1.14	1.1E-01	AW817618.1	EST_HUMAN	H.sapiens IL15 gene
8248	20843	34081	1.45	1.1E-01	AL134348.1	EST_HUMAN	PM1-ST0270-080200-001-009 ST0270 Homo sapiens cDNA
							DKFZp547P194.1 547 (synonym: hbf1) Homo sapiens cDNA clone DKFZp547P194 5'
							Pedococcus acidilactici H plasmid pSMB74 pediocin AcH production (pap) gene cluster papA, papB, papC and papD genes, complete cds
8717	21409	34552	2.08	1.1E-01	U02482.1	NT	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element
8810	21602	34649	0.88	1.1E-01	A1807474.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
8906	21597	34739	0.47	1.1E-01	AF050031.1	NT	zp93b12.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
8941	21632	34775	2.04	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
8941	21632	34776	2.04	1.1E-01	AA192153.1	EST_HUMAN	P.furiosus partial dph5 gene and argF gene
9033	21723	34877	0.74	1.1E-01	Y12727.1	NT	yd18n03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to
9083	21762	34912	2.04	1.1E-01	T72676.1	EST_HUMAN	gb.M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9090	21778		0.6	1.1E-01	BE883280.1	EST_HUMAN	601436972F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3822048 5'
9322	21989		0.88	1.1E-01	BE142305.1	EST_HUMAN	GM3-HT0142-271089-026-q11 HT0142 Homo sapiens cDNA
9396	22058		2	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-q08 GN0027 Homo sapiens cDNA
9810	22461		0.5	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10017	22665		0.45	1.1E-01	BE315509.1	EST_HUMAN	601140231F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3049543 5'
10106	22764		1.57	1.1E-01	R80590.1	EST_HUMAN	y98a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
10235	22883	36096	1.26	1.1E-01	U60528.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10708	15796	28442	2.05	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'

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10840	23622		2.76	1.1E-01	AF169032.1	NT	Cerastus auratus activin beta A precursor, mRNA, complete cds
10974	23650	36903	3.91	1.1E-01	R23708.1	EST_HUMAN	Y13512.1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:131769 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
10983	23658	36911	1.39	1.1E-01	6981351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfk), mRNA
11002	18480	31399	1.31	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11134	23802	37079	1.58	1.1E-01	X70058.1	NT	M.musculus cyclidine gene
11169	23836	37117	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
11169	23836	37118	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
11277	23938	37230	2.81	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11674	24269		1.65	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
11990	24529		1.36	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.11 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
12098	24598		3.92	1.1E-01	BE767023.1	EST_HUMAN	RG2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
12341	25160		1.97	1.1E-01	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850604 3'
12780	25012	30977	3.15	1.1E-01	BF239753.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1179	13932		2.74	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1249	13998	26665	2.63	1.0E-01	AI985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_K411 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
1371	14119	28794	1.95	1.0E-01	AL181504.2	NT	MER7 repetitive element;
2493	15210	27952	1.11	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3503	16259	28913	1.19	1.0E-01	BF033991.1	EST_HUMAN	UI-H-B3-alc-d-07-o-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738420 3'
3708	16461	29100	1.03	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3859849 5'
3817	16569	29200	0.98	1.0E-01	AF297081.1	NT	601906499F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3817	16569	29201	0.96	1.0E-01	AF297081.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3935	16685	29326	2.53	1.0E-01	BF365703.1	EST_HUMAN	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4518	17253		0.95	1.0E-01	AI792349.1	EST_HUMAN	QV2-NT0048-160800-318-e05 NT0048 Homo sapiens cDNA
4684	17398	30032	1.19	1.0E-01	U50450.1	NT	en32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4966	17594	30217	2.35	1.0E-01	AW952344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isofrm (for) mRNA, complete cds
5238	18044		9.73	1.0E-01	W86490.1	EST_HUMAN	EST1364414 IMAGE resequences, MAG8 Homo sapiens cDNA
5789	18580		1.21	1.0E-01	AK024472.1	NT	z62204.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5934	18717	31675	14.15	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6243	19017	31991	0.99	1.0E-01	AA481879.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6256	19030	32005	0.7	1.0E-01	AA406039.1	EST_HUMAN	z41910.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:766258 3' similar to contains L1.13.L1 repetitive element;
						EST_HUMAN	zu67c12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'

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6924	19660		1.81	1.0E-01	R23821.1	EST_HUMAN	y34406.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131676 5' similar to contains Alu repetitive element;
7635	20300		2.67	1.0E-01	Y12488.1	NT	M.musculus wfm gene
7709	20373	33486	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7709	20373	33487	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7834	20529	33656	0.65	1.0E-01	AA861091.1	EST_HUMAN	ak32g01.e1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8066	20760		0.5	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8390	21083		0.96	1.0E-01	AW189787.1	EST_HUMAN	x09601.x1 NCJ CGAP U14 Homo sapiens cDNA clone IMAGE:2875689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.3 TAR1 repetitive element;
9084	21773	34837	1.04	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNA, complete cds
9395	22057	35228	0.51	1.0E-01	R44983.1	EST_HUMAN	y93404.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9407	22069		1.6	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9450	22000		3.02	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9464	22074	35245	0.75	1.0E-01	W01855.1	EST_HUMAN	zc68c10.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:327282 3'
9721	22372	35571	1.67	1.0E-01	BF240194.1	EST_HUMAN	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9835	22486	35687	8.12	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
9835	22486	35688	8.12	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10043	22691		0.97	1.0E-01	AW957425.1	EST_HUMAN	EST369815 MAGE resequences, MAGE Homo sapiens cDNA
10048	22696	35912	0.51	1.0E-01	T51952.1	EST_HUMAN	y628a06.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10229	22877	36089	0.89	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3839096 5'
10554	23250		1.95	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
10858	23634	36884	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10858	23634	36885	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11376	23983	37283	5.22	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836734 5'
11510	24110		1.52	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain:RIMD 0509962
11594	24183	37511	1.46	1.0E-01	Z71446.1	NT	A.thaliana mRNA for CLC-b chloride channel protein
11594	24183	37512	1.46	1.0E-01	Z71446.1	NT	A.thaliana mRNA for CLC-b chloride channel protein
11832	24418	37755	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLCBPG01 3'
11832	24418	37756	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLCBPG01 3'
12083	24921		4.32	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12300	24725		1.71	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA

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12317	24738		2.22	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
12814	24921		2.74	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12677	25318		5.03	1.0E-01	U06834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12733	25002		9.8	1.0E-01	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2781	15486	28224	1.27	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1) mRNA, complete cds
2790	15495	28235	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2790	15495	28236	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3260	16022	28671	1.32	9.9E-02	AF098810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
3933	16683	29324	0.75	9.9E-02	A1921637.1	EST_HUMAN	zu45c03.x6 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:740932 3'
4632	17367	30003	0.93	9.9E-02	BE674249.1	EST_HUMAN	7d77c12x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
6875	17951	30547	9.17	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
7815	20510	33634	0.93	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI CGAP_Oy23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
7815	20510	33635	0.93	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI CGAP_Oy23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
9156	21887	35055	0.98	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
550	13333		1.43	9.8E-02	X56338.1	NT	O.sativa RAMy3C gene for alpha-amylase
3100	15665		0.9	9.8E-02	4504578	NT	Homo sapiens I factor (complement) (IF) mRNA
3142	15906	28550	3.64	9.8E-02	AF184274.1	NT	Daucus carota leucoanthoxyanthidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4198	16939	28564	6.24	9.8E-02	AF257329.1	NT	Leptocapharia maculans beta-tubulin mRNA, complete cds
4198	16939	28565	6.24	9.8E-02	AF257329.1	NT	Leptocapharia maculans beta-tubulin mRNA, complete cds
7381	20061		0.77	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9153	21884		1.18	9.8E-02	M61943.1	NT	Human lamitin B1 chain gene, exon 26
11437	23204	36436	2.05	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12052	24570		1.78	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1328	14077	26752	1.31	9.7E-02	AB005808.1	NT	Alcea arborescens mRNA for NADP-malic enzyme, complete cds
1590	14326		1.49	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2257	14984	27724	2.08	9.7E-02	BE186600.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3965	16714		3.48	9.7E-02	D99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5261	18067	30895	0.94	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5261	18067	30696	0.94	9.7E-02	AF069189.1	NT	Caulobacter crescentius thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5924	18708	31662	1.43	9.7E-02	AW064476.1	EST_HUMAN	EST368548 MAGC resequences, MAGC Homo sapiens cDNA
7198	19884	32958	3.24	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
7882	20577	33705	1.28	9.7E-02	N22788.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7882	20577	33706	1.28	9.7E-02	N22788.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8748	21440	34587	1.49	9.7E-02	AI953984.1	EST_HUMAN	wz78b08.x1 NCI_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_mel1
11152	23819		2.84	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2009	14744	27470	1.11	9.6E-02	AI080721.1	EST_HUMAN	Mus musculus ligatin (lgin) mRNA, partial cds
2009	14744	27471	1.11	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4311	17050	29675	5.8	9.6E-02	Z32686.2	NT	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4940	17688	30276	0.99	9.6E-02	AW066230.1	EST_HUMAN	Protein mirabilis fmbrial operon, strain HI4320
6014	18795		3.13	9.6E-02	BE910039.1	EST_HUMAN	EST378303 MAGC resequences, MAGI Homo sapiens cDNA
8274	20968		0.6	9.6E-02	AU137084.1	EST_HUMAN	60148088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
9444	22121	35300	1.31	9.6E-02	AV687988.1	EST_HUMAN	AV687988 GKG Homo sapiens cDNA clone PLACE1005740 5'
9772	22423		1.12	9.6E-02	BE884895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916963 5'
9839	22587	35790	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
9839	22587	35791	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10020	22668	35884	0.5	9.6E-02	BF67270.1	EST_HUMAN	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10051	22689	35915	1.54	9.6E-02	AB013985.1	NT	Anthrithum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10051	22689	35916	1.54	9.6E-02	AB013985.1	NT	Anthrithum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10158	22806	36024	3.35	9.6E-02	P08174	SWISSPROT	COMPLEMENT DEGRADATION-ACCELERATING FACTOR PRECURSOR (CD55)
10543	23334	36572	7.22	9.6E-02	Z79702.1	NT	Myobacterium tuberculosis H37Rv complete genome, segment 102/162
12652	24954		3.34	9.6E-02	H14588.1	EST_HUMAN	Myobacterium tuberculosis H37Rv complete genome, segment 102/162
4081	16825	29452	2.1	9.5E-02	AW092395.1	EST_HUMAN	ym18n03.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
5578	18376	31289	0.85	9.5E-02	P51854	SWISSPROT	CM2-BN0023-050200-087-112 BN0023 Homo sapiens cDNA
6988	19681	32729	0.55	9.5E-02	AA790728.1	EST_HUMAN	TRANSETOLASE 2 (TK 2) (TRANSETOLASE RELATED PROTEIN)
7202	19888	32963	4.72	9.5E-02	AB003473.1	NT	ac68a09.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:867736 3'
7467	20141	33234	7.68	9.5E-02	AL161538.2	NT	Timoreus flaviviridis DNA for phospholipase A2 inhibitor, complete cds
7597	18376	31289	0.84	9.5E-02	P51854	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7780	20475	33600	1.83	9.5E-02	BF035861.1	EST_HUMAN	TRANSETOLASE 2 (TK 2) (TRANSETOLASE RELATED PROTEIN)
7780	20475	33601	1.83	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10378	23273	36509	2.36	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'

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10578	23273	36510	2.36	9.5E-02	BF035981.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1825	14564	27275	2.82	9.4E-02	BF671083.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
1857	14595	27310	0.99	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1857	14595	27311	0.99	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3860	16610	28249	4.43	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
6225	18989	31876	0.63	9.4E-02	AF097383.1	NT	Trifolium aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8498	21180		2.46	9.4E-02	Z46863.1	NT	Acetobacter sp. cysD, cobQ, cobQ, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
10851	20166	33258	2.44	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vati genes, complete cds, and p65 gene, partial cds
11941	25255		1.76	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12871	24985		1.92	9.4E-02	AF198036.1	NT	Mycoplasma pneumoniae hypodermal membrane protein P83 gene, complete cds
2988	15754		1.97	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3028	15782		6.32	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3251	16013	28665	1.85	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4132	16874	29502	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4132	16874	29503	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4685	17419		2.04	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5576	18373		0.67	9.3E-02	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8146	20940	33972	0.82	9.3E-02	AW866007.1	EST_HUMAN	EST69 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9610	22263	35449	2.15	9.3E-02	BE962631.2	EST_HUMAN	601655988R1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3855981 3'
10091	22739	35953	3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10091	22739	35954	3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10218	22866		3.5	9.3E-02	AW206117.1	EST_HUMAN	UI-HB11-afk-h-05-0-UI.s1 NCL_OGAP Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12194	25181		2.51	9.3E-02	AJ249650.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
12550	25209		8.43	9.3E-02	AW468850.1	EST_HUMAN	hd281r12.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daax (DAXX) gene, partial cds; Bmg1 (BING1), tapasin (tapasin), RelGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr
12752	25254		2.1	9.3E-02	AF100956.1	NT	Mollusca contagiosum virus subtype 1, complete genome
222	13034	25668	8.37	9.2E-02	U60315.1	NT	Mollusca contagiosum virus subtype 1, complete genome
222	13034	25669	8.37	9.2E-02	U60315.1	NT	Mollusca contagiosum virus subtype 1, complete genome
222	13034	25670	8.37	9.2E-02	U60315.1	NT	Mollusca contagiosum virus subtype 1, complete genome
2224	14952		1.68	9.2E-02	R54156.1	EST_HUMAN	yg8807.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:41618 5'
3175	15938	28587	3.28	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3289	16061	28709	0.85	9.2E-02	AA534354.1	EST_HUMAN	n70e01.s1 NCL_OGAP_Co3 Homo sapiens cDNA clone IMAGE:928138 3'

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3573	16328		1.28	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4213	16954		0.89	9.2E-02	U62048.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region
4274	17013		0.76	9.2E-02	BE289722.1	EST_HUMAN	60094366F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860176 5'
7907	20602	33732	1.98	9.2E-02	T49920.1	EST_HUMAN	ya89c08.r1 Strategene placenta (#837225) Homo sapiens cDNA clone IMAGE:69808 5' similar to
8076	20770	33899	2.2	9.2E-02	X95256.1	NT	gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
11695	24290	37614	1.27	9.2E-02	AF028552.3	NT	H. vulgare xylose isomerase gene
12736	25412		1.4	9.2E-02	11468872	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
414	12825	25439	4.19	9.1E-02	X77665.1	NT	Podospira anserina mitochondrion, complete genome
4451	17187	28812	1.33	9.1E-02	AL161554.2	NT	O. cuniculus K12 keratin gene
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5643	18438	31352	1.44	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b,
7285	19868	33045	14.94	9.1E-02	AW160658.1	EST_HUMAN	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7575	20244	33349	0.79	9.1E-02	AP000061.1	NT	au74a03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7609	20275	33383	0.72	9.1E-02	U39073.1	NT	Aeropyrum pernix genome DNA, section 417
8822	21514	34659	0.88	9.1E-02	Y14379.1	NT	Mus musculus thymopolein zeta mRNA, complete cds
10327	22874		1.37	9.1E-02	T02984.1	EST_HUMAN	Homo sapiens gamma adducin gene, exon 9
10354	23001	36218	1.25	9.1E-02	S74059.1	NT	FB19F10 Fetal brain, Strategene Homo sapiens cDNA clone FB19F10 3' end
10383	23029	36244	1.19	9.1E-02	Y11187.1	NT	Tg616=Oyl actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 5275 nt]
12110	25348		1.4	9.1E-02	AA179901.1	EST_HUMAN	A.thaliana RH1, TCI, G14587-5, G14587-6, and PRL1 genes
12181	24653		2.12	9.1E-02	AF052895.1	NT	zp38h12.s1 Strategene muscle 887209 Homo sapiens cDNA clone IMAGE:611783 3' similar to
12637	25204		1.93	9.1E-02	AJ291390.1	NT	SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA;
						NT	Rattus norvegicus cell cycle protein p56CDC gene, complete cds
						NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
						SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE
727	13501	26155	4.3	9.0E-02	P15328	SWISSPROT	RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED
						EST_HUMAN	ANTIGEN MOV18) (KB CELLS FBP)
1631	14377	27064	5.28	9.0E-02	BE220482.1	EST_HUMAN	h399g10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu
2806	15511	28252	6.45	9.0E-02	AF138522.1	NT	repetitive element
2806	15511	28253	6.45	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3331	16091	28744	0.94	9.0E-02	AF279135.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
4619	17354	28969	3.27	9.0E-02	X65740.2	NT	Dicystotellium discoidium spore coat structural protein SP65 (cotE) gene, complete cds
						NT	Plasmodium falciparum P-type ATPase 3 gene

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5906	18691	31640	5.21	9.0E-02	W56037.1	EST_HUMAN	z68a12.r1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
6619	19381		1.14	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element
6668	19585	32619	0.72	9.0E-02	R62805.4	EST_HUMAN	y11b08.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3' Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OriU (oriU), >
12486	24845		2.01	9.0E-02	AF022236.1	NT	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285851 5'
1418	14166	26849	1.99	8.9E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285851 5'
1418	14166	26850	1.98	8.9E-02	BF701593.1	EST_HUMAN	PMO-H70339-251199-003-401 HT0339 Homo sapiens cDNA
2386	15107	27846	1.22	8.9E-02	BE153572.1	EST_HUMAN	Arichium angustatum AtranFib2 protein (AtranFib2) gene, partial cds
4175	16915		1.93	8.9E-02	AF286055.1	NT	UI-HB3-abc-f08-Q-U1 st NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5760	18552	31474	3.22	8.9E-02	AW452122.1	EST_HUMAN	UI-HB3-abc-f08-Q-U1 st NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5760	18552	31475	3.22	8.9E-02	AW452122.1	EST_HUMAN	Homo sapiens similar to endoglycan (H. sapiens) (LOC83107), mRNA
5776	18567	31496	3.39	8.9E-02	11433478	NT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
7093	19782	32848	1.64	8.9E-02	P47259	SWISSPROT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SO6pA20F8
7458	20132		2.06	8.9E-02	Z79021.1	NT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
7949	20644	33768	1.08	8.9E-02	P29475	SWISSPROT	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8030	20725	33858	0.72	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8030	20725	33859	0.72	8.9E-02	BF701665.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
8496	21188	34331	4.72	8.9E-02	AA308319.1	EST_HUMAN	q455005.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1668680 3' similar to contains MER10.b1 MER10 repetitive element ;
9520	22173	35356	0.8	8.9E-02	AI285627.1	EST_HUMAN	q455005.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1668680 3' similar to contains MER10.b1 MER10 repetitive element ;
9520	22173	35357	0.8	8.9E-02	AI285627.1	EST_HUMAN	EST44454 Fetal brain I Homo sapiens cDNA 5' end
9632	22284	35477	0.76	8.9E-02	AA339356.1	EST_HUMAN	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
11882	25173		1.49	8.9E-02	P30143	SWISSPROT	MYOSIN-2 ISOFORM
11840	25207		1.48	8.9E-02	P19524	SWISSPROT	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12085	24591		3.05	8.9E-02	BF686918.1	EST_HUMAN	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
12284	24716		1.61	8.9E-02	U28895.1	NT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
1352	14100	26775	1.59	8.8E-02	Q27474	SWISSPROT	EST11595 Uterus Homo sapiens cDNA 5' end
3883	16633	29272	1.03	8.8E-02	AA299128.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4014	16760		3.55	8.8E-02	O00288	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII130) (TAFII130)
4214	16955		0.99	8.8E-02	450280.4	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4269	17009		1.27	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7444	20120		0.57	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
8886	21577	34719	1.07	8.8E-02	AA151872.1	EST_HUMAN	z09a05.s1 Stragene clone (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
11062	23732	37003	2.7	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11062	23732	37004	2.7	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11228	23891	37178	6.92	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5'
11805	24395	37729	1.49	8.8E-02	P97803	SWISSPROT	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10)
12155	24641	31098	2.66	8.8E-02	Z71581.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285w
1642	14388	27077	1.15	8.7E-02	AI167281.1	EST_HUMAN	aa65b01.s1 Soares_NIHMPUL S1 Homo sapiens cDNA clone IMAGE:1661161 3'
3681	16434	29077	3.66	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3681	16434	29078	3.66	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4658	17392	30027	1.19	8.7E-02	AF178636.1	NT	Mus musculus JNK Interacting protein-3a (Jip3) mRNA, complete cds
5231	18037	30683	5.88	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:701438 3'
5231	18037	30684	5.88	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:701438 3'
6745	19578	32612	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6745	19578	32613	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6943	19425	32440	0.71	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
7761	20457		0.45	8.7E-02	AA284532.1	EST_HUMAN	z20e03.s1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:713692 3'
8413	21106	34246	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8413	21106	34246	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
10610	23304		2.46	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11282	23943	37237	2.55	8.7E-02	AJ007763.1	NT	Glucobacter oxydans tRNA-Ile and tRNA-Ala genes
12145	24833		2.1	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12340	24750		1.75	8.7E-02	6679057	NT	Mus musculus nidogen 2 (Nkd2), mRNA
1230	13979	26949	7.02	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2240	14968	27706	1.82	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3183	15946	28596	4.57	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds

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3635	18388		3.77	8.6E-02	AF153362.1	NT	Dicystostellum discoideum adenyl cyclase (accA) gene, complete cds
5134	17852		0.86	8.6E-02	BF570296.1	EST_HUMAN	602185716T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310259 3'
6003	18784	31746	4.75	8.6E-02	Y10928.1	NT	Homo sapiens LCN1b gene
6281	19054	32033	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6281	19054	32034	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7481	20153	33248	1.34	8.6E-02	P14816	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7831	20526	33651	1.25	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
7831	20526	33652	1.25	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
7969	20664	33788	0.62	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
8031	20726		0.81	8.6E-02	U60168.1	NT	Dicystostellum discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9637	22289	35482	1.76	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9673	22325		0.58	8.6E-02	AW662163.1	EST_HUMAN	h20cd08.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872846 3'
10053	22701	35918	0.81	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
10865	23545	36792	1.8	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10865	23545	36793	1.8	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11214	23877	37163	4.64	8.6E-02	BF305606.1	EST_HUMAN	601833437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11214	23877	37164	4.64	8.6E-02	BF305606.1	EST_HUMAN	601833437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11417	23184	36414	5.97	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11568	24167	37481	2.11	8.6E-02	AF293860.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2395	15116	27853	3.3	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5583	18380	31292	0.75	8.5E-02	AA985491.1	EST_HUMAN	0483b07.s1 NCL_CGAP_Kd6 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gbK01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5621	18417		1.29	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5921	18706	31658	6.95	8.5E-02	AF233985.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8504	21196	34340	1.65	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
9736	22387	35591	2.81	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
9736	22387	35592	2.81	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10261	22909	36119	0.54	8.5E-02	X76731.1	NT	V. lamidocytes gene for arimodiyoxin C
10382	23028	36243	0.87	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11105	23775		8.87	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11125	23764	37070	4.43	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds

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12700	24981		3.8	8.5E-02	AJ362934.1	EST_HUMAN	EST172736 Ovary II Homo sapiens cDNA 5' end
2672	15602	28121	3.73	8.4E-02	W68330.1	EST_HUMAN	z444e11.r1 Soares_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:343532 5'
3801	16553	29184	1	8.4E-02	A1827586.1	EST_HUMAN	w10f11.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2350221 3' similar to contains element MSR1 repetitive element;
4321	17060	29885	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4321	17060	29886	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
5137	17855	30472	4.97	8.4E-02	AB042556.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
5229	18035	30661	9.84	8.4E-02	BE207153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6590	18553	32366	1.72	8.4E-02	AK024488.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7928	20623	33751	7.18	8.4E-02	BE096074.1	EST_HUMAN	GM3-BT0790-260400-162-405 BT0790 Homo sapiens cDNA
8741	21433	34578	1.01	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10260	22808	36118	1.83	8.4E-02	A1735184.1	EST_HUMAN	es88g10.x1 Barstead codon HPLB87 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR-O88312 O88312 GOB-4;
12070	24584	31122	1.68	8.4E-02	RT9408.1	EST_HUMAN	yf83h12.r1 Soares placenta Nb24IP Homo sapiens cDNA clone IMAGE:145895 5'
2005	14741	27465	0.92	8.3E-02	5835680	NT	bodes hexagonus mitochondrion, complete genome
2005	14741	27466	0.92	8.3E-02	5835680	NT	bodes hexagonus mitochondrion, complete genome
3580	16335	28980	6.91	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3607	16360	29001	0.83	8.3E-02	A1436797.1	EST_HUMAN	fh82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3607	16360	29002	0.83	8.3E-02	A1436797.1	EST_HUMAN	fh82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6166	18943	31914	1.05	8.3E-02	A1842338.1	EST_HUMAN	w078f11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
6273	19046	32023	3.05	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7890	20575	33702	2.98	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
7911	20608		1.46	8.3E-02	AA865285.1	EST_HUMAN	og88g08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L.11 L1 L1
8198	20892		1.32	8.3E-02	AA987873.1	EST_HUMAN	og81f10.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592778 3'
9438	22118	35281	1.41	8.3E-02	AW583503.1	EST_HUMAN	la05h10.x1 Human Pancreatic islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
9451	22001		1.88	8.3E-02	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10240	22888		0.49	8.3E-02	AF020496.1	NT	Dicystellum discoidium DocA (docA) mRNA, complete cds
12158	25353		1.67	8.3E-02	BE958458.1	EST_HUMAN	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928993 5'
1357	14105		7.15	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1481	14228	26914	1.98	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3071	15837		2.07	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3784	16536		1.35	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10

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3989	16737	29371	1.07	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
4251	16982	29617	4.97	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	16982	29618	4.97	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	16982	29619	4.97	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5022	17743	30354	2.44	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5070	17789		2.39	8.2E-02	Z69893.1	NT	T. Inflatum transposon Resless DNA
5252	18058	30687	1.49	8.2E-02	BE897030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
6925	19661	32707	3.09	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7632	20298		0.67	8.2E-02	AV743341.1	EST_HUMAN	AV743341 OB Homo sapiens cDNA clone CBLANF07 5'
8870	21362	34509	2.95	8.2E-02	AW876126.1	EST_HUMAN	RC2-PT0004-031299-011-405 PT0004 Homo sapiens cDNA
9499	22152	35332	5.36	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
9663	22315	35512	2.24	8.2E-02	BE284318.1	EST_HUMAN	601150555F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355588 5'
12164	24846	31102	4.03	8.2E-02	AE002246.2	NT	Chlamydomonas reinhardtii AR39, section 73 of 94 of the complete genome
12554	25138		3.65	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5668	18463	31378	0.79	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 162 of 229 of the complete genome
6286	19059	32040	1.19	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7097	19786		0.66	8.1E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
7482	20154		1.25	8.1E-02	AI692681.1	EST_HUMAN	wd86f08.x1 NCJ_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338603 3'
8238	20932	34067	0.61	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8238	20932	34068	0.61	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
9812	22463		1.64	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lectin precursor, gene, complete cds
11482	24083	37395	2.08	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	15634	25447	5.03	8.0E-02	AW954653.1	EST_HUMAN	EST356723 MAGE resequences, MAGEC Homo sapiens cDNA
915	13682	26344	0.79	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1694	15576	27134	9.85	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1694	15576	27135	9.85	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1896	14633	27343	3.27	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA
2374	15096	27835	1.09	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2374	15096	27836	1.09	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2473	15191		4.2	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075819 5'
2823	13827	26486	0.98	8.0E-02	M23449.1	NT	Dictyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2901	15667	28315	1.45	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3797	16549	29182	1.01	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGE Homo sapiens cDNA

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4725	17457	30093	1.43	8.0E-02	AI434202.1	EST_HUMAN	U31602.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114.3'
4764	17496		6.33	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
5108	17826	30443	0.87	8.0E-02	AW207037.1	EST_HUMAN	U1-H-B1+add.f-10-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721547.3'
5801	18591	31516	3.15	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7080	18591	31516	1.82	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8027	20722	33854	3.79	8.0E-02	AL114993.1	NT	Bordetis ciferia strain T4 cDNA library under conditions of nitrogen deprivation
9289	21956	35127	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9289	21956	35128	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10058	22706		0.55	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10892	23383	36823	2.27	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12195	24665	31070	6.39	8.0E-02	AI006375.1	NT	Drosophila arena hunchback region
12748	17903		2.21	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2171	14900	27634	3.52	7.8E-02	BE250008.1	EST_HUMAN	600943101F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510.5'
2878	15744	28392	7.25	7.9E-02	AI582029.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173648.3' similar to gb:Z26876
3177	16529	29168		7.9E-02	AF030694.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 88 (HSP88), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG9 (cg9), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3832	16583	29217	5.01	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3832	16583	29218	5.01	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4845	17379	30011	0.99	7.9E-02	BF348454.1	EST_HUMAN	60201970F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155401.5'
4760	17492		1.31	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
4851	17581	30204	1.02	7.9E-02	L24757.1	NT	Human bone sialoprotein (BNSP) gene, exons 2, 3 and 4
6597	19360		1.16	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310900-024-r11 GN0042 Homo sapiens cDNA
7931	20928	33754	2.79	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
9927	22575	35773	4.21	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632466.3' similar to WP:C37A2.2
9927	22575	35774	4.21	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465.3' similar to WP:C37A2.2
1188	13940	28604	1.77	7.8E-02	AI793275.1	EST_HUMAN	oo59402.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467.5' similar to contains L1.13 L1
1188	13940	28605	1.77	7.8E-02	AI793275.1	EST_HUMAN	oo59402.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467.5' similar to contains L1.13 L1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression- Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5027	16484		2.47	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859893 5'
6976	19457	32479	0.88	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
6976	19457	32480	0.88	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8684	21376	34520	0.71	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8779	21471	34616	0.66	7.8E-02	X78344.1	NT	S. cerevisiae CAT8 gene
8951	21842	34789	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8951	21842	34790	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9261	22015	35183	1.07	7.8E-02	AA469354.1	EST_HUMAN	nc88808.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:771731
9701	22352	35547	0.62	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
10562	23258	36494	4.58	7.8E-02	U32323.1	NT	Human Interleukin-11 receptor alpha chain gene, complete cds
12754	25015		3.92	7.8E-02	AF068349.1	NT	HIV-1 strain 97USNG30 from USA, envelope glycoprotein (env) gene, partial cds
1378	15588	26800	1.25	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3574	16329		1.97	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5456	18255	31145	0.59	7.7E-02	AF062638.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
7809	20504	33625	5.37	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to
9735	22386	35590	3.94	7.7E-02	P38080	SWISSPROT	TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN. ; PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10031	22879	35895	0.85	7.7E-02	AI318662.1	EST_HUMAN	la80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10031	22879	35896	0.85	7.7E-02	AI318662.1	EST_HUMAN	la80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10933	23613	36863	4.51	7.7E-02	11422767	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
12389	25215		2.68	7.7E-02	11436859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3382	16141	28798	1.97	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3403	16161	28812	1.14	7.6E-02	AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3547	16302	28952	0.71	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6006	18787	31749	0.81	7.6E-02	AI061276.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6263	18037	32012	0.92	7.6E-02	BE378328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9270	22024	35194	1.47	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
9797	22448		1.63	7.6E-02	AL138078.2	NT	Campylobacter jejuni NCTC11188 complete genome; segment 5/6
10119	22767	35979	0.49	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0545-020800-017-006 HT0545 Homo sapiens cDNA
10247	22895		0.75	7.6E-02	BE95638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10487	23133	36359	0.71	7.6E-02	X92688.1	NT	L. esculentum mRNA for trice phosphate translocator
10487	23133	36360	0.71	7.6E-02	X92688.1	NT	L. esculentum mRNA for trice phosphate translocator
11678	24273	37595	2.45	7.6E-02	AW998945.1	EST_HUMAN	QV3-BN0046-150400-161-e04 BN0046 Homo sapiens cDNA
767	13540	26199	1.44	7.5E-02		NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	13540	26200	1.44	7.5E-02		NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4472	17207	29833	1.17	7.5E-02	AB015981.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5762	18553	31477	0.91	7.5E-02	A1948714.1	EST_HUMAN	wq24t09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8236	20930	34066	1.05	7.5E-02	A1864387.1	EST_HUMAN	w52b02.x1 NCL CGAP_Bm28 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA
8406	21098	34234	1.17	7.5E-02	AU116913.1	EST_HUMAN	ENOLASE (HUMAN);
9932	22580		0.54	7.5E-02	BF221730.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
10390	23036	36252	0.7	7.5E-02	BF206809.1	EST_HUMAN	7061c05.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10488	23134	36361	0.72	7.5E-02	X79460.1	EST_HUMAN	MER27 repetitive element
465	13250	25891	1.46	7.4E-02	AW838547.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
1445	14192		0.92	7.4E-02	AF030027.1	EST_HUMAN	C.fiml DSM 20113 16S rDNA
2585	15299		1.32	7.4E-02	6765069	NT	RCS-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
3591	16336	28981	0.86	7.4E-02	A1807885.1	EST_HUMAN	Equine herpesvirus 4 strain NS0587, complete genome
4658	17390	30024	2.03	7.4E-02	L78810.1	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
4741	17473	30108	2.94	7.4E-02		NT	wf43h01.x1 Soares_NFL_T_GBC ST Homo sapiens cDNA clone IMAGE:2358385 3'
4889	17616	30235	2.1	7.4E-02	6978442	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
8403	19172		2.18	7.4E-02	R17477.1	EST_HUMAN	Rattus norvegicus Actin receptor like kinase 1 (Acvrl1), mRNA
7801	20496	33618	1.52	7.4E-02	BE880112.1	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrlp), mRNA
8399	21092	34228	1.03	7.4E-02	U56089.1	NT	y914g08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
9064	21753	34913	1.12	7.4E-02	AW628605.1	EST_HUMAN	601493366F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3895284 5'
							Human peridic typtophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
							h167d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
							O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2;

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9084	21753	34914	1.12	7.4E-02	AW629605.1	EST_HUMAN	h167d11.y1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW_SCA2_HUMAN
9339	20410	33525	0.52	7.4E-02	AI672939.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9339	20410	33526	0.52	7.4E-02	AI672939.1	EST_HUMAN	w74402.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9374	22365	35563	1.03	7.4E-02	U62293.1	NT	w74402.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9841	22492	35982	0.52	7.4E-02	BF512678.1	EST_HUMAN	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10939	23619	36869	1.26	7.4E-02	AA059187.1	EST_HUMAN	UL-HBW1-emb-g-06-Q-U1_s1 NCI_CGAP_Sub07 Homo sapiens cDNA clone IMAGE:3068688 3'
12126	24618		1.53	7.4E-02	11525893	NT	z64e01.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381720 5'
12381	25329		2.21	7.4E-02	AW379431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
456	13242	25881	1.5	7.3E-02	BE964981.2	EST_HUMAN	CMA-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
456	13242	25882	1.5	7.3E-02	BE964981.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
669	13445	26085	3.9	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1464	15570	26900	3.62	7.3E-02	AW900281.1	EST_HUMAN	Thermopoga maritima section 101 of 136 of the complete genome
1837	15580		12.41	7.3E-02	AL163302.2	NT	CMD-NIN1004-130300-284-g08 NN1004 Homo sapiens cDNA
6381	19131	32126	1.32	7.3E-02	AA779977.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
7368	20048	33128	2.58	7.3E-02	P05143	SWISSPROT	z24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7368	20048	33128	2.58	7.3E-02	P05143	SWISSPROT	gb.L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
8068	20762		1.15	7.3E-02	7662107	NT	PROLINE-RICH PROTEIN MP-3
9110	21798		1.14	7.3E-02	AB011090.1	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
11179	19131	32126	2.06	7.3E-02	AA779977.1	EST_HUMAN	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
11844	24428		5.07	7.3E-02	11560138	NT	z24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
117	12937	25577	1	7.2E-02	AE000882.1	NT	gb.L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
117	12937	25578	1	7.2E-02	AE000882.1	NT	Rattus norvegicus caspase recruitment domain protein 9 (LOC64171), mRNA
1458	14205	26890	2.72	7.2E-02	AL163301.2	NT	gb.L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
1458	14205	26891	2.72	7.2E-02	AL163301.2	NT	Rattus norvegicus caspase recruitment domain protein 9 (LOC64171), mRNA
2552	15267		2.83	7.2E-02	U14794.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
3665	16615	29254	0.95	7.2E-02	AW268322.1	EST_HUMAN	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
4312	17051	29676	4.65	7.2E-02	BF572307.1	EST_HUMAN	genome
4644	17378	30010	0.7	7.2E-02	11466563	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome

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5205	18013	30635	2.88	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5206	18014	30636	10.1	7.2E-02	P11120	SWISSPROT	CALMODULIN
7068	19759	32824	1.58	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7085	19775	32840	0.64	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metallopeptase (zmpB) genes, complete cds
7109	19797		1.5	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8087	20781	33910	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8087	20781	33911	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8962	21653		0.61	7.2E-02	Y17217.1	NT	Lactococcus lactis capE gene
9474	22127		0.49	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9511	22164	35346	2.32	7.2E-02	AV112452.1	EST_HUMAN	AV112452 DCA Homo sapiens cDNA clone DCAUG01 5'
9659	22311	35509	3.8	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9814	22465	35667	0.93	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5'
9903	22552	35747	2.53	7.2E-02	AW873187.1	EST_HUMAN	hq24f11.x1 NCI CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR-Q9Z340 Q9Z340
10092	22740	35955	0.62	7.2E-02	AA768204.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN. ; ca62c07.e1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10250	22898	36108	1.93	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10372	23018	36234	5.54	7.2E-02	BE65003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3665951 5'
10395	23041		3.68	7.2E-02	BE59214.1	EST_HUMAN	601066194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451569 5'
10609	23155	36381	0.48	7.2E-02	AA706897.1	EST_HUMAN	z28f05.e1 Soares_fetal_liver_epilepsy_infls_S1 Homo sapiens cDNA clone IMAGE:451641 3'
10830	23512	36753	3.3	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11849	24433	37775	1.34	7.2E-02	AY009090.1	NT	Homo sapiens putative transmembrane protein decin-1 mRNA, complete cds
12035	24560	31113	1.57	7.2E-02	AA773696.1	EST_HUMAN	af61a04.f1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12068	24583		4.45	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seraid P) Homo sapiens cDNA clone PS13D5 3'
12182	24654		1.73	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12196	25185		8.19	7.2E-02	AW900962.1	EST_HUMAN	CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
12599	25362		3.62	7.2E-02	AF020439.1	NT	Homo sapiens ATP-citrate lyase gene, intron 3
1887	14834	27344	2.01	7.1E-02	U02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2290	15015	27751	5.07	7.1E-02	BF208802.1	EST_HUMAN	60187228F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
7807	20502	33622	0.77	7.1E-02	AI125264.1	EST_HUMAN	qd92a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736822 3'

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11822	24483		8.41	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
515	13289	25831	1	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1486	14233		1.27	7.0E-02	X96677.1	NT	Martellia Mitcut-1 gene
1756	14498	27199	1.08	7.0E-02	AA056343.1	EST_HUMAN	2166104.s1 Stratiocoma colon (#637204) Homo sapiens cDNA clone IMAGE:609599 3'
3027	15793	28440	2.1	7.0E-02	AW138162.1	EST_HUMAN	UI-H-B11-acy-c-07-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
							a165a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
3878	16828	29266	0.74	7.0E-02	AA815438.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4119	16861		1.28	7.0E-02	AW792862.1	EST_HUMAN	GMO-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4189	16930	29560	1.06	7.0E-02	AF077821.1	NT	Carls familiaris inducible nitric oxide synthase mRNA, complete cds
4877	17604	30227	7.24	7.0E-02	BF381687.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
5293	18098		0.57	7.0E-02	Y09143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7300	18983	33059	1.29	7.0E-02	AV689285.1	EST_HUMAN	AV689285 GKC Homo sapiens cDNA clone GKCCAE06 5'
7506	20177	33271	0.84	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial acornin, XL spliced variant (acz gene)
8996	21686	34836	1.28	7.0E-02	6628113	NT	African swine fever virus, complete genome
9497	22150	35331	1.24	7.0E-02	K02901.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' and
9852	22502	35702	0.51	7.0E-02	U27266.1	NT	Human myosin binding protein H (MyBP-H) gene, complete cds
11345	24035	37338	4.98	7.0E-02	AA724295.1	EST_HUMAN	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
501	13285	25917	4.3	6.9E-02	AL163210.2	NT	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
501	13285	25918	4.3	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens chromosome 21 segment HS21C010
1310	14058		1.2	6.9E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3773	16525	29163	1.41	6.9E-02	Q06384	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3773	16525	29164	1.41	6.9E-02	Q06384	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB precursor (entB), enterocin B immunity protease precursor (entB), enterocin B immunity protease
5113	17831	30448	0.89	6.9E-02	AF121254.1	NT	601192383F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3636253 5'
5127	17845	30462	1.25	6.9E-02	BE284605.1	EST_HUMAN	Cervine distemper virus strain A75/17, complete genome
7516	20187		0.61	6.9E-02	AF164967.1	NT	Human calmodulin (CALM) gene, exons 2,3,4,5 and 6, and complete cds
7851	20646		1.12	6.9E-02	U12022.1	NT	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8451	21143	34282	1.01	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8451	21143	34283	1.01	6.9E-02	BE567435.1	EST_HUMAN	Barbary duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
9018	21708	34860	0.7	6.9E-02	U22967.1	NT	X.laeviis XFD2 mRNA for fork head protein
12085	24580		1.82	6.9E-02	X74315.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12232	24686		1.69	6.9E-02	P44821	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFG HOMOLOG
12447	24817		1.46	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1875	14613	27321	1.56	6.8E-02	AA496759.1	EST_HUMAN	ae30702.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1875	14613	27322	1.56	6.8E-02	AA496759.1	EST_HUMAN	ae30702.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1900	14637	27346	3.77	6.8E-02	AF156673.1	NT	Homo sapiens putative hepatic transcription factor (WBSR14) gene, complete cds
3097	15862	28503	1.19	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376628 3'
3097	15862	28504	1.19	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376628 3'
3097	15862	28505	1.19	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376628 3'
4516	17251		0.86	6.8E-02	BE141076.1	EST_HUMAN	MRO-HT0069-071069-001-c05 HT0069 Homo sapiens cDNA
6525	19291		0.6	6.8E-02	P20792	SWISSPROT	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
6799	19460		1.09	6.8E-02	BE061890.1	EST_HUMAN	RC1-BT0254-080300-017-009 BT0254 Homo sapiens cDNA
7180	19866	32939	8.73	6.8E-02	AL103268.2	NT	Homo sapiens chromosome 21 segment HS21C068
7584	20252	33358	0.63	6.8E-02	U16856.1	NT	Dicystellum discoideum myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8186	20880	34017	5.01	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11873	26379	34018	5.01	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
12001	24537		2.3	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Strabagene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
12551	24888		2.85	6.8E-02	AA758014.1	EST_HUMAN	ah6705.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
12613	24920		1.65	6.8E-02	AW976839.1	EST_HUMAN	EST387948 IMAGE resequences, MAGN Homo sapiens cDNA
1519	14266		3.06	6.8E-02	9910585	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1866	14623	27333	1.93	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1'01 allele, complete cds
3708	16459	29097	2.27	6.7E-02	AI220285.1	EST_HUMAN	qg70e04.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1841406 3'
7749	20445	33567	4.52	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD4 (CHOX-A)
7749	20445	33568	0.55	6.7E-02	XG2695.1	NT	H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8337	21030	34167	0.56	6.7E-02	XG2695.1	NT	H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
9500	22153	35333	0.47	6.7E-02	AW082688.1	EST_HUMAN	xb61c11.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2580788 3'
9500	22153	35334	0.69	6.7E-02	AW137398.1	EST_HUMAN	UI-HB1-acr-q-01-Q.U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1348	14096	26771	0.69	6.7E-02	AW137398.1	EST_HUMAN	UI-HB1-acr-q-01-Q.U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
2180	14909	27641	1.07	6.6E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
3456	16212	28665	3.31	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3471	16227	28881	10.57	6.6E-02	IR64306.1	EST_HUMAN	Y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:199579 3'
3471	16227	28882	2.59	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3471	16227	28882	2.59	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA

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4090	16805	29436	1.29	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4921	17649	30281	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4921	17649	30282	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6489	19256	32258	3.44	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6701	19283	32286	0.56	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6701	19283	32287	0.56	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
7847	20542	33670	1.81	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8372	21065	34206	0.84	6.6E-02	AF050555.1	NT	Dicystostellum discoideum darlin (darA) gene, complete cds
8678	21370		0.53	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8819	21511	34654	0.58	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
8819	21511	34655	0.58	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9851	22501	35701	0.65	6.6E-02	A1458752.1	EST_HUMAN	h97g06.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
9987	22635	35845	1.66	6.6E-02	Y07848.1	NT	Homo sapiens EW's, gar22, rnp22 and bam22 genes
10022	22670		0.63	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10883	23563	36811	6.88	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0084-010600-008-a12 SN0084 Homo sapiens cDNA
11887	24451	37793	1.46	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
12442	24812		2.66	6.6E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
12740	25008		1.38	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
568	13349	25977	2.49	6.6E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
966	13732	26398	1.32	6.6E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1370	14118	26793	3.08	6.6E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1728	14470	27169	1.77	6.6E-02	AE000764.1	NT	Aquifex acidicus section 96 of 109 of the complete genome
5471	18270	31162	2.03	6.6E-02	AA443991.1	EST_HUMAN	z468112.s1 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:758743 3' similar to gb:M26038
6877	17953	30549	0.95	6.6E-02	U22661.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
9842	22493	35893	0.55	6.6E-02	BE963200.2	EST_HUMAN	Azobacter vinelandii ATCC 8046 negative regulator MucB (mucB) gene, partial cds
9842	22493	35894	0.55	6.6E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10363	23010	38225	0.48	6.6E-02	BF108300.1	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10635	23232	38468	5.56	6.6E-02	AA195848.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11894	24463		3.73	6.6E-02	M21496.1	NT	zr32q05.s1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12240	24691		4.66	6.6E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
561	13343	25970	2.08	6.4E-02	X94549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
3014	15780	28429	0.86	6.4E-02	6896923	NT	A. carterae precursor of peridinin-chlorophyll-protein (PCP) gene
4839	15780	28429	1.18	6.4E-02	6896923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA

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5363	18165	30850	1.67	6.4E-02	AH191956.1	EST_HUMAN	q07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element:
5791	18382	31509	0.65	6.4E-02	7305186	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6022	18802	31763	4.21	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1.4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6022	18802	31764	4.21	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1.4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6308	19080	32065	0.62	6.4E-02	AF072896.1	EST_HUMAN	we73g12.x1 Soares_Deckgraeft_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6719	19634	32877	6.43	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
7390	20041	33119	0.64	6.4E-02	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8234	20928		2.91	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
8563	21255	34392	3.42	6.4E-02	AA083305.1	EST_HUMAN	k1419.seq, F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9025	21716	34988	0.77	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDA1A10
9486	22139		0.55	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-q08 OT0083 Homo sapiens cDNA
9617	22270	35457	1.73	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0854 protein, partial cds
10161	22809	36027	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10161	22809	36028	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11709	24304	37629	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP-T3) gene, complete cds
11709	24304	37630	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP-T3) gene, complete cds
12141	25288		2.7	6.4E-02	AF107890.1	NT	Homo sapiens nucln 6B (MUC5B) gene, partial cds
12188	24659	31065	2.47	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1749	14491	27191	2.57	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III region Hsc701 gene, partial cds; smRNP, G7A, NG23, MUS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
3590	16344		2.38	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6045	18825	31786	1.18	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4097489 5'
7142	19829		0.82	6.3E-02	X97899.1	NT	H. sapiens gene encoding La autoantigen
9191	21861	35026	1.04	6.3E-02	AJ243916.1	NT	Drosophila melanogaster DmRNA gene, exons 1-3
9613	22562	35758	2.64	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: QMR-192
10171	22819		0.85	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GK Homo sapiens cDNA clone GKCAHE01 5'
10615	18825	31786	2.96	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4097489 5'
4224	16965	29590	2.81	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68

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4304	17043		1.02	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4542	17277		6.31	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6698	18615	32656	0.65	6.2E-02	D4850.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7527	20198	33292	1.03	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8846	25429		0.6	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9243	21922	35092	0.52	6.2E-02	AA778450.1	EST_HUMAN	af20a06.s1 Soares_fetus_Homo sapiens cDNA clone IMAGE:10321783
9380	22042	35214	1.85	6.2E-02	6877898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdfr2) mRNA
11095	23765	37039	1.56	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
11320	24011	37315	1.53	6.2E-02	AJ242735.1	NT	Melanizium anisopliae mRNA for Chymotrypsin (chyt1 gene)
11865	24449	37781	1.74	6.2E-02	AF200359.1	NT	Rattus norvegicus UDP-glucose glycoprotein:glucosyltransferase precursor (Uggt) mRNA, complete cds
11889	25405		13.39	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12394	24782	31037	2.5	6.2E-02	BF112039.1	EST_HUMAN	737h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:35238153 similar to TR-Q8Y4S6 Q8Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
249	13058	25697	5.59	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
3972	18721		2.29	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
6023	18803		1.4	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8161	20855	33986	3.75	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8559	21251	34388	0.57	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:39346043
8559	21251	34389	0.57	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:39346043
10630	23323	36560	4.91	6.1E-02	BE179543.1	EST_HUMAN	IL3-H10618-110500-136-006 HT0618 Homo sapiens cDNA
11862	24446	37787	1.27	6.1E-02	AB025333.1	NT	Eptatretus burgeri mRNA for RNA polymerase III largest subunit, partial cds
11845	25323		2.27	6.1E-02	X70969.1	NT	S. japonicum mRNA for serine-enzyme
12633	24833		5.61	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
98	12922	25559	0.76	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:9263105
96	12922	25560	0.76	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:9263105
1239	13988	26655	1.54	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2882	15391	28130	1.09	6.0E-02	AW669848.1	EST_HUMAN	EST380824 IMAGE resequences, MAGJ Homo sapiens cDNA
2775	15480		1.62	6.0E-02	AB031289.1	NT	Mesocricetus cord mitochondrial DNA, NADH dehydrogenase subunit 4, rRNA-Gh, rRNA-Phe, rRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2937	12922	25559	0.9	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:9263105
2937	12922	25560	0.9	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:9263105

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3223	15988	28639	1.48	6.0E-02	AA372376.1	EST_HUMAN	EST184268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3223	15988	28640	1.48	6.0E-02	AA372376.1	EST_HUMAN	EST184268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3625	16378		0.72	6.0E-02	BE984443.2	EST_HUMAN	601658150RT NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5037	17756	30370	0.69	6.0E-02	AF146738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
5313	18117		0.94	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011189-013-004 BT0253 Homo sapiens cDNA
6122	18900	31888	0.77	6.0E-02	AI807637.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1 L1 L1 repetitive element:
6891	17987	30524	3.07	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6891	17987	30525	3.07	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7088	19777	32842	2.33	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:4049228 5'
7580	20249	33355	2.13	6.0E-02	AI204275.1	EST_HUMAN	qf58h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764199 3'
8321	21014		0.54	6.0E-02	11466495	NT	Reclinomonas americana mitochondrion, complete genome
9172	21842	35007	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCL_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2237362 3'
9172	21842	35008	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCL_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2237362 3'
9306	21973	35147	1.66	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9306	21973	35148	1.66	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9805	22456	35659	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
9805	22456	35660	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
11306	23965		1.69	6.0E-02	AA128386.1	EST_HUMAN	zr87c08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X68181.80S RIBOSOMAL PROTEIN L31 (HUMAN);
12187	24658	31084	2.19	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12564	24894		2.31	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60288
223	13035	25671	3.87	5.9E-02	AW934719.1	EST_HUMAN	O60288 KIAA0551 PROTEIN:
2882	15748	28386	2.88	5.9E-02	AF190289.1	NT	RC1-DT0001-280100-012-e10 DT0001 Homo sapiens cDNA
4817	17548	30173	1	5.9E-02	AF006304.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
5123	17841	30457	0.73	5.9E-02	AW028748.1	EST_HUMAN	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
5123	17841	30458	0.73	5.9E-02	AW028748.1	EST_HUMAN	wf34e02.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65388
8515	12107	34350	1.68	5.9E-02	9055249	EST_HUMAN	O65388 F12F1.20 PROTEIN ;
9351	20422		0.8	5.9E-02	BF24247.1	EST_HUMAN	wf34e02.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							Mus musculus Iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
							601877608F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10885	23376		3.2	5.9E-02	6679870	NT	Mus musculus follistatin-like (Foll), mRNA
10944	23623	36872	1.44	5.9E-02	11433356	NT	Homo sapiens nlnh1 (LOC51199), mRNA
11544	24144		1.59	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
912	13679		5.18	5.8E-02	D80110.1	NT	Thibacillus ferrooxidans merC, merA genes and URF-1
2864	16632		0.96	5.8E-02	AJ223821.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
4322	17061	29687	4.9	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4322	17061	29688	4.9	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4510	17245	28879	4.95	5.8E-02	AJ247505.1	EST_HUMAN	gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4510	17245	28880	4.95	5.8E-02	AJ247505.1	EST_HUMAN	gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4535	17270		2.62	5.8E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7578	20247	33352	2.99	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7578	20247	33353	2.99	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8565	21257	34394	0.67	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12084	24590		1.79	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12373	25396		7.06	5.8E-02	AA604269.1	EST_HUMAN	no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3053	15819	28463	1.36	5.7E-02	AJ081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:G37A2.2
3068	15834	28478	1.29	5.7E-02	AF119117.1	NT	CE08611;
3694	16448		0.97	5.7E-02	AF001282.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3783	16535	29173	2.45	5.7E-02	AW966791.1	EST_HUMAN	Chironomus thummi thummi globin VIIA.1 (cit-7A.1), globin 8.1 (cit-8.1), globin II-beta (cit-2beta), non-functional globin XIII (cit-13RT), globin XII (cit-12) and globin XI (cit-11) genes, complete cds
4637	17371		1.01	5.7E-02	M95099.1	NT	EST1378865 IMAGE resequences, MAGI Homo sapiens cDNA
7438	20115	33203	0.69	5.7E-02	D78003.1	NT	Bos taurus lysozyme gene (cov 3), complete cds
7438	20115	33204	0.69	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8055	20749	33880	1.42	5.7E-02	AJ285090.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
9750	22401	35606	0.64	5.7E-02	6681260	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv2.2 gene)
11143	23810	37090	4.42	5.7E-02	AJ752685.1	EST_HUMAN	Mus musculus ecd2 oncogene (Ecd2), mRNA
11143	23810	37091	4.42	5.7E-02	AJ752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn18b09 random
11321	24012		1.59	5.7E-02	AL163303.2	NT	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn18b09 random
12285	25213		7.24	5.7E-02	D50320.1	NT	Homo sapiens chromosome 21 segment HS21C103
							Plg DNA for SPAL-2, complete cds

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12515	25283		3.18	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12650	25387		2.61	5.7E-02	AF281280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1518	14265	26951	1.57	5.6E-02	AF094455.1	NT	Hydroxycylo rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
4595	17330	29957	1.12	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4648	17382	30014	1.46	5.6E-02	AA290599.1	EST_HUMAN	zs45c07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6562	19327	32334	6.57	5.6E-02	AW172708.1	EST_HUMAN	x02a10.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIAA0805 PROTEIN. ;
6791	19535	32563	1.25	5.6E-02	AA868182.1	EST_HUMAN	od4711.2.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7051	19742	32804	3.05	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA
7063	19754	32819	0.69	5.6E-02	AI983738.1	EST_HUMAN	wz34r05.x1 NCL CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2559989 3' similar to gb:X08409 RAF
7725	20388	33502	0.66	5.6E-02	AI163593.1	EST_HUMAN	PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
8701	21393	34539	2.88	5.6E-02	BE542863.1	EST_HUMAN	qd84g11.x1 Scores, tests, NHT Homo sapiens cDNA clone IMAGE:1734308 3'
8701	21393	34540	2.88	5.6E-02	BE542863.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9712	22363	35561	1.09	5.6E-02	AA482864.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
11556	24155		2.35	5.6E-02	AF260225.1	NT	m49407.s1 NCL CGAP_A1V1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C. ;
2660	15370	28108	6.8	5.6E-02	X97869.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3209	15972	28925	3.93	5.6E-02	6755501	NT	H. sapiens gene encoding La autoantigen
4191	16932	29561	1	5.6E-02	L41561.1	NT	Mus musculus SH3 domain protein 1B (SH3d1B), mRNA
5573	18370	31281	3.05	5.6E-02	Q01174	SWISSPROT	Gallid herpesvirus mRNA fragment
5935	18370	31281	3.58	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7277	19961	33038	2	5.6E-02	6755802	NT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
8019	20714	33845	0.63	5.6E-02	AF170911.1	NT	Mus musculus tufalin 1 (Tuf1), mRNA
8019	20714	33846	0.63	5.6E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9555	22208	35392	0.6	5.6E-02	10947034	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9555	22208	35393	0.8	5.6E-02	10947034	NT	Homo sapiens eIF4E-transcripter (4E-T), mRNA
9650	22302	35497	1.32	5.6E-02	U69482.1	NT	Homo sapiens aIF4E-transcripter (4E-T), mRNA
10943	23622	36871	7.26	5.6E-02	U09771.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
							Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (chaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB).>

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12797	26349	30604	1.49	5.5E-02	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
3019	15785		0.91	5.4E-02	AI277468.1	NT	Oryza sativa rib3-1 gene for putative Bowman Birk trypsin inhibitor
3416	17885		5.78	5.4E-02	BE073468.1	EST_HUMAN	R05-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3891	16641	29281	0.76	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8024	20719		0.88	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395281 to 2613730
8969	21659	34809	0.55	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10537	23234	36467	1.62	5.4E-02	AU120889.1	EST_HUMAN	AU120889 HEMBB1 Homo sapiens cDNA clone HEMBB1001630 5'
10598	23292	36530	2.01	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11132	23800	37076	1.32	5.4E-02	BF371289.1	EST_HUMAN	R06-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
11132	23800	37077	1.32	5.4E-02	BF371289.1	EST_HUMAN	R06-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
1031	13791	26450	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV6-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1031	13791	26451	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV6-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1495	14242	26929	14.72	5.3E-02	T84759.1	EST_HUMAN	ye37f12.1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506
2501	15218	27961	2.47	5.3E-02	AI278408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2943	15709	28360	0.95	5.3E-02	M58417.1	NT	Pseudomonas putida tgsS gene
2943	15709	28361	0.95	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3150	15913	28558	5.51	5.3E-02	AI278408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
5029	17749	30381	6.34	5.3E-02	M80463.1	NT	Pseudomonas putida tgsS gene
5236	18042	30670	1.98	5.3E-02	AE000527.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5236	18042	30671	1.98	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6785	19529	32556	5.01	5.3E-02	9695413	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6992	19685	32733	1	5.3E-02	U32832.1	NT	Lymphocystis disease virus 1, complete genome
7260	19944		2.06	5.3E-02	S78221.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7777	20399	33514	0.65	5.3E-02	P38742	SWISSPROT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8304	20988		0.7	5.3E-02	U10098.1	NT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
9023	21713	34857	1.56	5.3E-02	X03127.1	NT	Mus musculus 129/Sv cyslain C (cst3) gene, complete cds
10032	22680	35897	0.62	5.3E-02	AB022605.1	NT	Podospira anserina mitochondrial epsilon-sen DNA
10032	22680	35898	0.62	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA [guanine-7-methyltransferase, complete cds
10156	22804		0.63	5.3E-02	Y07907.1	NT	Homo sapiens hCMT1b mRNA for mRNA [guanine-7-methyltransferase, complete cds
10230	22878	36090	0.7	5.3E-02	X68432.1	NT	D. rerio mRNA for ap-23 POU gene, splice variant (neurula, 9-16 hpf and postmitogenesis, 20-28 hpf)
							B. rerio pou1c mRNA for transcription factor

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12778	25030	30964	1.43	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2283	15008		160.56	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA, peptide hydrolase) (MEP1A) mRNA
3112	15877	28516	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3112	15877	28517	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3919	16689	28310	1.23	5.2E-02	AF226101.1	NT	Arabidopsis thaliana putative dicarboxylate diion protein (Crd1) mRNA, complete cds
3921	16671		1.19	5.2E-02	6671757	NT	Mus musculus cytokine inducible SH2-containing protein 3 (Cish3), mRNA
4245	16986	28609	3.02	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nsr-1 mRNA, complete cds
5053	17772		0.9	5.2E-02	AA297940.1	EST_HUMAN	EST113552 Uterus Homo sapiens cDNA 5' end
5828	18617	31548	0.61	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6016	18797		0.96	5.2E-02	AI830965.1	EST_HUMAN	w80e04.x1 NCJ_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1
7174	18860	32932	3.13	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROGRESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8095	20789		2.19	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9629	22282	35472	1.87	5.2E-02	D10927.1	NT	Tumip mosaic virus genomic RNA for Capsid protein, complete cds
9629	22282	35473	1.87	5.2E-02	D10927.1	NT	Tumip mosaic virus genomic RNA for Capsid protein, complete cds
12414	24795		1.93	5.2E-02	Q03030	SWISSPROT	OXALOOCTATE DECARBOXYLASE ALPHA CHAIN
2364	15086		1.17	5.1E-02	AL134071.1	EST_HUMAN	DKFZp447D073_11 647 (synonym: h1b1) Homo sapiens cDNA clone DKFZp447D073 5'
4178	16919	28547	1.03	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4960	17685		49.38	5.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6576	19339	32350	0.72	5.1E-02	AF280369.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds
6760	17929	30564	1.44	5.1E-02	BF378825.1	EST_HUMAN	QVQ-LJM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8151	20845	33975	0.84	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8151	20845	33976	0.84	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8245	20839	34076	1.48	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
8783	21475	34622	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
8783	21475	34623	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9709	22360	35556	6.2	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Sed1 homolog (SSD1) gene, complete cds
10082	22730	35945	1.89	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10733	23420	36661	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
10733	23420	36662	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11620	24217	37540	1.3	5.1E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 3/8
12421	24797		2.56	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds

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12679	24968		1.41	5.1E-02	AA534104.1	EST_HUMAN	n7302.s1 NCI CGAP_P10 Homo sapiens cDNA clone IMAGE:898139
470	13256	25884	1.84	5.0E-02	AF080004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1182	13934	26599	6.54	5.0E-02	Z89104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1983	14719	27438	3.91	5.0E-02	P02810	SWISSPROT	SALVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2821	13731	26397	1.28	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3332	16092		1.42	5.0E-02	7305810	NT	Mus musculus Urc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3582	16337		1.04	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 87 of 163 of the complete genome
3672	16425	28066	5.83	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
4770	17502		0.98	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6039	18318	31780	0.95	5.0E-02	AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6216	18990		1.3	5.0E-02	AJ242825.1	NT	Mus musculus Dmp-1 gene, exons 1-8
7437	20114	33202	12.48	5.0E-02	P35816	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10100	22748	35963	1.28	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
10521	23167		0.45	5.0E-02	BF213280.1	EST_HUMAN	601844753F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4070101 5'
11473	24074	37383	2.5	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
11956	25246		3.5	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
217	13028		24.03	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
360	13158	25800	2.66	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
360	13158	25801	2.68	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3282	16043	28682	2.53	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3556	16311		0.69	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632928 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3579	16334	28978	0.99	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares Testis NHT Homo sapiens cDNA clone IMAGE:728428 3'
3579	16334	28979	0.99	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares Testis NHT Homo sapiens cDNA clone IMAGE:728428 3'
4788	17519	30141	1.91	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4788	17519	30142	1.91	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5286	18091	30751	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5286	18091	30752	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7042	19733	32783	0.91	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8513	21205		0.8	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8552	21344	34489	0.71	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10181	22839	36054	0.48	4.9E-02	P18532	SWISSPROT	TRANSCRIPTION FACTOR E3
10494	23140	36366	0.46	4.9E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11378	23985	37285	3.22	4.9E-02	AF068303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12345	24752		1.77	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12598	24912		3.41	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
321	13123	25760	1.54	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
322	13123	25760	3.94	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
476	13262	25899	9.96	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2271	14997	27735	1.82	4.8E-02	W51983.1	EST_HUMAN	z49b02.s1 Soares, senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30838 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3203	15966	28620	2.1	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4623	17358		1.15	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle myosin receptor
5144	17863	30478	1.03	4.8E-02	11693131	NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
5144	17863	30479	1.03	4.8E-02	11693131	NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
8037	20732	33864	1.32	4.8E-02	AW388497.1	EST_HUMAN	MF2-ST0129-221099-012-502 ST0129 Homo sapiens cDNA
9027	21717	34870	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9027	21717	34871	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
6731	19565	32597	3.83	4.7E-02	W01153.1	EST_HUMAN	y29709.r1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element
6819	19480	32503	2.02	4.7E-02	M62752.1	NT	Rat stalin-related protein (st1) gene, complete CDS
8149	20843	33973	8.24	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
8852	21543	34690	0.96	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8875	21566		2.68	4.7E-02	AB026678.1	NT	Gallus gallus Wpici-8 gene, complete cds
9127	21815	34981	6.89	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9547	22200	35382	0.67	4.7E-02	BF305237.1	EST_HUMAN	601892692F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
9635	22287		0.57	4.7E-02	A1873042.1	EST_HUMAN	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
10654	23345	36582	1.4	4.7E-02	6754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
11545	24145	37453	1.39	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11545	24145	37454	1.39	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
264	13072	25712	0.93	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0338-25159-003-p05 HT0338 Homo sapiens cDNA
722	13496	26149	2.91	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1269	14018		0.99	4.6E-02	A1014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1638979 3' similar to TR:P60533
1338	14086	26762	3.47	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA :contains element LTR1 repetitive element ;
							AV727059 HTC Homo sapiens cDNA clone HTCBCWC01 5'

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2482	15209	27951	2.31	4.6E-02	AW236023.1	EST_HUMAN	xt24f03.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2684853 3' similar to SW:GRF1_HUMAN
2811	13072	25712	1.9	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1:
3325	15774	28423	0.74	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3487	15774	28423	0.73	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4103	16846		1.35	4.6E-02	AF220365.1	NT	Mus musculus nucleolar RNA helicase II/Gu (dbp21) gene, complete cds
5121	17639	30455	0.89	4.6E-02	AA079157.1	EST_HUMAN	zms2c10.s1 Stragene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gb:X03212 KERATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
5647	18442	31355	1.57	4.6E-02	AF076982.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6136	18914	31883	3.51	4.6E-02	X61624.1	NT	C.reinhardtii alp2 (alpB) mRNA
6136	18914	31884	3.51	4.6E-02	X61624.1	NT	C.reinhardtii alp2 (alpB) mRNA
6702	19617	32659	1.47	4.6E-02	AH49574.1	EST_HUMAN	q60b006.x1 Soares_placenta_8tc9weeks_2NhtP8tk9W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.3 L1 repetitive element;
8554	21246	34386	2.69	4.5E-02	BE154006.1	EST_HUMAN	PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11379	23986	37286	4.94	4.6E-02	AA913328.1	EST_HUMAN	ol27h08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12325	24744		1.88	4.6E-02	AV712871.1	EST_HUMAN	AV712871 DCA Homo sapiens cDNA clone DCAAZF07 5'
12705	24985		3.98	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
434	13220	25866	1.72	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1196	13948	28612	1.11	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1196	13948	28613	1.11	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1797	14537	27247	4.57	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2103	14834	27568	3.76	4.5E-02	AE003964.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3710	18463	29102	3.66	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6137	18915	31885	1.61	4.5E-02	AJ400877.1	NT	Homo sapiens ASQ3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6415	19183	32182	0.77	4.5E-02	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6779	19523	32550	0.61	4.5E-02	L28487.1	NT	Methanosarcina frisa carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
6779	19523	32551	0.61	4.5E-02	L28487.1	NT	Methanosarcina frisa carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8262	20986	34125	1.96	4.5E-02	AF036694.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
9849	22499	35689	4.57	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to similar to neuro-D4 protein
10000	22648	35660	0.48	4.5E-02	X55508.1	NT	A.europeum mRNA for legumin-like protein

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10116	22764	35978	0.95	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12164	24840	31097	1.94	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
12537	25290	30733	6.91	4.5E-02	AA191097.1	EST_HUMAN	zq43111.11 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
213	13025		5.52	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3835388 5'
2089	14821		5.42	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2494	15211	27953	2.4	4.4E-02	AW875475.1	EST_HUMAN	QV2.PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3631	16384	28024	1.95	4.4E-02	AF159180.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4584	17319	29945	1.24	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4584	17319	29946	1.24	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4883	17427		2.28	4.4E-02	AJ22589.1	NT	Ovis aries CCAAT-archancer binding protein epsilon gene
7018	19710	32768	0.64	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7018	19710	32767	0.64	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8650	21342	34486	2.14	4.4E-02	AA736969.1	EST_HUMAN	nm131h03.s1 NCJ CGAP SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11007	23679	36636	2.02	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11137	23824	37104	2.78	4.4E-02	AA498739.1	EST_HUMAN	ac33f04.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
11890	24480		2.57	4.4E-02	AB040826.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12087	25408		1.87	4.4E-02	BF241245.1	EST_HUMAN	601878748F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
783	13536	28195	7.07	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2573	16287	28024	1.23	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0408 5'
3423	16180	28830	7.84	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3631	16404		1.37	4.3E-02	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5152	17889	30482	0.95	4.3E-02	U11788.1	NT	Grapevine fanleaf virus coat protein gene, partial cds
6404	19173	32171	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6404	19173	32172	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6633	19395	32410	0.73	4.3E-02	AA652286.1	EST_HUMAN	ns66c12.s1 NCJ CGAP P12 Homo sapiens cDNA clone IMAGE:1188888
8411	21104	34243	0.73	4.3E-02	AF283359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8700	21392	34537	1.02	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
8700	21392	34538	1.02	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
803	13575	26238	2.7	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
846	13616		2.32	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'

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876	13645	26315	1.35	4.2E-02	AW003645.1	EST_HUMAN	w34901.x1 NCI CGAP_P41 Homo sapiens cDNA clone IMAGE:2545684 3' similar to TR:Q63291 Q63291
1714	14457		1.02	4.2E-02	AL445086.1	NT	L1 RETROPOSON, ORF2 MRNA, contains L1.13 L1 repetitive element;
1771	14513	27213	1.01	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
3655	16408	29047	2.43	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4100	16843	29471	0.7	4.2E-02	BE262605.1	EST_HUMAN	601150933FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
4284	17023	29648	1.83	4.2E-02	U26874.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4284	17023	29649	1.83	4.2E-02	U26874.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4895	17429	30060	2.32	4.2E-02	BF342995.1	EST_HUMAN	602017105FT NCI CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4162672 5'
5530	18328	31231	0.68	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5530	18328	31232	0.68	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6886	17962	30517	0.56	4.2E-02	BE268285.1	EST_HUMAN	601124596FT NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2889319 5'
7426	20103	33190	4.7	4.2E-02	AF278752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
8710	21402	34547	3.96	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10064	22712	35930	1.22	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
10869	23645	36898	2.82	4.2E-02	AA976118.1	EST_HUMAN	on33b11.st NCI CGAP_Li6 Homo sapiens cDNA clone IMAGE:1658461 3' similar to gb:M66290
11278	23939	37231	2.54	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11278	23939	37232	2.54	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11489	24090	37402	1.68	4.2E-02	AF176458.1	NT	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
12415	25335		3.43	4.2E-02	AB83494.1	EST_HUMAN	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
497	13281	25916	1.24	4.1E-02	AF200629.1	NT	w49g10.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
2683	15392	28131	1.04	4.1E-02	AE002330.2	NT	Homo sapiens HPS1 gene, intron 5
4439	17175		7.52	4.1E-02	AW893494.1	EST_HUMAN	Chlamydia muridarum, section 60 of 85 of the complete genome
5556	18353	31262	0.82	4.1E-02	BE251894.1	EST_HUMAN	QV1-NN0012-180400-164-06 NN0012 Homo sapiens cDNA
5556	18353	31263	0.82	4.1E-02	BE251894.1	EST_HUMAN	601107535FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6783	19527		0.87	4.1E-02	X78881.1	NT	601107535FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6899	19691	32742	1.25	4.1E-02	AE002132.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7413	20090	33174	2.09	4.1E-02	7662347	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
							Homo sapiens KIAA0867 protein (KIAA0867), mRNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7502	20173	33265	0.66	4.1E-02	L02110.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7665	20329	33439	3.12	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitotic-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8541	21233	34378	0.68	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9082	21741	34899	0.81	4.1E-02	AA372398.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
12728	25336	30715	4.07	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3238	16000	28650	3.26	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3780	16532	29170	1.27	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5265	18100	30759	5.4	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6120	18888	31868	0.93	4.0E-02	BF110434.1	EST_HUMAN	7n62h07.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:35688380 3' similar to TR:O75298 O75298 R29124_1;
7560	20258	33366	6.57	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7650	20314		0.86	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7666	20330	33440	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7668	20330	33441	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8617	21309	34461	2.22	4.0E-02	P08940	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9544	22197		0.78	4.0E-02	BF679376.1	EST_HUMAN	602153884FT NIH_MGC_B3 Homo sapiens cDNA clone IMAGE:4294724 5'
9587	22220	35408	4.01	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol fumarate reductase subunit A
9884	22534		1.21	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11778	24369		1.54	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Cgt+ ATPase
12053	25158	30898	3.31	4.0E-02	AJ01056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1098	13856	26516	2.75	3.9E-02	BF516149.1	EST_HUMAN	UHL-BW1-arx-h-09-o-UJ.st NC1 CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1323	14072	26745	2.45	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1954	14688	27402	2.4	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmethyl-binding fragment DesD7
2708	15415		1.69	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
4119	16860	29487	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4118	16860	29488	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5408	18207	30913	0.55	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5408	18207	30914	0.55	3.8E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5644	18439	31353	1.04	3.9E-02	BE68841.1	EST_HUMAN	601849874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
5766	18557	31484	0.95	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
6957	19439	32454	1.18	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7739	20435	33557	1.14	3.9E-02	BF239613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
7959	20654	33778	0.79	3.9E-02	AJ220041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
7959	20654	33779	0.79	3.9E-02	AJ220041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
11386	20396	33511	2	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11913	25298		15.38	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12543	24883		1.83	3.9E-02	U66081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV1S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TORBU1S1, TORBU1S2, >
12666	25223		5.31	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contig8; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mirxq28orf
1945	14880	27394	1.16	3.8E-02	BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
2114	14845		1.77	3.8E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
4878	17603	30228	1.1	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001688 5'
5354	18157	30840	1	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
5996	18777	31739	1.32	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7218	19903	32978	1.66	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8562	21254		1.33	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10549	23245	36481	2.62	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
971	13736	28401	4.94	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1367	14115	28790	0.91	3.7E-02	L14861.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2230	14958	27698	3.84	3.7E-02	A1984803.1	EST_HUMAN	wR65e08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2582	15286	28034	0.92	3.7E-02	AB018281.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3045	15811	28457	0.9	3.7E-02	P78944	SWISSPROT	ECMESODERMIN
3047	15813	28458	2.99	3.7E-02	BF312963.1	EST_HUMAN	601886233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125884 5'
3447	16203		1.17	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
6978	25422		0.83	3.7E-02	AF000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7

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7592	20260	33368	0.56	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
9814	22863		1	3.7E-02	AA782516.1	EST_HUMAN	af55c09.s1 Soares parathyroid tumor_NhpHPA Homo sapiens cDNA clone 1360912 3'
11954	24506	37811	3.86	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12803	25183	30813	1.94	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3646	16399	29039	1.38	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3654	16407	29046	0.88	3.6E-02	AL096906.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
5341	18144	30806	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5341	18144	30823	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5413	18212	30921	0.64	3.6E-02	AF181722.1	NT	Homo sapiens RUC2AS (RUC2) mRNA, complete cds
6607	19370	32382	5.47	3.6E-02	AW945516.1	EST_HUMAN	GM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6607	19370	32383	5.47	3.6E-02	AW945516.1	EST_HUMAN	GM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6885	19678	32725	2.5	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cy2 precursor (sgp2) gene, complete cds
7206	19891	32967	2.76	3.6E-02	AA714521.1	EST_HUMAN	rw20605.s1 NCI_CGAP_G080 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2
7533	20203	33298	1.03	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN)
9291	21958	35130	1.72	3.6E-02	U20608.1	NT	MR0-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA
9291	21958	35131	1.72	3.6E-02	U20608.1	NT	Dicystotellium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9512	22165	35347	0.83	3.6E-02	BF347586.1	EST_HUMAN	602020463F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4156116 5'
11135	23803	37080	1.4	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11135	23803	37081	1.4	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11852	24436		1.46	3.6E-02	AL280966.1	EST_HUMAN	qk48809.x1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:1872185 3'
875	13644	26314	1.08	3.5E-02	U09508.1	NT	Drosophila melanogaster figgin mRNA, complete cds
988	13751	26413	1.39	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1566	14303	26891	1.55	3.5E-02	BF578085.1	EST_HUMAN	602065136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1556	14303	26992	1.55	3.5E-02	BF578085.1	EST_HUMAN	602065136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4188	16829	29559	1.83	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4281	17020	29647	1.27	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6127	18905	31973	1.77	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAc1), complete cds

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7877	20572		0.78	3.5E-02	H28951.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element
8521	21213	34357	2.7	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:3828737 3'
8917	22566	35782	1.45	3.5E-02	X76842.1	NT	Llactis MG1363 grpE and dnaK genes
9965	22613	35817	0.5	3.5E-02	BE561042.1	EST_HUMAN	601344661F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3617654 5'
11477	24078	37988	1.82	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-H03 CT0326 Homo sapiens cDNA
11477	24078	37989	1.82	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-H03 CT0326 Homo sapiens cDNA
12596	25234		5.69	3.5E-02	BE276848.1	EST_HUMAN	601178765F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3543933 5'
564	13346	25973	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
564	13346	25974	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25973	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25974	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1029	13789	26448	2.92	3.4E-02	AW274020.1	EST_HUMAN	xx26407.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to
1184	13936		7.14	3.4E-02	11345459	NT	SW:C211_HUMAN P3801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
2391	15112	27649	2.06	3.4E-02	T57160.1	EST_HUMAN	Homo sapiens lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains
3424	16181	28831	1.4	3.4E-02	AL163208.2	NT	MER29 repetitive element
3757	16509	29145	0.7	3.4E-02	BE839514.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
3900	16650	29291	3.19	3.4E-02	AW794952.1	EST_HUMAN	RC3-FN0155-060700-011-410 FN0155 Homo sapiens cDNA
4559	17294	29922	2.41	3.4E-02	X59799.1	NT	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
5000	17723		3.59	3.4E-02	Q26457	SWISSPROT	M.musculus S-antigen gene promoter region
5019	17740	30349	1.2	3.4E-02	AJ012489.1	NT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
6754	17923	30558	4.73	3.4E-02	U24393.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
8159	20853		3.25	3.4E-02	A1890629.1	EST_HUMAN	Human lysyl oxidase-like protein gene, exon 3
8646	21338	34482	1.38	3.4E-02	AA664886.1	EST_HUMAN	w89404.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'
							nu70708.s1 NCL_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element ;
							zq0411.s1 Stratagene muscle 697208 Homo sapiens cDNA clone IMAGE:628749 3' similar to
8814	21506		5.97	3.4E-02	AA194306.1	EST_HUMAN	TR-G1017425 G1017425
9878	22330		0.63	3.4E-02	AB02719.1	EST_HUMAN	IPISGKLPKVTLSRDGKPLKATMRNFTEAENLTINLKESVTADAGRYEITAAANSSTGTTKAFINVLDRPG
983	13161		9.61	3.3E-02	AA398735.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGGQVNTYLLKREITSTAVWTEVSATVARTMMKMKL ... ;
1143	13898	26559	17.86	3.3E-02	AB035887.1	NT	oz89h08.x1 Soares_papillary tumor NIH-PA Homo sapiens cDNA clone IMAGE:1683519 3'
							z75608.s1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:728198 3'
							Cricetus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds

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1489	14236	26923	1.15	3.3E-02	L18870.1	NT	Homo sapiens cytochrome P4502C18 (CYP2C18) gene, exons 2 and 3
1835	14381	27068	1.47	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1732	14474		1.29	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2077	14809		2.48	3.3E-02	R09112.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
2453	15171	27910	1.31	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tret1), mRNA
4156	14381	27068	2.44	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4435	17171	29800	1.78	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tret1), mRNA
6336	19108	32095	27.38	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6336	19108	32096	27.38	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7408	20085	33169	0.63	3.3E-02	AF124162.1	NT	Nicotiana plumbaginifolia molybdopterin synthase sulphurylase (nxs5) gene, partial cde
9222	21901	35071	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9222	21901	35072	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9324	21991	35162	0.66	3.3E-02	AA488202.1	EST_HUMAN	ad08R09.s1 Soares NIHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
9324	21991	35163	0.66	3.3E-02	AA488202.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24;1D5 (HUMAN);
11065	23735	37008	3.63	3.3E-02	BF691107.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24;1D5 (HUMAN);
12142	24630		3.24	3.3E-02	T96545.1	EST_HUMAN	60224717F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4332497 5'
12259	24704		1.52	3.3E-02	AF289665.1	NT	ye49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
12288	24718		2.92	3.3E-02	M81890.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
129	12944	25588	0.74	3.2E-02	AJ002005.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
1104	13861	26520	7.01	3.2E-02	AF096275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1104	13861	26521	7.01	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2112	14843		3.01	3.2E-02	P28955	SWISSPROT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
3131	15898	28540	10.08	3.2E-02	BE867353.1	EST_HUMAN	LARGE TEGUMENT PROTEIN
3701	16454	29094	0.92	3.2E-02	AL163203.2	NT	60144243F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3942	16892	29330	1.64	3.2E-02	Z74103.1	NT	Homo sapiens chromosome 21 segment HS21C003
3942	16892	29331	1.64	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4193	16934		14.21	3.2E-02	X94768.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4716	17448	30081	3.42	3.2E-02	AF114182.1	NT	H.sapiens RPB3 gene (XLRP gene 3)
4894	17621		1.09	3.2E-02	AF109908.1	NT	Saxifraga nultifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
6448	18247	31135	1.83	3.2E-02	X68709.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; GTA gene, partial cds; and unknown genes

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	18247	31138	1.83	3.2E-02	X88708.1	NT	S. griseocaneum whiG-Stv gene
6431	19198	32198	3.13	3.2E-02	M32437.1	NT	Rat polyomavirus left junction in cell line W98.14
6432	19200		33.46	3.2E-02	T89387.1	EST_HUMAN	Y433H12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element contains LTR1 repetitive element;
6513	19278	32279	4.14	3.2E-02	AF173845.1	NT	Seguinus oedipus tissue kallikrein gene, complete cds
7662	20328	33436	0.64	3.2E-02	11424049	NT	Homo sapiens cyclochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8199	20893	34030	4.64	3.2E-02	6880565	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
8839	21531		0.73	3.2E-02	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
9125	21813	34978	1.21	3.2E-02	A1278971.1	EST_HUMAN	gm17604.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9126	21813	34979	1.21	3.2E-02	A1278971.1	EST_HUMAN	gm17604.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9957	22605		4.07	3.2E-02	AA719795.1	EST_HUMAN	zp54b12.s1 Soares pineal_gland_N3-HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gbt108441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10256	22904	36114	0.95	3.2E-02	U96762.1	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1237	13986		2.14	3.1E-02	4503418	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1282	14032	26702	1.72	3.1E-02	F18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1885	14822	27332	1.09	3.1E-02	6671584	NT	Mus musculus adapter-related protein complex AP-3, delta subunit (Ap3d), mRNA
1967	14703		1.34	3.1E-02	Z50097.1	NT	Drosophila melanogaster mRNA for headcase protein
5182	17990	30508	1.13	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5276	18081		2.12	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5561	18358	31288	0.74	3.1E-02	BF68742.1	EST_HUMAN	602068783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066789 6'
5628	25072	31338	0.59	3.1E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flaC-homologs, unknown genes) and flanking genes, strain FAM18
8840	21532	34677	0.46	3.1E-02	BE965082.2	EST_HUMAN	601658879R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3886291 3'
9931	22579	35778	2.93	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
11765	24356	37689	1.78	3.1E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
1619	14366		1.88	3.0E-02	AF187125.1	NT	Ptychokeles minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2590	15304	28040	0.97	3.0E-02	AA402242.1	EST_HUMAN	z056h03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727283 5'
3645	16398	28038	2.78	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3728	16480		0.74	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0286-150200-040-e09 ST0286 Homo sapiens cDNA
3929	16678		1.42	3.0E-02	AA364003.1	EST_HUMAN	EST174530 Pineal gland II Homo sapiens cDNA 5' end
4991	17714	30318	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4991	17714	30319	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5307	18112		3.43	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KAA1573 protein, partial cds

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6160	19837	31905	1.4	3.0E-02	N98915.1	EST_HUMAN	z338a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TARI repetitive element ;
6160	19837	31906	1.4	3.0E-02	N98915.1	EST_HUMAN	z338a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TARI repetitive element ;
6892	19609	32648	3.32	3.0E-02	AJ242806.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
6806	19467	32488	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6806	19467	32489	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6971	19453	32472	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6971	19453	32473	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7132	19619	32885	1.4	3.0E-02	M86524.1	NT	Human dystrophin gene
7483	20155		0.59	3.0E-02	BF246361.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8025	20720		0.48	3.0E-02	BF679706.1	EST_HUMAN	602154394F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295854 5'
8539	21231	34373	0.66	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-290600-108-c04 HT0704 Homo sapiens cDNA
8692	21384		1.8	3.0E-02	AF275654.1	NT	Omithorhynchus anatinus coagulation factor X mRNA, complete cds
10357	23004	36221	1.49	3.0E-02	AE001797.1	NT	Thermidoga maritima section 109 of 138 of the complete genome
10446	23092	36322	0.49	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11197	23982	37148	2.73	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11690	24285	37607	7.75	3.0E-02	AA483216.1	EST_HUMAN	ne87804.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:311283
12243	25389	30618	2	3.0E-02	R32019.1	EST_HUMAN	Y683404.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12587	24909		2.46	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-r05 NN0038 Homo sapiens cDNA
12629	25383		2.06	3.0E-02	AF048897.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2436	15594	27891	1.27	2.8E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2890	15756	28402	1.04	2.9E-02	BE565044.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680895 5'
2890	15756	28403	1.04	2.8E-02	BE565044.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680895 5'
3908	16658	29299	0.89	2.9E-02	H72805.1	EST_HUMAN	yu07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5972	18764	31715	0.97	2.8E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6198	18975	31953	7.39	2.9E-02	BF032293.1	EST_HUMAN	601452661F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856588 5'
6955	19555	32585	0.56	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (fhaB- and fhaC-homologs, unknown genes) and flanking genes, strain FAM18
7148	19835	32604	12.03	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'

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Table 4
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7897	20582	33723	0.87	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendella chitrensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
7897	20582	33724	0.87	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendella chitrensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9558	22211	35396	2.49	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9558	22211	35397	2.49	2.9E-02	AW876979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9774	22425		0.75	2.9E-02	AW976597.1	EST_HUMAN	EST388706 MAGC resequences, MAGN Homo sapiens cDNA
10243	22891	38103	1.25	2.9E-02	AP000084.1	NT	Aeropyrum pernix genomic DNA, section 777
10977	17902	30590	1.91	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
552	13335		0.96	2.8E-02	AW970153.1	EST_HUMAN	EST382234 MAGC resequences, MAGK Homo sapiens cDNA
3360	16119	28775	1.3	2.8E-02	AF069063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3360	16119	28776	1.3	2.8E-02	AF069063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
5400	18200	30905	11.62	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3948067 5'
6711	19526	32670	1.15	2.8E-02	T78960.1	EST_HUMAN	yd21608.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:711486 5'
8228	20920	34058	1.61	2.8E-02	AJ005820.1	NT	Craterosigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
8915	21806	34749	0.85	2.8E-02	AA280762.1	EST_HUMAN	zs96c06.r1 NCI_CGAP GC81 Homo sapiens cDNA clone IMAGE:711486 5'
9108	21796	34960	1	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9212	21891	35058	0.69	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12528	25229		1.5	2.8E-02	R06968.1	EST_HUMAN	Yf12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126675 5'
12530	24876		1.48	2.8E-02	X069322.1	NT	Yeast CN3TC chromosome III RAHS DNA (right arm transcription hot-spot)
							Human geminine T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2P1, TCRBV7S2A1N4T, TCRBV13S9/13S>
1472	14219	26905	1.23	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3425	16182	28632	1.74	2.7E-02	AL161494.2	NT	Yw68h12.r1 Soares multiple sclerosis 2NBHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4178	16918	29645	1.92	2.7E-02	N47268.1	EST_HUMAN	Yw68h12.r1 Soares multiple sclerosis 2NBHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4178	16918	29646	1.92	2.7E-02	N47268.1	EST_HUMAN	Yw68h12.r1 Soares multiple sclerosis 2NBHMSP Homo sapiens cDNA clone IMAGE:280487 5'
							SP-JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
5355	18158	30841	1.2	2.7E-02	R12245.1	EST_HUMAN	T.aestivum p1TH20 mRNA for wheat type V thionin
5812	18601	31529	0.86	2.7E-02	X61670.1	NT	Onyza salvia mRNA for ascorbate oxidase, partial cds
5885	18671	31612	0.64	2.7E-02	AB004799.1	NT	A.bisporus p6kA gene
6505	19270		0.93	2.7E-02	X97680.1	NT	cd86h03.a1 Soares fetal_Nb2IF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
6867	19449	32467	2.29	2.7E-02	AA983571.1	EST_HUMAN	

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8252	20946		1.06	2.7E-02	AI377036.1	EST_HUMAN	tc28g08.x1 Soares_t01a_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
8514	21206	34349	0.49	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
558	13340	25988	1.12	2.8E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2369	15088	27825	3.29	2.8E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2368	15090	27827	4.49	2.8E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2368	15090	27828	4.49	2.8E-02	6764241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2916	15682		1.86	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
4847	17577	30200	2.25	2.8E-02	L12032.1	NT	Chicken dorazih-1 mRNA, complete cds
5005	17728	30332	1.58	2.8E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5032	17752	30364	2.35	2.6E-02	AW241154.1	EST_HUMAN	xs52b04.x1 NCI_CGAP_Ser4 Homo sapiens cDNA clone IMAGE:2570363 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069
6754	18546		0.7	2.8E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
5800	18590		0.59	2.8E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
8126	18903		7.34	2.6E-02	AI206030.1	EST_HUMAN	9827111.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6331	19101	32089	1.9	2.6E-02	BE821748.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6728	19582	32593	0.9	2.6E-02	Z99084.1	NT	Vaccinia virus ORF1L, strain Wyeth
6728	19582	32594	0.9	2.6E-02	Z99084.1	NT	Vaccinia virus ORF1L, strain Wyeth
6810	19471	32494	7.11	2.6E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngf), mRNA
8403	21096	34232	0.71	2.6E-02	AA869948.1	EST_HUMAN	sk22f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9260	22014	35182	1.15	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9614	22267	35453	0.75	2.6E-02	AF114952.1	NT	Saccharomyces daltensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9614	22267	35454	0.75	2.6E-02	AF114952.1	NT	Saccharomyces daltensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10303	22950	36185	4.39	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11161	23856		1.87	2.6E-02	4506466	NT	Homo sapiens radixin (RDX) mRNA
11361	24049		2.33	2.6E-02	AA279351.1	EST_HUMAN	zs84q02.r1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:704162 5'
11553	24152	37465	2.2	2.6E-02	AW500547.1	EST_HUMAN	UI-HF-BNO-akf-e-10-o-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077468 5'
12170	23375	30615	2.09	2.6E-02	BF343827.1	EST_HUMAN	602015501F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150944 5'
519	13303	25935	1.75	2.5E-02	AI793130.1	EST_HUMAN	on28f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
519	13303	25936	1.75	2.5E-02	AI793130.1	EST_HUMAN	on28f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
791	13563	26224	15.9	2.5E-02	BE974314.1	EST_HUMAN	601880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'

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849	13619	26289	7.2	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
2768	16471		2.24	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2956	16722	28371	4.35	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2956	15722	28372	4.35	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4023	17879	28399	1	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4023	17879	29400	1	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4182	16922	28650	4.23	2.5E-02	AW592114.1	EST_HUMAN	H36H08.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
5825	18422	31335	0.61	2.5E-02	A173276.1	EST_HUMAN	z83c10.x5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:810354 3'
6100	18878		5.01	2.5E-02	BE670128.1	EST_HUMAN	7e30e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.11 L1 repetitive element
6115	18893		4.1	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6244	19018	31992	1.04	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7563	20233	33338	1.7	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213406 5'
7563	20233	33337	1.7	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213406 5'
8724	21416	34580	0.81	2.5E-02	Q81713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8863	21554	34698	0.47	2.5E-02	AW025821.1	EST_HUMAN	wu08c10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2516370 3'
9968	22614		0.55	2.5E-02	X71303.1	NT	D. radiatum 28S ribosomal RNA, D2 domain
10482	23128	36356	0.65	2.5E-02	A147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1686982 3'
10712	23401	36640	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
10712	23401	36641	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
10773	23456	38700	2.32	2.5E-02	AJ237836.1	NT	Bos taurus peridial stidB gene, exons 17-19
10795	23478						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (I-Ealpha) and major histocompatibility protein class II beta chain (I-Ebeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-lp
11770	24361		3.46	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
12134	25311		2.55	2.5E-02	AB007548.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12311	25182		2.89	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
12432	24804	31043	1.76	2.5E-02	11433220	NT	601682365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
1593	14339	27028	1.94	2.5E-02	BE973327.1	EST_HUMAN	y776f11.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211149 5'
2037	15584	27501	1.7	2.4E-02	H65884.1	EST_HUMAN	I-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2037	15584	27502	1.92	2.4E-02	P01901	SWISSPROT	I-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4335	17074	29702	1.65	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4485	17220	29847	1.68	2.4E-02	P01901	SWISSPROT	I-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4485	17220	29848	1.58	2.4E-02	P01901	SWISSPROT	I-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5068	17787	30403	0.95	2.4E-02	8922702	NT	Homo sapiens hypothetical protein FLJ10844 (FLJ10844), mRNA
6121	18699	31867	0.9	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:410791 3'
6267	19040	32018	0.58	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
6267	19040	32017	0.58	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7121	19808	32875	0.8	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7138	19825	32892	0.9	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7138	19825	32893	0.9	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7791	20486		0.72	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-06 ST0186 Homo sapiens cDNA
7844	20539		0.5	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8340	21033		0.69	2.4E-02	H78376.1	EST_HUMAN	yu12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element;
8429	21122	34280	9.78	2.4E-02	N69442.1	EST_HUMAN	gb K02809 JCATSR7K Rat (rRNA); contains A3R.b1 A3R repetitive element;
8885	21576	34718	0.57	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
8907	21598	34740	0.78	2.4E-02	AA625660.1	EST_HUMAN	zu01c06.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 [SLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR XTR repetitive element;
9591	22244	35427	0.52	2.4E-02	AF124180.1	NT	Arabidopsis thaliana myoeloplasm synthase sulphurylase (crx5) gene, complete cds
9591	22244	35428	0.52	2.4E-02	AF124180.1	NT	Arabidopsis thaliana myoeloplasm synthase sulphurylase (crx5) gene, complete cds
9706	22357	35553	2.38	2.4E-02	AV692954.1	EST_HUMAN	AV692954 GKG Homo sapiens cDNA clone GKDCSC03 5'
9881	22531	35728	2.73	2.4E-02	AA493894.1	EST_HUMAN	th07b12.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element;
10512	23158		0.46	2.4E-02	BE387111.1	EST_HUMAN	601274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:361602 5'
11565	24164	37475	1.89	2.4E-02	AF109605.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11565	24164	37476	1.89	2.4E-02	AF109605.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11838	24495		2.28	2.4E-02	9627909	NT	Bacteriophage b1L87, complete genome
12081	24589	31124	1.91	2.4E-02	6753635	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
12138	24625	31094	2.37	2.4E-02	BE928899.1	EST_HUMAN	MRO-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA
12186	24657	31063	1.66	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12188	24857	31104	1.68	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (GAMP-GEF1) mRNA, complete cds
12216	24878		1.34	2.4E-02	AF163864.1	NT	Homo sapiens SINCA isoform (SINCA) gene, complete cds, alternatively spliced
12360	24764		3.88	2.4E-02	AB008569.1	NT	Ceenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1885	14603		4.29	2.3E-02	W05340.1	EST_HUMAN	zab4g08.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:289294 5'
1880	14617		10.45	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT8 (INT8) gene, exon 4
2350	15072	27809	2.08	2.3E-02	Z74293.1	NT	S cerevisiae chromosome IV reading frame ORF YDL245c
3670	18423	29064	6.19	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH.P. Human foetal Brain Whole tissue Homo sapiens cDNA
3702	18455		0.8	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3'end
4129	18871	29499	1.06	2.3E-02	L24798.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4129	18871	29500	1.08	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4386	17123	29755	0.93	2.3E-02	AW899107.1	EST_HUMAN	GM4-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4415	17152	29780	0.88	2.3E-02	BE93225.1	EST_HUMAN	GM4-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4415	17152	29781	0.88	2.3E-02	BE93225.1	EST_HUMAN	GM4-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4416	17880	29782	1.14	2.3E-02	AW593693.1	EST_HUMAN	xs28d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4416	17880	29783	1.14	2.3E-02	AW593693.1	EST_HUMAN	xs28d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4555	17290	29919	2.56	2.3E-02	BF028487.1	EST_HUMAN	801672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4555	17290	29920	2.56	2.3E-02	BF028487.1	EST_HUMAN	801672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5291	18096	30756	3.63	2.3E-02	U68303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6522	19288	32292	4.08	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
6883	17959	30513	0.69	2.3E-02	BE141475.1	EST_HUMAN	MRO-HT0080-011069-002-c09 HT0080 Homo sapiens cDNA
7776	20472	33595	6.28	2.3E-02	U63810.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8370	21063	34204	0.94	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8370	21063	34205	0.94	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8597	21288	34429	0.68	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8597	21289	34430	0.68	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9036	21726	34890	0.98	2.3E-02	P41998	SWISSPROT	HYPOPHOSPHATE 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9769	22410	35617	0.77	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
9829	22577	35776	1.33	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
9829	22577	35777	1.33	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10524	23170	36397	0.46	2.3E-02	AF282894.1	NT	Bacillus licheniformis isolate N57N1 KcrA gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10982	23373	36615	2.16	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN
12058	25166		5.07	2.3E-02	BE278331.1	EST_HUMAN	GLUCOHYDROLASE)
12562	24892	30997	2.19	2.3E-02	U38394.1	NT	601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546587 5'
12816	25409		2.42	2.3E-02	U11077.1	NT	Straptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12807	25260		1.62	2.3E-02	11426388	NT	Dictyostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
720	13494	26147	4.13	2.2E-02	AF018267.1	NT	Homo sapiens dead finger (Drosophila)-like 1 (DRIL1), mRNA
1741	14483		1.38	2.2E-02	4557448	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1755	14497	27197	1.06	2.2E-02	P07313	SWISSPROT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1755	14497	27198	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
2008	14743	27469	2.13	2.2E-02	Z62001.1	NT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
3428	18185		1.49	2.2E-02	AA577785.1	EST_HUMAN	S.pneumoniae pcpA gene and open reading frames
3637	18390		4.01	2.2E-02	AF083094.1	NT	m24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3834	16585	29221	1.28	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3899	16649	29290	0.75	2.2E-02	Z74293.1	NT	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
5006	17729	30333	1.05	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome IV reading frame ORF YDI245c
7146	19833	32902	3.63	2.2E-02	AV698721.1	EST_HUMAN	S.cerevisiae chromosome XVI reading frame ORF YPL241c
8269	20963	34104	1.62	2.2E-02	AL161515.2	NT	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8269	20963	34105	1.62	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8709	21401	34546	0.82	2.2E-02	X79468.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9586	22239	35422	2.22	2.2E-02	AB026898.1	NT	P. vulgata alpha tub 2 mRNA
9586	22239	35423	2.22	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10105	22753		0.89	2.2E-02	6678140	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
11167	23834	37115	1.68	2.2E-02	BE197601.1	EST_HUMAN	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
11841	24425	37768	1.54	2.2E-02	11423632	NT	601584309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938571 5'
12315	24737		4.07	2.2E-02	AA503553.1	EST_HUMAN	Homo sapiens transmembrane protein 1 (TMEM1), mRNA
410	13195		6.11	2.1E-02	AV761502.1	EST_HUMAN	nc47n07.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
436	13222		9.98	2.1E-02	AF028726.1	NT	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
						NT	Dictyostellum discoideum histidine kinase C (dhkc) mRNA, complete cds

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1240	13989	26656	10.32	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1366	14113	26787	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1366	14113	26788	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1775	14517	27218	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27219	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27220	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2028	14763	27492	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
2028	14763	27493	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
2591	15305	28041	1.32	2.1E-02	AA225096.1	EST_HUMAN	nc21603.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008920
2819	13534	26193	4.48	2.1E-02	N29266.1	EST_HUMAN	y43h07.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264541 5'
3147	14763	27492	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
3147	14763	27493	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
3571	16326	29873	1	2.1E-02	AA461271.1	EST_HUMAN	z63308.1 Soares fetal, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:786121 5'
4110	16953	29480	0.81	2.1E-02	Z74283.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
4275	17014	29641	0.81	2.1E-02	BF343655.1	EST_HUMAN	602015306F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4151161 5'
4410	17147	29775	1.47	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
4421	17157	29788	1.53	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4461	17197		0.69	2.1E-02	Y19213.1	NT	Homo sapiens putative psbHbA pseudogene for hair keratin, exons 2 to 7
4662	17398	30031	4.51	2.1E-02	Y08501.1	NT	A. thaliana mitochondrial genome, part A
4762	17494	30122	1.05	2.1E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4769	17501	30124	0.76	2.1E-02	A1823432.1	EST_HUMAN	wt54405.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2384528 3'
5553	18350	31259	1.13	2.1E-02	AW379529.1	EST_HUMAN	GM4-HT0244-111189-040-h05 HT0244 Homo sapiens cDNA
6066	19448	32466	0.88	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120600-328-e12 GN0058 Homo sapiens cDNA
8417	21110	34249	0.8	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9403	22065	35236	0.5	2.1E-02	AA984288.1	EST_HUMAN	am83607.s1 Stratagene echizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element/contains element MER11 repetitive element;
9531	22184	35368	2.61	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9531	22184	35369	2.61	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9883	22533	35730	1.15	2.1E-02	L28324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds, and unknown genes
9961	22809	35814	0.69	2.1E-02	AA984288.1	EST_HUMAN	am83607.s1 Stratagene echizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element/contains element MER11 repetitive element;
10522	23168	36395	0.45	2.1E-02	AP001519.1	NT	Bacillus halodurans genomic DNA, section 13/14

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11479	24080	37391	1.38	2.1E-02	8754255	NT	Mus musculus heat shock protein, 74 kDa, A (Hspa9a), mRNA
12206	17197		8.62	2.1E-02	Y18213.1	NT	Homo sapiens putative psithHbA pseudogene for hair keratin, exons 2 to 7
12339	25163	30801	1.89	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12714	24988	30869	5.71	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
16	12844	25457	1.1	2.0E-02	BF002832.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Py28 Homo sapiens cDNA clone IMAGE:3309898 3' similar to contains MER1.13
17	12845	25458	14.4	2.0E-02	AW896585.1	EST_HUMAN	MER1 repetitive element ;
252	13051	25699	3.76	2.0E-02	8753635	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
288	13094	25736	2.72	2.0E-02	AA456638.1	EST_HUMAN	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
781	13563	26214	2.11	2.0E-02	8753635	NT	aa15b10.11 Soares_NHMPV_ST Homo sapiens cDNA clone IMAGE:813307 5'
1065	13823	26483	1.6	2.0E-02	AL096805.1	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1177	13930	26595	1.17	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [p36.33] of Homo sapiens
1177	13930	26596	1.17	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1866	14604	27313	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1866	14604	27314	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2801	15506		3.24	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3077	12844	26457	2.11	2.0E-02	BF002832.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Py28 Homo sapiens cDNA clone IMAGE:3309898 3' similar to contains MER1.13
3141	15905		1.4	2.0E-02	7305474	NT	MER1 repetitive element ;
3221	15984		2.35	2.0E-02	AF095688.1	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 68 (Sema68), mRNA
3988	16736	28370	1.3	2.0E-02	M18095.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
5548	18345	31254	0.58	2.0E-02	U34778.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
6807	18596	31523	0.7	2.0E-02	L35321.2	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
7450	20128	33217	1.11	2.0E-02	AP000004.1	NT	Dicystoslellum discoidium class VII unconventional myosin (myosin) gene, complete cds
7450	20126	33218	1.11	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
9777	22428		2.21	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
10259	23907	36117	1.62	2.0E-02	AI640342.1	EST_HUMAN	Japanese encephalitis virus envelope protein mRNA, partial cds
10539	23236	36489	1.78	2.0E-02	Z73996.1	NT	wal7b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288315 3'
11344	24034	37337	2.17	2.0E-02	D88184.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 83/182
11682	24277	37598	2.21	2.0E-02	10947055	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11682	24277	37599	2.21	2.0E-02	10947055	NT	Homo sapiens ankryrin 3, node of Ranvier (ankryrin G) (ANK3), transcript variant 1, mRNA
							Homo sapiens ankryrin 3, node of Ranvier (ankryrin G) (ANK3), transcript variant 1, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11880	17809	30595	1.9	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12336	15506		1.82	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12786	26038		6.4	2.0E-02	T80037.1	EST_HUMAN	y04c09.1 Soares infant brain 1N19 Homo sapiens cDNA clone IMAGE:24876 5'
677	13452	26095	2.15	1.9E-02	AA572764.1	EST_HUMAN	n19a07.s1 NCL_OGAP_P1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.1 L1
1611	14358	27047	1.15	1.9E-02	P16488	SWISSPROT	repetitive element;
2032	14767	27496	2.68	1.9E-02	AL163303.2	NT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2032	14767	27497	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2510	15227	27898	0.97	1.9E-02	AL161550.2	NT	Homo sapiens chromosome 21 segment HS21C103
2906	15672	28320	7.48	1.9E-02	AA713558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2952	15718	28369	1.66	1.9E-02	AV648669.1	EST_HUMAN	rw04f05.s1 NCL_OGAP_S51 Homo sapiens cDNA clone IMAGE:1288337 3'
3568	16351		1.18	1.9E-02	N52250.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GL08LH07 3'
3691	16444		9.58	1.9E-02	BE738088.1	EST_HUMAN	y22b02.s1 Soares_multiple sclerosis_2NHMPSP Homo sapiens cDNA clone IMAGE:284331 3'
3703	16456	29095	0.95	1.9E-02	AI301183.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
4025	16770	29402	1.49	1.9E-02	AF141940.1	NT	q04c07.x1 NCL_OGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;
4170	16910	29539	1.83	1.9E-02	P09081	SWISSPROT	Mycoplasma imitans VHA1 precursor (VHA1) and VHA2 precursor (VHA2) genes, partial cds
4170	16910	29540	1.83	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4504	17239	29872	3.21	1.9E-02	AI452898.1	EST_HUMAN	HOMEOTIC BICOID PROTEIN (PRD-4)
4951	15227	27968	4.09	1.9E-02	AL161550.2	NT	j46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5233	18039	30687	0.99	1.9E-02	AF037552.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5382	18182	30872	1.41	1.9E-02	L47572.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5701	18495	32744	0.88	1.9E-02	AB019507.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
7001	19693	32744	1.38	1.9E-02	U19241.1	NT	Drosophila karekai gene for glyceral-3-phosphate dehydrogenase, complete cds
7001	19693	32745	1.38	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8469	21161		1.23	1.9E-02	AL162764.2	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
9230	21909	35082	1.03	1.9E-02	BF316129.1	EST_HUMAN	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 317
9613	22266	35452	0.6	1.9E-02	L10114.1	NT	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128462 5'
9945	22593	35798	1.05	1.9E-02	BF695932.1	EST_HUMAN	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10152	22800	36017	0.54	1.9E-02	D64001.1	NT	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076263 5'
10681	23372	36614	1.44	1.9E-02	AF008938.1	NT	Synochocystis sp. PCO6803 complete genome, 2027, 2539000-2644794
12090	25171	30903	2.82	1.9E-02	AF101065.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12646	25147		1.36	1.9E-02	L11088.1	NT	Hirudo medicinalis intermediate filament glialin mRNA, complete cds
							Candida albicans lambda Ca31B fragment

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
338	13137	25772	1.4	1.8E-02	AW771104.1	EST_HUMAN	Im52-06.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
670	13448	26086	0.83	1.8E-02	BF308122.1	EST_HUMAN	MER28 repetitive element;
1137	13892	26553	1.32	1.8E-02	X17684.1	NT	601854329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1416	14184	26847	1.73	1.8E-02	AF243382.1	NT	H.francisci mRNA for myelin basic protein (MBP)
2885	15394	28133	1.71	1.8E-02	AE004544.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
3205	15968		0.94	1.8E-02	AI805828.1	EST_HUMAN	Pseudomonas aeruginosa PAO1, section 105 of 528 of the complete genome
4085	16810		0.99	1.8E-02	AA861446.1	EST_HUMAN	Is52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080296 3'
4396	17133	29784	1.17	1.8E-02	AW936363.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406835 3'
6712	19627	32671	5.02	1.8E-02	P14310	SWISSPROT	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
8029	20724	33857	0.89	1.8E-02	U37091.1	NT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
8367	21060	34200	0.91	1.8E-02	AW905327.1	EST_HUMAN	Mus musculus carbonic anhydrase IV gene, complete cds
8410	21103	34242	0.8	1.8E-02	8678943	NT	QV2-NN1073-220400-159-H08 NN1073 Homo sapiens cDNA
8392	22054	35225	0.49	1.8E-02	BF241924.1	EST_HUMAN	Mus musculus microtubule-associated protein 2 (Map2), mRNA
8392	22054	35228	0.49	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
8542	22185		2.41	1.8E-02	AA897643.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
8963	22611	35815	1.51	1.8E-02	BE778274.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:1394921 3' similar to gbL11672 ZINC
10128	22774	35987	1.37	1.8E-02	X96833.1	NT	601463545F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866963 5'
11414	23181	36409	2.31	1.8E-02	AB002337.2	NT	L.stagnalis mRNA for myomodulin neuropeptide precursor
11414	23181	36410	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11613	24211	37535	1.59	1.8E-02	AF000006.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11626	24223	37545	3.32	1.8E-02	U62749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 116001-1485000 nt. position (617)
886	13655	26323	1.86	1.7E-02	BE394689.1	EST_HUMAN	Zea mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA, partial cds
1783	14524	27230	2.17	1.7E-02	AW573183.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632180 5'
1783	14524	27231	2.17	1.7E-02	AW573183.1	EST_HUMAN	h134a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains
1884	14602		3.41	1.7E-02	AL163204.2	NT	L1.1 L1 repetitive element;
2106	14837		10.5	1.7E-02	AB004048.1	NT	Homo sapiens chromosome 21 segment HS21C004
2291	15016	27752	0.89	1.7E-02	S74186.1	NT	Oryzopsis cuniculatus mRNA for misugumih29, complete cds
2846	15356		1.01	1.7E-02	7657495	NT	[microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
2898	15762	28411	1.44	1.7E-02	AI147615.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
							qb22a08.x1 Soares_pregnant_uterus_Nb4-IPU Homo sapiens cDNA clone IMAGE:1696982 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3502	16258		4.67	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
3614	16367		0.73	1.7E-02	P04929	SWISSPROT	MER18.b1 MER19 repetitive element; HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4148	16890		1.23	1.7E-02	AA669618.1	EST_HUMAN	act1904.s1 Stratigene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu
4176	16916		2.04	1.7E-02	R02506.1	EST_HUMAN	repetitive element; contains element MER24 repetitive element; y88f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4420	17156	29787	1.49	1.7E-02	A1305278.1	EST_HUMAN	qm08g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb-X52359 ZINC
4491	17227	28856	1.78	1.7E-02	AW873183.1	EST_HUMAN	FINGER PROTEIN 30 (HUMAN); h134a03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains
4666	17400	30034	1.61	1.7E-02	V00841.1	NT	L1.1 L1 repetitive element; Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4763	17495		5.84	1.7E-02	A1015076.1	EST_HUMAN	ov51a02.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1640858 3'
5007	17730	30334	0.69	1.7E-02	6981289	NT	Rattus norvegicus N-arginine diisomerase 1 (Nrd1), mRNA
5096	17815		0.91	1.7E-02	AJ229041.1	NT	Homo sapiens 989 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6035	18815	31775	2.07	1.7E-02	A1769247.1	EST_HUMAN	wg35f09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to
6484	19251	32250	1.47	1.7E-02	A1038280.1	EST_HUMAN	contains Alu repetitive element; oy85h03.x1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
6950	19432	32448	1.27	1.7E-02	AF180930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7103	19781	32856	2.44	1.7E-02	8400718	NT	Homo sapiens nebulin (NEB), mRNA
7257	19841	33018	1.06	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7257	19841	33017	1.06	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7642	20307		1.78	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
9336	20407	33523	0.98	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9598	22251	35437	1.3	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434i0314_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434i0314 5'
11801	24391	37724	1.38	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE55), mRNA
12831	25337	30716	2.39	1.7E-02	AW803482.1	EST_HUMAN	GM4-NN1030-040400-130-06 NN1030 Homo sapiens cDNA
498	13282		3.19	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/182
1653	14399	27088	1.04	1.6E-02	Y18899.1	NT	Treponema mallophilum flaB2, flaB3 and flilD genes for flagellin subunit proteins and CAP protein homologue
2246	14874	27711	0.9	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2246	14974	27712	0.9	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2570	15284	28022	1.05	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ71 gene
2649	15359	28102	1.48	1.6E-02	AA484872.1	EST_HUMAN	ne81008.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910687
2699	15408		0.96	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds

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3016	15782	28431	0.71	1.6E-02	AF112282.1	NT	Laccase sp. isolate IBD cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3516	16272	28928	5.9	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
3630	16581	29215	1.32	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4154	16896		2.49	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4267	17007	29640	0.97	1.6E-02	AW875407.1	EST_HUMAN	OV2-PT0012-140100-030-007 PT0012 Homo sapiens cDNA
5536	18334	31241	1.25	1.6E-02	6871715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6546	19311	32316	2.05	1.6E-02	AB015281.1	NT	Candida albicans CaGC83 gene, complete cds
6832	19494	32517	1.75	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
6832	19494	32518	1.75	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7610	20276	33384	0.86	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8020	20715	33847	0.76	1.6E-02	AJ277682.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8078	20772		1.88	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
8940	22588		2.72	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10319	22966	36184	1.29	1.6E-02	AA572818.1	EST_HUMAN	nt19g03.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN, [1]:
10319	22966	36185	1.29	1.6E-02	AA572818.1	EST_HUMAN	nt19g03.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN, [1]:
10826	26132	36748	2.38	1.6E-02	Z94828.1	NT	G.gallus microsatellite DNA (LE10260 (=T161IE11))
11174	23841	37124	2.64	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11174	23841	37125	2.54	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11495	24096	37407	1.54	1.6E-02	AI373558.1	EST_HUMAN	q286e10.x1 Soares_pregnant_uterus_Nb1pU Homo sapiens cDNA clone IMAGE:2042442 3'
734	13508		23.05	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2138	14868	27598	4.24	1.5E-02	N39521.1	EST_HUMAN	w27b07.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:243925 3'
2172	14901	27635	1.69	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
3057	15823	28467	1.6	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3057	15823	28468	1.6	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3711	16464	28103	0.98	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080600-201-b12 TN0115 Homo sapiens cDNA
6201	18977	31955	1.56	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
7219	19904		1.63	1.5E-02	11467282	NT	Gyanophora paradoxa cyanelle, complete genome
7301	19984	33060	1.2	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA

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7773	20469	33592	1.63	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7781	20476	33602	3.59	1.5E-02	11417739	NT	Homo sapiens val-tRNA synthetase 2 (VAR32), mRNA
8728	21421	34565	0.9	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4154504 5'
8668	21943		0.51	1.5E-02	AF088774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9470	22079	35251	1.47	1.5E-02	D44806.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9711	22362	35559	0.98	1.5E-02	R32687.1	EST_HUMAN	Y154b10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
9711	22362	35560	0.98	1.5E-02	R32687.1	EST_HUMAN	Y154b10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
11121	23790	37068	3.49	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds
11163	23830	37109	2.14	1.5E-02	AL111238.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11856	24440	37781	1.38	1.5E-02	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
12277	26214		1.74	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
12787	26039		1.45	1.5E-02	AI763127.1	EST_HUMAN	w08h03.x1 NCI_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2389493 3' similar to contains Alu repetitive element/contains element MER28 MSR1 repetitive element ;
408	13193		2.29	1.4E-02	AE002230.2	NT	Gilamorphia pneumoniae AR39, section 58 of 94 of the complete genome
1096	13854	26513	4.42	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1234	13983		1.24	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1275	14025		3.77	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1375	14123		1.45	1.4E-02	AF216854.1	NT	Homo sapiens headpin gene, complete cds
1507	14253		1.26	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3207	15970	28622	2	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhb), cytosolic deaminase, and alpha-galactosidase (egl) genes, complete cds; and N-acetylglucosaminyl/xylose repressor protein (nagCxyR) gene, partial cds
3393	16152	28605	1.07	1.4E-02	AW074212.1	EST_HUMAN	x509409.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3478	16234	28888	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3478	16234	28889	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3948	16401	29041	8.63	1.4E-02	8698918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4455	17191	29817	7.77	1.4E-02	AW662688.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4455	17191	29818	7.77	1.4E-02	AW662688.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4821	17552	30174	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4821	17552	30175	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6321	19091	32079	5.47	1.4E-02	AA556930.1	EST_HUMAN	nt1104.e1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029890 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6321	18091	32080	5.47	1.4E-02	AA558030.1	EST_HUMAN	nt11c04.a1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1028890 3' similar to contains Alu repetitive element;
8038	20733		1.94	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
8796	21488	34634	0.75	1.4E-02	M81702.1	NT	Candida bodinii methanol oxidase (AOD1) gene, complete cds
9053	21742	34900	0.84	1.4E-02	AL27265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9300	21967	35141	2.27	1.4E-02	BE544561.1	EST_HUMAN	601078238F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484241 5'
10455	23101		0.76	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11985	24526	37287	2.2	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12331	24747		1.37	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12801	24913		2.36	1.4E-02	11428668	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1948	14683	27395	2.21	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3208	15971	28623	2.23	1.3E-02	BF697081.1	EST_HUMAN	602129476F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3208	15971	28624	2.23	1.3E-02	BF697081.1	EST_HUMAN	602129476F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3951	16701		1.31	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
							Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
4874	17601	30223	0.93	1.3E-02	U66061.1	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
5168	17975	30532	1.31	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
5166	17975	30533	1.31	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
6072	18851	31816	1.05	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6105	18883	31851	0.88	1.3E-02	M62862.1	NT	C. reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
6865	17942	30535	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
6865	17942	30538	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
							ow08g05.x1 Soares_parathyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
7477	20150	33244	4.9	1.3E-02	AI031593.1	EST_HUMAN	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
8380	21073	34212	1.65	1.3E-02	AF15961.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10107	22755	35967	1.91	1.3E-02	M63707.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10178	22826	36040	0.68	1.3E-02	AE001304.1	NT	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10913	23593	36838	3.97	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10913	23593	36839	3.97	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12337	25352		1.44	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12437	24807		2.41	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
12807	25145		28.18	1.3E-02	AF152238.1	NT	Human sapiens V1b vasopressin receptor (VPR3) gene, complete cds
345	13145	25783	3.48	1.2E-02	AA059298.1	EST_HUMAN	z65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
440	13226	25669	1.66	1.2E-02	P38888	SWISSPROT	HYPOPHYSICAL 17.1 KD PROTEIN IN PUR5.3 REGION
721	13495	26148	2.02	1.2E-02	AI183522.1	EST_HUMAN	q68e12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.H1.L1 repetitive element;
2175	14804	27637	1.81	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2178	14907	27640	1.71	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2444	15163	27901	1.39	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2842	15163	27901	1.07	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3088	15863		6.66	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Stratigene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3281	16042	26897	2.1	1.2E-02	R62805.1	EST_HUMAN	y11b08.e1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3284	16045	26894	0.92	1.2E-02	AI688884.1	EST_HUMAN	z66a07.x6 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
4875	17409	30045	0.91	1.2E-02	AI887378.1	EST_HUMAN	wm39f04.x1 NCJ CGAP_UK4 Homo sapiens cDNA clone IMAGE:2438335 3'
4859	17588	30211	2.03	1.2E-02	U61328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4981	17704		1.13	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiqT mRNA, partial cds
5025	17746	30358	1.41	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5666	18481	31375	1.73	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calcitriol, complete cds
6026	18806	31767	0.72	1.2E-02	AF045555.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
6907	19845	32691	6.46	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7192	19878	32852	1.36	1.2E-02	H02187.1	EST_HUMAN	y84h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7212	19897	32972	10.54	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBHG11 5'
7456	20130	33222	0.57	1.2E-02	BF216650.1	EST_HUMAN	601882849F1 NIH_JMGC_57 Homo sapiens cDNA clone IMAGE:4086253 5'
7896	20591	33722	2.18	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL4.2) (SIAT4-B)
8092	20786	33917	1.35	1.2E-02	AF183612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8082	20786	33918	1.35	1.2E-02	AF183612.1	NT	Homo sapiens fringe protein mRNA, partial cds

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8788	21480		1.03	1.2E-02	T79987.1	EST_HUMAN	yd72d08.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 3'
9539	22192	35376	2.46	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9570	22223	35408	1.35	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12034	24559	31112	2.88	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU1) (HPER)
12615	24922		8.02	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN:557G06 5'
1246	13995	26662	1.49	1.1E-02	AA070364.1	EST_HUMAN	zm69e11.s1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530824 3'
1701	14444	27143	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1701	14444	27144	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2031	14766	27495	4.92	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153808 5'
2880	15647		4.05	1.1E-02	N89523.1	EST_HUMAN	zsf40e06.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:285040 5'
3513	16269	28824	2.98	1.1E-02	AI653508.1	EST_HUMAN	tg95b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPf_HUMAN
4086	16829		0.86	1.1E-02	AW813766.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4778	17510	30192	1.5	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 S10197 Homo sapiens cDNA
							DKFZp686E0924 .s1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp686E0924
6057	18837	31796	1	1.1E-02	U68480.1	NT	Bacillus subtilis SpoIVK (spoVK), YnaA (ynaA), YnaB (ynbB), GlnR (glnR), glutamine synthetase (ghA), YnaA (ynaA), YnaB (ynbB), YnaC (ynnC), YnaD (ynAD), YnaE (ynAE), YnaF (ynAF), YnaG (ynAG), YnaH (ynAH), YnaI (ynAI), YnaJ (ynAJ), YnaK (ynAK), xylan beta-1,4-xylosyl-
7497	20169	33261	2.51	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
8538	21230	34372	0.91	1.1E-02	AW996160.1	EST_HUMAN	OV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
8721	21413	34556	0.67	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC:4040
8800	21492	34639	0.45	1.1E-02	C81982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9829	22480	35682	2.03	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratiogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
9994	22642	35854	3.55	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10900	23580	36830	3.23	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11823	24484		4.16	1.1E-02	AA688239.1	EST_HUMAN	ab77f11.s1 Stratiogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12678	18829		1.62	1.1E-02	AW813766.1	EST_HUMAN	Alu repetitive element;
6	12833	25448	9.16	1.0E-02	AW848120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 S10197 Homo sapiens cDNA
1513	14260	26946	1.66	1.0E-02	AW368126.1	EST_HUMAN	MR3-C10176-111099-003-e10 C10176 Homo sapiens cDNA
2577	15291		1.57	1.0E-02	AA606369.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3087	15852	28494	2.7	1.0E-02	BE835556.1	EST_HUMAN	cc22h08.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1350495 3'
3257	16019	28666	1.49	1.0E-02	BE988969.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3861	16611	29250	0.79	1.0E-02	AI065086.1	EST_HUMAN	60164967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
							HA0921 Human fetal liver cDNA library Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3876	16626	29264	0.7	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4728	17458	30094	4.24	1.0E-02	8753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4783	17524	30146	5.16	1.0E-02	R96667.1	EST_HUMAN	yq54h01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:159833 5'
5331	18134	30783	0.72	1.0E-02	H52681.1	EST_HUMAN	yq36h11.1 Soares ovary tumor NtHOT Homo sapiens cDNA clone IMAGE:235941 5'
5661	18456	31370	0.57	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-A Tc4 (Nfatc4) gene, exons 1 and 2
6025	18805	31768	1.4	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Syk) gene, complete cds
6088	18868	31831	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6088	18868	31832	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6664	19581	32616	1.92	1.0E-02	Z29642.1	NT	Z mays U3snRNA pseudogene
9283	21960	35133	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459870F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3863177 5'
9283	21960	35134	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459870F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3863177 5'
11229	23892		1.97	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11263	23925		1.46	1.0E-02	AI417961.1	EST_HUMAN	ig59h07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183_cds1
11340	24030	37334	1.97	1.0E-02	AV760018.1	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5
12003	25416		1.83	1.0E-02	Q62203	SWISSPROT	repetitive element;
12059	25189	30811	3.76	1.0E-02	AW935521.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12075	25243		5.93	1.0E-02	S70330.1	NT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12592	25289		3.74	1.0E-02	X62654.1	NT	RC2-DT0007-120200-016-H02 DT0007 Homo sapiens cDNA
12903	25050	30957	1.84	1.0E-02	AB039887.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
873	13642	26312	2.1	9.0E-03	AI796126.1	EST_HUMAN	H.sapiens gene for Me-491/CD63 antigen
1241	13990		2.07	9.0E-03	BE781889.1	EST_HUMAN	Homo sapiens WDR4 gene for WD repeat protein, complete cds
1463	14211	26899	1.1	9.0E-03	AE001270.1	NT	W44209.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
2394	15115	27852	2.48	9.0E-03	AI161559.2	NT	MER22 MER22 repetitive element;
2403	15124	27861	0.92	9.0E-03	AF096934.1	NT	601470242F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3873348 5'
3659	18412	29050	1.21	9.0E-03	J05184.1	NT	Treponema pallidum section 88 of 87 of the complete genome
4927	17655	30267	1.03	9.0E-03	BE047949.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
4964	17689	30297	0.95	9.0E-03	T70044.1	EST_HUMAN	Mus musculus MHC class III (Rp1) mRNA, partial cds
4964	17689	30298	0.95	9.0E-03	T70044.1	EST_HUMAN	S. acidocaldarius thermophil gene, complete cds
5720	18512		1.15	9.0E-03	AI809782.1	EST_HUMAN	iz44e10.y1 NCL CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2281466 5'
6533	19288		4.88	9.0E-03	BE745988.1	EST_HUMAN	yv17b08.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
							yv17b08.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
							w77704.x1 Soares NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2381631 3'
							601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7362	20043	33122	0.57	9.0E-03	AI242219.1	EST_HUMAN	q187c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7371	20051	33132	0.8	9.0E-03	8222570	NT	Homo sapiens hypothetical protein FLJ10850 (FLJ10850), mRNA
7774	20470		1.05	9.0E-03	AL036991.1	EST_HUMAN	DKFZp434L0412.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L0412 5'
8147	20841		0.65	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9745	22396	35601	0.47	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M230 IEL ANTIGEN)
9762	22413	35620	1.44	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10907	23587		2.07	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10935	23615	36866	1.57	9.0E-03	BE395380.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'
11651	24248	37568	1.55	9.0E-03	L11144.1	NT	Homo sapiens preprogalactin (GAL1) gene, exons 1, 2, and 3
11651	24248	37569	1.55	9.0E-03	L11144.1	NT	Homo sapiens preprogalactin (GAL1) gene, exons 1, 2, and 3
12411	25411		2.37	9.0E-03	BE348385.1	EST_HUMAN	hw17609.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12703	24983		23.46	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281289-001-e09 HT0452 Homo sapiens cDNA
489	13274		4.06	8.0E-03	AA723007.1	EST_HUMAN	Zf30e03.s1 Soares_pithecus_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element
968	13734	26399	36.32	8.0E-03	AF106956.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2154	14884	27617	2.2	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2960	15726		0.93	8.0E-03	U47048.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mdbA), immunity protein (mif), microcin 24 (mifS), and microcin transport protein (mifA, mifB) genes, complete cds
3353	16113	28768	1.08	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3665	16418	29058	1.21	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3665	16418	29059	1.21	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4350	17089	29721	4.88	8.0E-03	BF363327.1	EST_HUMAN	OM4-NN0119-300600-223-405 NN0119 Homo sapiens cDNA
5083	17802	30420	1.09	8.0E-03	AU140261.1	EST_HUMAN	AU140261 PLACE2 Homo sapiens cDNA clone PLACE2000223 5'
5436	18235	30949	2.82	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fae-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6106	25085	31852	1.45	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
6851	19413	32427	4.89	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE YANA
6820	19481		0.95	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7107	19785	32860	1.79	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
7442	20119		2.03	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
8781	21473	34619	0.63	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)

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8808	21500	34646	3.29	8.0E-03	AW808692.1	EST_HUMAN	MR1-ST0111-111199-011-h06 ST0111 Homo sapiens cDNA
8816	21508	34653	0.49	8.0E-03	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 2/6
8878	21669	34713	0.58	8.0E-03	9789956	NT	Mus musculus fusion 2 (human) (Fus2), mRNA
9848	22498		4.63	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0877-040400-131-g03 BT0877 Homo sapiens cDNA
10656	23357	36597	1.38	8.0E-03	BE788441.1	EST_HUMAN	601476618F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
10906	23586		3.58	8.0E-03	Z49662.1	NT	S. cerevisiae chromosome X reading frame ORF YJR152w
11715	24309	37632	4.74	8.0E-03	AF084589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
11814	24402		22.71	8.0E-03	AA016180.1	EST_HUMAN	2a32a11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360716 5'
11853	24437	37779	1.36	8.0E-03	BF342436.1	EST_HUMAN	602013941F1 NCJ_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149418 5'
11933	24491		1.74	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
11980	24523		1.74	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
678	13453	26096	16.16	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
678	13453	26097	16.16	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
956	13721	26387	3.57	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1094	13852	26611	3.48	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1343	14091		2.67	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX-PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1374	14122	26797	5.71	7.0E-03	AA668298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HFH-2)
1491	14238	26924	3.37	7.0E-03	AW303599.1	EST_HUMAN	ab79b09.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:863145 3'
1735	14477	27175	1.24	7.0E-03	AW950556.1	EST_HUMAN	x121b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
1735	14477	27176	1.24	7.0E-03	AW950556.1	EST_HUMAN	EST362628 MAGE resequences, MAGA Homo sapiens cDNA
2254	15689	27722	1.86	7.0E-03	P04928	SWISSPROT	EST362628 MAGE resequences, MAGA Homo sapiens cDNA
3546	16301	28951	0.71	7.0E-03	A1150273.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3749	16502	29137	0.8	7.0E-03	AW444463.1	EST_HUMAN	q34402.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3792	16544	29179	1.32	7.0E-03	AF196344.1	NT	UI-H-B13-alk-c-10-Q-UJ.s1 NCJ_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4000	16502	29137	0.83	7.0E-03	AW444463.1	EST_HUMAN	UI-H-B13-alk-c-10-Q-UJ.s1 NCJ_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4560	17285			7.0E-03	AW630888.1	EST_HUMAN	hh89a05.y1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969838 5'
4929	17657		2.17	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5729	18521		0.75	7.0E-03	HT1108.1	EST_HUMAN	y82g01.r1 Soares_fetal_liver_spleen_1NfLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6021	25083		4.9	7.0E-03	AW861059.1	EST_HUMAN	gb:Y14723 CLUSTERIN PRECURSOR (HUMAN);
6222	18996	31972	1.47	7.0E-03	W68251.1	EST_HUMAN	RC1-GT0286-050400-018-c08 C10288 Homo sapiens cDNA
							z333f10.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:342475 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6443	19211	32207	3.44	7.0E-03	AA327129.1	EST_HUMAN	EST30874 Colon I Homo sapiens cDNA 5' end
6470	19237	32237	0.75	7.0E-03	BE857385.1	EST_HUMAN	7q34b10.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
6979	19504	32529	1.67	7.0E-03	BE828133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.12 TAR1 repetitive element;
7420	20097	33184	5.48	7.0E-03	Z35838.1	NT	CM2-GT0478-230800-347-b11 C10478 Homo sapiens cDNA
7420	20097	33185	5.48	7.0E-03	Z35838.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077w
8010	20705	33833	2.47	7.0E-03	BE175667.1	EST_HUMAN	hd22a05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
8511	21203	34348	0.51	7.0E-03	AF281074.1	NT	RC5-H10582-190300-011-D02 HT0582 Homo sapiens cDNA
9287	21964		0.75	7.0E-03	AF111108.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
9495	22148	35330	0.72	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens sarfin palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9620	22273	35460	2.57	7.0E-03	P48982	SWISSPROT	y48c10.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248088 3' similar to contains
9620	22273	35461	2.57	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
10204	22852		1.32	7.0E-03	AV687378.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10384	23030		0.77	7.0E-03	A1789734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10729	23417	36658	2.63	7.0E-03	AB008852.1	NT	AV687378 GK Homo sapiens cDNA clone GKAF007 5'
10818	23501	36739	1.71	7.0E-03	AJ004862.1	NT	wc37a09.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:2320840 3'
10818	23501	36740	1.71	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP62, complete cds
10982	23657		1.26	7.0E-03	AJ242804.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12466	24833		1.79	7.0E-03	BE263253.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12553	24880		1.81	7.0E-03	Y17455.1	NT	Sporobolus stipitatus mRNA for putative glycine and proline-rich protein
12691	25400		1.72	7.0E-03	AL163300.2	NT	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
1218	13969	26637	12.34	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSFR2 gene, penultimate exon
1218	13969	26638	12.34	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
2774	15479	28220	1.3	6.0E-03	AF112374.1	NT	hd22a05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2893	15660	28305	3.36	6.0E-03	AA759135.1	EST_HUMAN	SW_PXR_HUMAN 075468 ORPHAN NUCLEAR RECEPTOR PXR;
2893	15660	28306	3.36	6.0E-03	AA759135.1	EST_HUMAN	SW_PXR_HUMAN 075468 ORPHAN NUCLEAR RECEPTOR PXR;
3240	16002		2.22	6.0E-03	H75690.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
3298	16090		1.31	6.0E-03	AF180338.1	NT	ah78e11.s1 Scores_bas1_NHT Homo sapiens cDNA clone 1321772 3'
3377	16136	28783	1.18	6.0E-03	U90880.1	NT	ah78e11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1321772 3'
							y77n04.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
							Noborus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
							Fugu rubripes zhc finger protein, isoform 1, fatty acid binding protein, sepiapterin reductase and vasodilator
							genes, complete cds

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3377	16136	28794	1.18	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isobutyrin, fatty acid binding protein, sepiapterin reductase and vasodilator genes, complete cds
3534	16280		1.19	6.0E-03	W37885.1	EST_HUMAN	zct13a1.1 r1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone IMAGE:322172 5'
3682	16405	29044	3.68	6.0E-03	BF510986.1	EST_HUMAN	UJ-H-B14-apm-c-08-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3682	16435	29079	1.08	6.0E-03	BE077356.1	EST_HUMAN	RC1-BT0606-260400-014-a07 BT0606 Homo sapiens cDNA
3769	16511	29147	1.22	6.0E-03	6754029	NT	Mus musculus glucosaminyl-6-phosphate deaminase (Gnp), mRNA
3902	16652	29284	0.76	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240899-021-b10 CT0204 Homo sapiens cDNA
3938	16888		1.29	6.0E-03	BE250108.1	EST_HUMAN	600942804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4331	17070		1.84	6.0E-03	A016833.1	EST_HUMAN	ov33c11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4647	17381	30013	5.67	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5073	17782	30407	2.58	6.0E-03	Q62209	SWISSPROT	SYNAPTONEVAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
6061	25084	31802	0.67	6.0E-03	9627521	NT	Varicella virus, complete genome
6718	18633	32676	1.16	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6755	17924	30559	0.57	6.0E-03	BE253748.1	EST_HUMAN	601112363F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7149	19836	32905	0.61	6.0E-03	AA298442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7149	19836	32906	0.61	6.0E-03	AA298442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7546	20216	33318	0.69	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
7702	20365	33479	0.62	6.0E-03	P17904	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
7767	20453	33578	6.9	6.0E-03	A033980.1	EST_HUMAN	ow13a04.x1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element
7874	20569	33695	2.17	6.0E-03	AW798337.1	EST_HUMAN	RCO-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
7945	20640		1.58	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3858626 5'
8454	22004	35176	7.26	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
8943	22591		2.13	6.0E-03	A1432661.1	EST_HUMAN	tt22c02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10052	22710	35928	0.86	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ; Bacillus subtilis fntD gene
10184	22842		1.14	6.0E-03	AF084655.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10304	22951	36166	0.59	6.0E-03	X68366.1	NT	M.thermoformicum complete plasmid pFV1 DNA
10645	23336	36575	1.75	6.0E-03	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGE Homo sapiens cDNA
10713	23402		2.54	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
10750	23435	36680	1.26	6.0E-03	A1420786.1	EST_HUMAN	tt61c12.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;

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10750	23435	36681	1.26	6.0E-03	A1420786.1	EST_HUMAN	te91c12.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519
10903	23583		4.6	6.0E-03	U14556.1	NT	FATTY ACID AMIDE HYDROLASE ;
10904	23584	36833	2.81	6.0E-03	BE737895.1	EST_HUMAN	Mus musculus zinc-finger protein mRNA, complete cds
12042	24653		3.25	6.0E-03	AF070496.1	NT	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
							Rhodococcus capsulatus strain SB1003, partial genome
12160	25174		6.69	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete genome
12239	25285		3.17	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12569	24698		1.64	6.0E-03	BE798019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3865388 5'
12588	24910		1.68	6.0E-03	AJ245480.1	NT	Brassica napus skg gene for S-locus glycoprotein, cultivar T2
654	13432	26072	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	13432	26073	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26072	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26073	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1090	13848	26507	1.15	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3
2686	15397	28135	2.5	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2936	15702	28351	0.88	5.0E-03	BE266057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3133	15898	28543	3.82	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3162	15915		2.83	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3164	15927	28575	1.3	5.0E-03	R71794.1	EST_HUMAN	y186g02.s1 Soares breast 2N1HBst Homo sapiens cDNA clone IMAGE:155666 3'
3272	16033		1.12	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3687	16440	28082	4.03	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3741	16494	29129	0.85	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
3954	16704		1.17	5.0E-03	AA239675.1	EST_HUMAN	EST12218 Ulerus tumor 1 Homo sapiens cDNA 5' end
4272	16494	29128	0.82	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4569	17304	29931	0.73	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4670	17404	30039	1.17	5.0E-03	AJ752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn15c02 random
5707	18501	31422	5.5	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED)(UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5953	18735	31694	2.97	6.0E-03	000507	SWISSPROT	
5983	18768		0.91	5.0E-03	AE002234.2	NT	Chlamydia pneumoniae AR39, section 62 of 84 of the complete genome
6499	19264		7.56	5.0E-03	BE300091.1	EST_HUMAN	800944564 T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6746	17915	30578	7.45	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6940	19422		0.64	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7395	20065	33143	0.73	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR93 similar to EST containing Alu repeat
7498	20170		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031099-011-07 CT0255 Homo sapiens cDNA
7667	20331	33442	7.5	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8119	20813	33948	0.48	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8119	20813	33949	0.48	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8137	20831	33965	3.29	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8509	21201		5.63	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8706	21398	34545	1.04	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA (19.1 - 19.4 min)
8838	21530	34676	0.71	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9482	22195	35315	0.45	5.0E-03	P33750	SWISSPROT	SOF1 PROTEIN
9739	22390	35595	0.89	5.0E-03	L21710.1	NT	Plasmodium berghei 68 kDa phosphoprotein mRNA, partial cds
9871	22521	35716	0.7	5.0E-03	AW821888.1	EST_HUMAN	RC9-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10057	22705	35923	0.45	5.0E-03	AA533143.1	EST_HUMAN	h46h10.e1 NCJ_CGAP_P08 Homo sapiens cDNA clone IMAGE:995587
10231	22879	36091	0.51	5.0E-03		NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10377	23023		0.48	5.0E-03	AA653261.1	EST_HUMAN	ap49c10.e1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3'
10621	23314		4.99	5.0E-03	T19686.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10859	23539	36785	3.42	5.0E-03	AW170334.1	EST_HUMAN	xr59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element ;
10859	23539	36786	3.42	5.0E-03	AW170334.1	EST_HUMAN	xr59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element ;
10971	23647	36900	1.89	5.0E-03	T49153.1	EST_HUMAN	y609e04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'
11021	23683	36956	1.47	5.0E-03	10946753	NT	Mus musculus hypothetical protein, MNCb-4780 (LOC58212), mRNA
11303	23982		3.54	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCJ_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291622 5'
11774	24365	37697	1.53	5.0E-03	AJ276905.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
11774	24365	37698	1.53	5.0E-03	AJ276905.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7

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12176	25367		9.26	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12307	24731		4.11	5.0E-03	AF067263.1	NT	Brugia malayi Y chromosome marker
12409	24792		2.52	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12441	24811		1.87	5.0E-03	AA456597.1	EST_HUMAN	xz75a03.s1 Soares ovary tumor NbtHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14685 PROBABLE DIPHEENOL OXIDASE A2 COMPONENT ;
12467	25183		2.78	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
12643	24940	30980	4.2	5.0E-03	AW449108.1	EST_HUMAN	UI-H-B13-ald7-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
12662	25253		1.76	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
226	13038	25675	2.98	4.0E-03	AW500196.1	EST_HUMAN	UI-H-B13-ald7-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3078831 5'
313	13117	25755	2.29	4.0E-03	R48482.1	EST_HUMAN	y951a04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
589	13369	25997	2.69	4.0E-03	AA69338.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:1562568 3'
857	13626	26298	2.03	4.0E-03	R48482.1	EST_HUMAN	y951a04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
891	13660		4.84	4.0E-03	AW749101.1	EST_HUMAN	RC3-B10333-110100-012-701 BT0333 Homo sapiens cDNA
1128	13884	26544	29.46	4.0E-03	AA089777.1	EST_HUMAN	z181a08.r1 Stratagene cdon (#937204) Homo sapiens cDNA clone IMAGE:510988 5'
1146	13901	26563	2.4	4.0E-03	AW784740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1280	14030	26699	1.57	4.0E-03	AA284374.1	EST_HUMAN	z559a01.r1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:701738 5'
1581	14327		1.52	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAK808 5'
1737	14479	27178	2.23	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
2011	14746	27474	10.56	4.0E-03	AA089777.1	EST_HUMAN	z181a08.r1 Stratagene cdon (#937204) Homo sapiens cDNA clone IMAGE:510988 5'
2244	14972		2.49	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2276	15002	27742	1.64	4.0E-03	AW784740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2579	15293	28030	1.97	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2879	15293	28031	1.97	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2696	15405	28140	3	4.0E-03	AJ27365.1	NT	CDM protein (CDM), adrenoleukodystrophy protein >
2696	15405	28141	3	4.0E-03	AJ27365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2701	15409	28144	1.41	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3219	15982	28634	1.16	4.0E-03	BE154734.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
3219	15982	28635	1.16	4.0E-03	BE154734.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3521	16277	28931	0.97	4.0E-03	AW189426.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA x98804.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'

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3521	16277	28932	0.97	4.0E-03	AW188426.1	EST_HUMAN	x98604.x1 NCI_CGAP_Cot8 Homo sapiens cDNA clone IMAGE:2865278 3'
3612	16365	29008	0.73	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 611 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3909	16659	29300	0.73	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
3977	16725		1.95	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5057	17776	30393	0.93	4.0E-03	AW103719.1	EST_HUMAN	x83403.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2814460 3' similar to contains L1.11 L1
5114	17832		0.97	4.0E-03	AA772898.1	EST_HUMAN	L1 repetitive element
5194	18002	30625	1.8	4.0E-03	AF005859.1	NT	ae73a05.s1 Streptococcus schiozo brain S11 Homo sapiens cDNA clone IMAGE:968776 3'
5314	18118	30774	23.91	4.0E-03	AF169825.1	NT	Drosophila melanogaster anan2D7 (anan2D7) mRNA, complete cds
5705	18499	31421	2.48	4.0E-03	P04196	SWISSPROT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5708	18502	31423	1.74	4.0E-03	P21849	SWISSPROT	(HPRG)
5792	18583	31510	0.88	4.0E-03	AL133871.1	EST_HUMAN	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
5993	18774		4.11	4.0E-03	U22180.1	NT	DKFZp7811014.1 r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7811014 5'
6140	18918	31888	0.95	4.0E-03	AW590572.1	EST_HUMAN	Rattus norvegicus opsin gene, complete cds
6217	18991	31967	1.6	4.0E-03	BE548453.1	EST_HUMAN	hg46c07.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2948852 3'
6572	19336	32347	1.28	4.0E-03	AA813222.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6677	19594	32632	1.61	4.0E-03	U76408.1	NT	g92f11.s1 Soares testis_NHT Homo sapiens cDNA clone 1392045 3'
6970	19452	32470	0.99	4.0E-03	AL163278.2	NT	Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds
6970	19452	32471	0.99	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7098	19787	32851	3.5	4.0E-03	Q02817	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
7331	20013	33091	1.23	4.0E-03	A081483.1	EST_HUMAN	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7333	20015	33093	0.78	4.0E-03	BE670170.1	EST_HUMAN	h37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7424	20101		0.74	4.0E-03	X92109.1	NT	7e31b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7843	20538	33666	0.7	4.0E-03	Q9T192	SWISSPROT	H. sapiens hcgIX gene
7947	20842	33767	5.45	4.0E-03	AF111944.1	NT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
8103	20797	33928	2.06	4.0E-03	7662067	NT	(ADAM-TS-5) (ADAM-TS) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8614	21306	34448	6.98	4.0E-03	A1553983.1	EST_HUMAN	Dicotyledon discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
8787	21479		4.25	4.0E-03	AL163209.2	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8797	21489	34635	2.97	4.0E-03	AL163278.2	NT	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
9827	22478	35679	0.87	4.0E-03	H30664.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
10276	22923	36135	1.3	4.0E-03	AL161556.2	NT	Homo sapiens chromosome 21 segment HS21C078
10466	23112		0.45	4.0E-03	AL163281.2	NT	yp42g12.r1 Soares retina N2b6HR Homo sapiens cDNA clone IMAGE:180150 5'
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
							Homo sapiens chromosome 21 segment HS21C081

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11074	23744	37017	4.09	4.0E-03	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
11777	24368	37700	1.82	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12147	25385		1.78	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-508 BN0138 Homo sapiens cDNA
12167	24649		2.38	4.0E-03	BE268290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12246	24694		2.27	4.0E-03	AW504273.1	EST_HUMAN	UI-HF-BN0-01p-9-04-0-UI-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12480	24841		3.41	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12521	25293		2.08	4.0E-03	AW614596.1	EST_HUMAN	h102c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element;
12801	25048	30956	2.17	4.0E-03	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
362	13160	25803	2.38	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
859	13628	26289	5.37	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1657	14403	27091	3.35	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2255	14982		1.38	3.0E-03	AF050666.1	NT	Homo sapiens MHC class 1 region
2292	15017		6.44	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2293	15018	27753	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2293	15018	27754	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3081	15846	28488	3.31	3.0E-03	BE379296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609833 5'
3149	15912	28557	2.62	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3412	16170	28819	1.72	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3420	16177		5.97	3.0E-03	Y12500.1	NT	C.elegans samde gene
3959	16708	29348	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3959	16708	29349	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4016	16762	29390	1.35	3.0E-03	AI792278.1	EST_HUMAN	ab04f09.j5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4130	16872		1	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
4364	17102	29737	5.63	3.0E-03	AI011432.1	NT	Rattus norvegicus cdrlf gene
4428	17164		0.73	3.0E-03	BE348739.1	EST_HUMAN	h66g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151934 3'
4482	17217	29844	4.97	3.0E-03	AI536141.1	EST_HUMAN	hu8.P10.H3 concam Homo sapiens cDNA 3'
4782	17514	30136	2.38	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4802	17533	30155	7.94	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5184	17992	30508	3.96	3.0E-03	8922498	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5468	18287	31159	1.98	3.0E-03	AJ249881.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)

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5539	18337	31244	0.99	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6458	19225	32226	11.75	3.0E-03	AA455701.1	EST_HUMAN	aa13f10.r1 Soares_NhiHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7104	19792	32857	1.38	3.0E-03	AJ011419.1	NT	Myxeromyces marianus pop3 gene for purine-cytosine permease
7422	20099	33187	3.84	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
7839	20534	33661	0.82	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
7839	20534	33662	0.82	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8056	20750	33881	1.54	3.0E-03	N92880.1	EST_HUMAN	z027b04.s1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:304783 3'
8214	20908		0.51	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8360	21063	34194	1.32	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8381	21074	34213	1.47	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8485	21177		1.29	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8890	21581		11.08	3.0E-03	AW613774.1	EST_HUMAN	h88f10.x1 NCL_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.t1 L1 repetitive element;
8943	21634	34778	4.01	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
8967	21657	34808	6.44	3.0E-03	AJ016731.1	EST_HUMAN	ov03d12.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_ma1
8977	21667	34817	0.73	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9309	21976		0.83	3.0E-03	D90901.1	NT	602035880F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183938 5'
9347	20418	33538	0.83	3.0E-03	BE154670.1	EST_HUMAN	Synochocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9536	22189		0.54	3.0E-03	P03355	SWISSPROT	PM3-HT0344-071299-003-d07 HT0344 Homo sapiens cDNA
9608	22259		3.88	3.0E-03	P08672	SWISSPROT	POL POLYPOLYMERIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
							CIRCUMSPOROITE PROTEIN PRECURSOR (CS)
							RETROVIRUS-RELATED POL POLYPOLYMERIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9795	22446	35651	1.3	3.0E-03	P11369	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
9896	22546	35740	1.29	3.0E-03	P51989	SWISSPROT	Homo sapiens chromosome 21 segment HS21C103
10040	22688	35906	3.97	3.0E-03	AL163303.2	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
10752	23437		1.9	3.0E-03	5803028	NT	Oryza sativa gene for bZIP protein, complete cds
11137	20096	33187	2.65	3.0E-03	AB021736.1	NT	Pneumocystis carinii kds-like serine endoprotease mRNA, partial cds
11353	24043	37346	1.69	3.0E-03	AF009222.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11424	23191	36422	2.52	3.0E-03	AF268285.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11482	24065	37372	2.72	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11482	24065	37373	2.72	3.0E-03	AF094481.1	NT	RETROVIRUS-RELATED POL POLYPOLYMERIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
11543	24143	37452	1.58	3.0E-03	P11369	SWISSPROT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11784	24374		1.48	3.0E-03	AW284812.1	EST_HUMAN	UIH-B12-art-4-08-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
11927	25196		2.86	3.0E-03	AB25056.1	EST_HUMAN	promoter-5.E07.7 bvtumor Homo sapiens cDNA 5'
11962	24510	37256	1.88	3.0E-03	AA993154.1	EST_HUMAN	α7b10.s1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER26 repetitive element;
12016	25321		2.26	3.0E-03	AB009688.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12190	24681	31066	2.71	3.0E-03	AL298282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
502	13286	25919	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
502	13286	25920	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	15552		12.31	2.0E-03	T70874.1	EST_HUMAN	y415h03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108341 5'
1342	14090	26768	2.07	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1345	14093	26768	1.4	2.0E-03	AA661605.1	EST_HUMAN	nu86f01.s1 NCI_CGAP_Av1 Homo sapiens cDNA clone IMAGE:1217593
1354	14102	26777	16.16	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1473	14220	26906	1.73	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD161 ANTIGEN)
1506	14252	26938	1.84	2.0E-03		NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1506	14252	26939	1.84	2.0E-03		NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1586	14332		6.31	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1764	14506	27207	1.13	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1872	14610		1.01	2.0E-03	BE144908.1	EST_HUMAN	GM2-H10183-061059-018-403 HT10183 Homo sapiens cDNA
1988	14724	27445	1.57	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2247	14975	27713	1.16	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2558	15272	28007	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2558	15272	28008	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2584	15298		4.57	2.0E-03	AW137782.1	EST_HUMAN	UIH-B11-art-g-10-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3411	16169	28818	4.3	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3417	16174	28823	1.13	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3657	16410	29048	6.62	2.0E-03	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPR2, LMP2, LMP7, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4093	16835	29461	1.96	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4195	16936		11.03	2.0E-03	U068491.1	NT	Rattus norvegicus 6-hydroxytryptamine? receptor gene, partial cds
4393	17130		1.12	2.0E-03	AW297380.1	EST_HUMAN	UIH-BW0-art-g-03-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4397	17134	29765	0.97	2.0E-03	AI084746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4509	17244	28877	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shc) mRNA, complete cds
4509	17244	28878	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shc) mRNA, complete cds
4683	17397		1.84	2.0E-03	R87773.1	EST_HUMAN	yo45c02.s1 Soares adult brain N2b4HB5Y Homo sapiens cDNA clone IMAGE:180890 3'
4958	17682	30290	2.57	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5092	17811	30427	1	2.0E-03	BE798380.1	EST_HUMAN	601583004F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937560 5'
5399	18199	30893	1.38	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5540	25070	31245	2.06	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5623	18420	31333	1.86	2.0E-03	U63711.1	NT	Xenopus laevis xanillin mRNA, complete cds
6019	18800	31760	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6019	18800	31761	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6253	19027	32001	2.17	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6253	19027	32002	2.17	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6255	19028	32004	7.5	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6291	19084	32046	2.44	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6292	19085	32047	0.98	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6320	19090	32078	1.62	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-RNA synthetase (LysRS)
6506	19271		1.16	2.0E-03	A1991089.1	EST_HUMAN	wu38h09.x1 Soares Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW-RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitive element ;
6541	19306	32311	0.61	2.0E-03	AA67783.1	EST_HUMAN	z13a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
6882	17939	30575	1.52	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galeflectin LEC-11, complete cds
6939	19674	32720	0.6	2.0E-03	5031864	NT	Homo sapiens lipoma HMIGIC fusion partner (LHFP) mRNA
6939	19674	32721	0.6	2.0E-03	5031864	NT	Homo sapiens lipoma HMIGIC fusion partner (LHFP) mRNA
6981	19506	32531	3.55	2.0E-03	BE067986.1	EST_HUMAN	CM4-BT03668-061299-054-401 BT03668 Homo sapiens cDNA
7044	19735	32795	0.58	2.0E-03	A1298883.1	EST_HUMAN	qim89d11.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896985 3'
7193	19879	32853	0.8	2.0E-03	T86569.1	EST_HUMAN	y477910.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114306 5'
7517	20188	33281	1.18	2.0E-03	P07364	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7950	20645	33769	1.96	2.0E-03	AW592004.1	EST_HUMAN	m73b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60976 Q60976 JERKY. ;
8116	20810	33944	6.07	2.0E-03	N20287.1	EST_HUMAN	yx42g06.a1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8116	20810	33945	6.07	2.0E-03	N20287.1	EST_HUMAN	y42q06.s1 Scores melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1 b2 L1 repetitive element;
8162	20856	33987	0.54	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C638.05 IN CHROMOSOME 1
8184	20878	34015	1.19	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8239	20933	34069	0.81	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8239	20933	34070	0.81	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8284	20958	34097	0.86	2.0E-03	AU136678.1	EST_HUMAN	AU136678 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8318	21011		0.91	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8570	21282	34400	0.54	2.0E-03	AB035256.1	NT	Oryzolagus curvicaulis mRNA for eukaryotic polypeptide chain release factor 3, partial cds
9094	18419	31331	0.74	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
9094	18419	31332	0.74	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
9139	21827	34992	0.64	2.0E-03	AF224688.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9426	22104	35276	0.89	2.0E-03	H50832.1	EST_HUMAN	y88a09.s1 Scores fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:194298 3'
9426	22104	35277	0.89	2.0E-03	H50832.1	EST_HUMAN	y88a09.s1 Scores fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:194298 3'
9458	22008	35178	3.46	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMIEM) (JI) (MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150- 225) (TENASCIN-C) (TN-C)
9566	22218	35404	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9566	22219	35405	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9623	22276	35484	0.53	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9623	22276	35465	0.53	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9815	22468	35668	0.81	2.0E-03	AW884289.1	EST_HUMAN	QV3-OT0084-060400-144-601 OT0084 Homo sapiens cDNA
9942	22690		5.75	2.0E-03	AA261376.1	EST_HUMAN	za10a08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
10506	23152	36377	0.45	2.0E-03	AW361178.1	EST_HUMAN	RC1-CT0251-141088-012-401 CT0251 Homo sapiens cDNA
10506	23152	36378	0.45	2.0E-03	AW361178.1	EST_HUMAN	RC1-CT0251-141088-012-401 CT0251 Homo sapiens cDNA
10938	23618		2.97	2.0E-03	M86524.1	NT	Human dystrophin gene
11470	20188	33281	2.56	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11531	24131		2.14	2.0E-03	BF30908.1	EST_HUMAN	RC3-BT0333-310800-115-q04 BT0333 Homo sapiens cDNA
11538	24138	37446	9.1	2.0E-03	Z11740.1	NT	H sapiens variable number tandem repeat (VNT) locus DNA
11909	24473		3.23	2.0E-03	AB25745.1	EST_HUMAN	y45h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW-VATG_MANSE Q26532 VACUOLAR ATP SYNTHASE SUBUNIT G;
11928	24487	37807	2.41	2.0E-03	AF157616.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds

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11949	24502	37810	2.41	2.0E-03	AI084325.1	EST_HUMAN	oy49g06.a1 Soares_parethyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to TR:P97636 P97635 PS-PLA1 PRECURSOR.;
11972	17907		9.37	2.0E-03	AJ245167.1	NT	Carnelius dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
12172	25361		2.99	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
12262	24707	31050	1.76	2.0E-03	Y00308.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12433	26224		1.48	2.0E-03	AI375037.1	EST_HUMAN	ta66f02.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element
12542	24882						Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12713	28175		1.64	2.0E-03	AF129756.1	NT	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
429	13215	25860	2.65	2.0E-03	AV697966.1	EST_HUMAN	y68c08.r1 Soares_pineal_gland_NbHPG Homo sapiens cDNA clone IMAGE:232334 5'
810	13581	26248	1.28	1.0E-03	H98471.1	EST_HUMAN	as70b08.x1 Barstead_colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
			2.31	1.0E-03	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE.;
810	13581	26249	2.31	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead_colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1073	13831	28489	3.78	1.0E-03	AI865789.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE.;
1093	13851	26510	1.78	1.0E-03	AI954572.1	EST_HUMAN	wk86a08.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
2021	14756	27486	3.38	1.0E-03	P47808	SWISSPROT	wx93a10.x1 NCL_CGAP_Mel18 Homo sapiens cDNA clone IMAGE:2551242 3'
2150	14880	27614	12.13	1.0E-03	AJ131016.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2879	15745	28393	1.37	1.0E-03	AB033117.1	NT	Homo sapiens SCL gene locus
3186	16949	28599	2.21	1.0E-03	P18915	SWISSPROT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3186	16949	28600	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3656	16409		1.65	1.0E-03	AB044400.1	NT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
4402	17139	29767	1.28	1.0E-03	BE639162.1	EST_HUMAN	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4441	17177	29803	4.05	1.0E-03	BE246536.1	EST_HUMAN	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
4615	17350	29895	0.84	1.0E-03	U28449.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4773	17505	30127	1.68	1.0E-03	AI073485.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4773	17505	30128	1.68	1.0E-03	AI073485.1	EST_HUMAN	TCBAP-1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBAP Homo sapiens cDNA clone TCBAP4809
4774	17506		4.29	1.0E-03	BE164067.1	EST_HUMAN	Cenchrabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
5018	17739	30348	7.24	1.0E-03	O46409	SWISSPROT	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840262 3'
							ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840262 3'
							PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
							APOLIPOPROTEIN A-IV PRECURSOR (APOA-IV)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5226	18032	30658	1.87	1.0E-03	AA280951.1	EST_HUMAN	z44401.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5317	18121	30778	3.12	1.0E-03	AIJ06345.1	NT	Homo sapiens KVLQ11 gene
5369	18170	30856	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG878 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5369	18170	30857	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG878 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5485	18284	31182	0.83	1.0E-03	BE766491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5491	18290	31187	2.07	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5546	18343	31251	0.67	1.0E-03	N41974.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2N1b-HM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5546	18343	31252	0.67	1.0E-03	N41974.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2N1b-HM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5930	18714		2.75	1.0E-03	X07698.1	NT	Mouse nucleolin gene
5930	18750	31711	1.07	1.0E-03	BE063339.2	EST_HUMAN	601657518R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875683 3'
6099	18877		8.76	1.0E-03	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6242	19016	31990	1.14	1.0E-03	T87761.1	EST_HUMAN	y083a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
6315	19096		1.7	1.0E-03	AW602585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6657	19418	32432	1.37	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7052	19743	32805	2.64	1.0E-03	D18826.1	NT	Human gene for fourth semaphorin receptor subtype
7539	20209	33308	1.8	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7608	20274	33382	3.37	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7656	20320	33429	0.86	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3883276 5'
7789	20484	33608	0.83	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7850	20545	33873	5.18	1.0E-03	AJ251873.1	NT	Homo sapiens partial abertin-1 gene
8043	20737	33870	1	1.0E-03	AA122270.1	EST_HUMAN	z497c08.e1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.1 L1 repetitive element;
8142	20836	33968	1.94	1.0E-03	AF153980.1	NT	Homo sapiens excrucies-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8329	21022	34158	0.86	1.0E-03	U28397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8492	21184	34326	0.61	1.0E-03	AA001613.1	EST_HUMAN	zh82a06.a1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8492	21184	34327	0.81	1.0E-03	AA001613.1	EST_HUMAN	zh82a06.a1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8842	21534		1.36	1.0E-03	Y11204.1	NT	V carlieri gene encoding vncroapsh
8869	21560	34705	0.62	1.0E-03	AW840353.1	EST_HUMAN	CH3-L1T0079-170200-092-507 LT0079 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	21688						Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (ORTR), CDM protein (CDM), adrenoleukodystrophy protein >
9017	21707	34858	0.58	1.0E-03	U52111.2	NT	
9017	21707	34858	3.68	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cdt subunit mRNA, complete cds
9017	21707	34859	3.68	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cdt subunit mRNA, complete cds
9507	22160	35340	1.68	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9507	22160	35341	1.68	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9720	22371	35570	0.81	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10083	22711	35929	0.85	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10088	22716		0.75	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10214	22882	36075	1.72	1.0E-03	AI024350.1	EST_HUMAN	ov7908.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1 MER39 MER39 repetitive element :
10503	23149		0.48	1.0E-03	AA706202.1	EST_HUMAN	ag93f12.s1 Stratagene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element:
10563	23259	36495	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-409 CT0279 Homo sapiens cDNA
10563	23259	36496	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-409 CT0279 Homo sapiens cDNA
10651	23342	36580	2.78	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-403 HT0543 Homo sapiens cDNA
10725	23413		3.29	1.0E-03	AI683847.1	EST_HUMAN	H73a12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195 PVA1 GENE :
10808	23491	36727	1.36	1.0E-03	AW237482.1	EST_HUMAN	xm72d12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2689751 3'
11106	23776		3.05	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11905	24470	37805	4.48	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12124	24616		1.38	1.0E-03	AV731520.1	EST_HUMAN	AV731520 HTF Homo sapiens cDNA clone HTFAJG05 5'
12371	25342		1.98	1.0E-03	AI347355.1	EST_HUMAN	bc05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element
12478	25365	30612	7.05	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
12821	25187	30809	1.37	1.0E-03	AW847341.1	EST_HUMAN	RCO-CT0205-240969-021-402 CT0205 Homo sapiens cDNA
5130	17848	30485	0.7	9.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5596	18391		1.26	9.0E-04	P06727	SWISSPROT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
6165	18942		0.6	9.0E-04	AI006345.1	NT	Homo sapiens KVLQ11 gene
6395	19164	32165	0.96	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VARI
9543	22168		1.42	9.0E-04	AB037203.1	NT	Glycylhistidyl tRNA for beta-amylin synthase, complete cds
1471	14218		1.02	8.0E-04	X96469.1	NT	X laevis mRNA for C4SR protein

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4159	18899		4.37	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4713	17445	30078	2.39	8.0E-04	U29186.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11092	23762		2.63	8.0E-04	AA77084.1	EST_HUMAN	z24c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11268	23926		1.96	8.0E-04	AI571098.1	EST_HUMAN	h85a08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
2398	15119	27858	0.97	7.0E-04	U29186.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2719	15428	28184	1.19	7.0E-04	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3274	16035	28685	1	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6005	18786	31748	0.94	7.0E-04	AA518212.1	EST_HUMAN	hg55g12.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:938718 similar to contains L1.83 L1 L1
6420	19188		2.47	7.0E-04	AI786331.1	EST_HUMAN	repetitive element
7128	18818		0.78	7.0E-04	AK024445.1	NT	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387209 3'
9703	22354	35549	0.53	7.0E-04	P13497	SWISSPROT	Homo sapiens mRNA for FLJ0035 protein, partial cds
9703	22354	35550	0.53	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11557	24158		2.28	7.0E-04	U78027.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11588	24185	37500	4.04	7.0E-04	Z40561.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
12642	24939		2.31	7.0E-04	R17338.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12689	24984		5.98	7.0E-04	6005855	NT	xg13c08.r1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:32288 5'
3941	18691	28328	1.83	6.0E-04	AI882526.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
4088	18812	28440	0.78	6.0E-04	K01315.1	NT	w15a11.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402878 3'
4088	18812	29441	0.78	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4162	18902	29531	3.79	6.0E-04	U45983.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
7478	20151	33245	0.81	6.0E-04	Q15034	SWISSPROT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
7765	20461		3.33	6.0E-04	P46408	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7914	20609		0.62	6.0E-04	H92947.1	EST_HUMAN	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
9880	22530		3.5	6.0E-04	AL048507.2	EST_HUMAN	y04c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element
9980	22828	35837	2.28	6.0E-04	BE005850.1	EST_HUMAN	DKFZ586M2024_r1 586 (synonym: hule1) Homo sapiens cDNA clone IMAGE:231956 3' similar to contains
10238	22886		0.71	6.0E-04	AF287478.1	NT	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
11487	24070	37378	2.53	6.0E-04	AJ228042.1	NT	Lytechinus variegatus embryonic blastocoel extracellular matrix precursor (ECM3) mRNA, complete cds
11558	24167	37467	3.48	6.0E-04	AW013847.1	EST_HUMAN	Homo sapiens 989 kb contig between AML1 and CBR1 on chromosome 21q22 segment 2/3
11638	24233		2.17	6.0E-04	Q01768	SWISSPROT	UHH-BJ0-aab-e-09-Q-UJ.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
12082	25249		2.81	6.0E-04	AW380519.1	EST_HUMAN	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)

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12816	25058		1.34	6.0E-04	AI817088.1	EST_HUMAN	wf76g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:240880.4 3' similar to contains element L1 repetitive element;
636	13415	26051	6.81	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)
1490	14237		1.4	5.0E-04	AW851844.1	EST_HUMAN	QV0-C10225-021098-030-507 C10225 Homo sapiens cDNA
3408	16166	28815	1.35	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3704	16457	29098	2.32	5.0E-04	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5386	18186	30877	2.99	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6532	19298	32303	7.89	5.0E-04	AA156080.1	EST_HUMAN	z033b08.r1 Stratiogene codon (#937204) Homo sapiens cDNA clone IMAGE:588663 5'
7276	19960	33037	3.75	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
7856	20551	33677	5.2	5.0E-04	AI188382.1	EST_HUMAN	qd13f06.x1 Soares placenta 8606weeks 2NBHP8b9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN) contains Alu repetitive element
8202	20896	34033	0.96	5.0E-04	AA814519.1	EST_HUMAN	cb86a02.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1339228 3' similar to contains element MER22 repetitive element;
9177	21847	35013	1.39	5.0E-04	AA846545.1	EST_HUMAN	ej56f03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9271	22025	35195	0.68	5.0E-04	N83765.1	EST_HUMAN	KK2748F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9418	22096	35268	1.44	5.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9509	22162	35344	4.1	5.0E-04	AW270938.1	EST_HUMAN	xs08e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768868 3'
10177	22825		0.48	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
10897	23577		2.38	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024.J1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586M2024
11713	18186	30877	14.08	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12020	25184		5.04	5.0E-04	AA568513.1	EST_HUMAN	mf15h02.e1 NCI_CGAP_Prl1 Homo sapiens cDNA clone IMAGE:913875
658	13435	26076	1.48	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
827	13597	26267	1.79	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOVYL-COA HYDRATASE.;
827	13597	26268	1.79	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOVYL-COA HYDRATASE.;
1449	14186	26380	3.18	4.0E-04	AW753356.1	EST_HUMAN	RC3-CT0254-130100-023-101 CT0254 Homo sapiens cDNA
2075	14807	27538	1.81	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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2129	14860		1	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
2833	15345	28088	2.21	4.0E-04	O98615	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3162	15925	28572	0.85	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4289	17028	29653	3.18	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4289	17028	29654	3.18	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4500	17236	29668	1.76	4.0E-04	AA086324.1	EST_HUMAN	zn61c08.s1 Striatum muscle 937209 Homo sapiens cDNA clone IMAGE:562870 3'
5028	17748	30360	3.1	4.0E-04	BE560660.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
7168	19855	32925	1.3	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7434	20111		0.76	4.0E-04	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
7618	20284	33394	0.56	4.0E-04	AU122079.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8434	21127	34284	1.07	4.0E-04	BF240712.1	EST_HUMAN	601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098700 5'
8442	21134	34270	1.5	4.0E-04	N25507.1	EST_HUMAN	yx39e12.1 Scores melanocyte 2NH-HM Homo sapiens cDNA clone IMAGE:264142 5'
9590	22243	35426	3.24	4.0E-04	A025698.1	EST_HUMAN	ov87h03.s1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1844341 3'
9740	22391		1.22	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2 (a17) mRNA, alternatively spliced, complete cds
12880	25157		2.05	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
152	12967	25608	3.46	3.0E-04	AL119426.1	EST_HUMAN	DKFZp781J221.J1 761 (synonym: harrm2) Homo sapiens cDNA clone DKFZp781J221 5'
190	13003	25644	2.24	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2R)
860	13629	26300	1.32	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1831	14570	27282	1.08	3.0E-04	AI262100.1	EST_HUMAN	q228403.y1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1846	14584		1.21	3.0E-04	AI399874.1	EST_HUMAN	th23a02.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2118082 3'
3303	15084	28712	3.43	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3308	16068	28717	0.7	3.0E-04	AA203342.1	EST_HUMAN	zx56a04.t1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:446478 5'
3946	16696	29335	4.07	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4034	16779		1.33	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4072	16816		1.12	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT0014-310589-028 HT0014 Homo sapiens cDNA
4766	17498		4.72	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT03339-180200-007.g12 HT0339 Homo sapiens cDNA
4827	17558	30180	0.95	3.0E-04	AW837723.1	EST_HUMAN	QV3-DT0045-221289-046-d08 DT0045 Homo sapiens cDNA
5063	17782	30389	0.96	3.0E-04	AA613145.1	EST_HUMAN	nc08g09.s1 NCL CGAP_Ju1 Homo sapiens cDNA clone IMAGE:1143328 3'
6052	18832		7.86	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6722	19598	32588	2.62	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7491	20163	33256	0.84	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8157	20851	33983	3.23	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9820	22471	35673	1.34	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
10078	22726	35943	0.85	3.0E-04	A1992139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); wt75a11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2613276 3'
10356	23003	36220	3.73	3.0E-04	AA781201.1	EST_HUMAN	q24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 80S
10495	23141	36367	0.54	3.0E-04	P13816	SWISSPROT	RIBOSOMAL PROTEIN L7A (HUMAN);
11555	24154	37498	1.38	3.0E-04	4501990	NT	GLUTAMIC ACID-RICH PROTEIN PRECURSOR Homo sapiens adrenepic, alpha -1A-, receptor (ADRA1A), mRNA
11976	25386	30817	4.91	3.0E-04	AA228301.1	EST_HUMAN	nc38e04.r1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
12338	25230	30818	3.08	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
12730	25000		2.75	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: ifbr1) Homo sapiens cDNA clone DKFZp547L185 5'
171	12984	25624	2.65	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
466	13251	25892	1.8	2.0E-04	AU148707.1	EST_HUMAN	AU148707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
887	13656	26324	10.71	2.0E-04	M86524.1	NT	Human dystrophin gene
887	13656	26325	10.71	2.0E-04	M86524.1	NT	Human dystrophin gene
1156	13911		3.93	2.0E-04	A1286021.1	EST_HUMAN	gh98e11.x1 Soares_NRL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3 b2 MER3 repetitive element;
1163	13917		2.18	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1824	14563		1.12	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pitx3 gene
2581	15295	28033	4.47	2.0E-04	U66081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRB1S1, TCRB1S2,>
2986	15752	28398	1.11	2.0E-04	A1124529.1	EST_HUMAN	am58c08.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3328	16088	28740	1.1	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3428	16186	28834	1.99	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-507 BT0636 Homo sapiens cDNA
3892	16542	29282	0.79	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE sequences, MAGP Homo sapiens cDNA
4122	16864		4.93	2.0E-04	U01029.1	NT	Phasodius vulgaris nitrate reductase (PVNR2) gene, complete cds
4620	17355	29990	1.74	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4620	17355	29991	1.74	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4742	17474		1.63	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4998	17721	30324	1.1	2.0E-04	AB037897.1	NT	Danio rerio heparinoma gene, exons 1 to 6, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5089	17808	30424	1.04	2.0E-04	P35748	SWISSPROT	MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC)
5457	18256	31146	0.73	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLODUH10 3'
5469	18268	31160	1.75	2.0E-04	AI690862.1	EST_HUMAN	IQ3511.1 NCI CGAP_U3 Homo sapiens cDNA clone IMAGE:2207709 3'
5664	18459	31373	0.96	2.0E-04	AA206652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' and similar to EST containing O family repeat
5857	18644	31584	0.81	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6144	18922	31892	0.59	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7130	19818		2.6	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7225	19910		0.55	2.0E-04	AW860963.1	EST_HUMAN	QV0-CT0387-18300-167-a10 CT0387 Homo sapiens cDNA
7520	20191		14.88	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7530	20200	33295	1.42	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7855	20550	33675	1.06	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7855	20550	33676	1.06	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8182	20876	34012	1.23	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8182	20876	34013	1.23	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8463	21155	34298	1.96	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
8642	21334	34478	0.49	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9233	21912	35086	0.49	2.0E-04	AA725700.1	EST_HUMAN	ai22a12 s1 Scores_testis_NHT Homo sapiens cDNA clone 1343518 3'
9319	21986	35158	0.6	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLGPF28.1
9875	22525	35719	1.19	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151068-011-005 HT0254 Homo sapiens cDNA
9916	22565	35761	1.77	2.0E-04	AA405777.1	EST_HUMAN	zu66a11.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
10755	23440	36684	5.23	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 6'
11128	23796		1.81	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11276	23937	37229	3.06	2.0E-04	AI440282.1	EST_HUMAN	ij01111.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
11403	24052	37356	2.86	2.0E-04	AW136740.1	EST_HUMAN	UJH-B11-adm-c-04-0-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
11857	24441	37782	2.77	2.0E-04	AI821304.1	EST_HUMAN	y97b10.x5 Stratiogene ovary (#937217) Homo sapiens cDNA clone IMAGE:77371 3'
1053	13812	26472	3.3	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1092	13850	26508	4.74	1.0E-04	AW013847.1	EST_HUMAN	UJH-B10-aab-e-09-0-UJ.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1092	13850	26509	4.74	1.0E-04	AW013847.1	EST_HUMAN	UJH-B10-aab-e-09-0-UJ.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'

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1309	14057		3.12	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1623	14370	27058	3.25	1.0E-04	AF14880.5.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1623	14370	27059	3.25	1.0E-04	AF14880.5.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1654	14592	27308	2.09	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
3278	16039	28689	1.06	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPlicing FACTOR 3A SUBUNIT 2) (SF3A66)
3719	16472	29110	0.91	1.0E-04	AI440282.1	EST_HUMAN	W11111.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains AU repetitive element
4037	16782	29412	2.11	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4062	16807	29437	1.15	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLC8BD04 3'
5036	17755	30368	1.28	1.0E-04	7682015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5036	17755	30369	1.28	1.0E-04	7682015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5769	18560	31487	1.49	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5834	18623	31556	0.57	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
5834	18623	31557	0.57	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6346	19116	32105	0.96	1.0E-04	AA17711.1	EST_HUMAN	nc02a12.s1 NCL_CGAP_Px3 Homo sapiens cDNA clone IMAGE:252
6738	19572	32605	0.92	1.0E-04	AA564561.1	EST_HUMAN	nl25a04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:963486 3' similar to gb:M87252
7086	19778	32841	15.6	1.0E-04	AI251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains AU repetitive element;
7470	19778	32841	17.82	1.0E-04	AI251980.1	EST_HUMAN	qv57d10.x1 NCL_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
7894	20589	33719	0.95	1.0E-04	AA630463.1	EST_HUMAN	qv57d10.x1 NCL_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
9236	21915	35088	2.27	1.0E-04	AI806220.1	EST_HUMAN	wf26a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9247	21926	35097	1.46	1.0E-04	O88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9325	21992	35381	0.49	1.0E-04	T77163.1	EST_HUMAN	yc72a08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 5'
9546	22199	35381	1.86	1.0E-04	10863878	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10079	22727	35975	2.74	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10115	22763	35975	1	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11312	23971		2.13	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11567	24166	37479	2.05	1.0E-04	AW205336.1	EST_HUMAN	UIH-B11-sew-a-02-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
11567	24166	37480	2.05	1.0E-04	AW205336.1	EST_HUMAN	UIH-B11-sew-a-02-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
11649	24246	37568	1.76	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds

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11692	24287	37609	2.01	1.0E-04	AW289081.1	EST_HUMAN	xv49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11725	24319	37643	2	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11725	24319	37644	2	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12131	25203		2.51	1.0E-04	BE076399.1	EST_HUMAN	7129a10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3266058 3' similar to contains L1.13 L1 repetitive element:
682	13457	26102	2.76	9.0E-05	AA718933.1	EST_HUMAN	an45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
1997	14733	27455	1.14	9.0E-05	AW868218.1	EST_HUMAN	QV4-SN0023-070400-166-b04 SN0023 Homo sapiens cDNA
5873	18660	31601	1.81	9.0E-05	Q80716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7476	20149	33242	0.6	9.0E-05	AW204958.1	EST_HUMAN	UI-HB11-aer-4-05-0-J1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
7476	20149	33243	0.6	9.0E-05	AW204958.1	EST_HUMAN	UI-HB11-aer-4-05-0-J1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9376	21951		3.02	9.0E-05	D85606.1	NT	Homo sapiens gene for cholesterylkin type-A receptor, complete cds
9376	21953	35125	2.78	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11082	23752	37027	2.68	9.0E-05	AW073078.1	EST_HUMAN	xx34g05.x1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2688728 3' similar to contains L1.12 L1 repetitive element:
11207	23870	37156	1.75	9.0E-05	AI237878.1	EST_HUMAN	q23f08.x1 NCL_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
11617	18660	31601	3.5	9.0E-05	Q80716	SWISSPROT	MIR repetitive element: PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12178	26259		6.63	9.0E-05	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
802	13574	26237	1.97	8.0E-05	AJ251648.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
844	13614		2.75	8.0E-05	AJ251648.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
2950	15716		0.73	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4448	17184	29808	0.87	8.0E-05	AW044805.1	EST_HUMAN	wy78a04.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
11059	23769	37045	1.84	8.0E-05	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
12765	25242		4.85	8.0E-05	AA279333.1	EST_HUMAN	z888h01.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:704693 3' similar to contains Alu repetitive element:contains element MSR1 repetitive element:
337	13138	25773	1.14	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
337	13138	25774	1.14	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
554	13337	25965	1.1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014
554	13337	25966	1.1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014
1033	13793	26453	1.4	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2724	15431	28168	2.99	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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3156	15919	28565	5.72	7.0E-05	AB009080.1	NT	Dictyostelium discoideum gene for TRIFA, complete cds
4339	17078	29707	1.71	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4412	17149	29776	0.95	7.0E-05	U60980.1	NT	Caenorhabditis elegans Stp1p homolog mRNA, complete cds
4871	17898	30221	0.71	7.0E-05	9845300	NT	Rat cytomegalovirus Measricht, complete genome
8124	20818	33954	1.09	7.0E-05	AA505582.1	EST_HUMAN	h83g01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966098 3'
9453	22003	35175	2.97	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stralagene (cat#936208) Homo sapiens cDNA clone HFBED60
11112	23782		3.09	7.0E-05	10835048	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2020	14755	27484	1.69	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2020	14755	27485	1.69	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2595	15309	28046	1.19	6.0E-05	A1655241.1	EST_HUMAN	w654h06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309631 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2690	15399	28137	1.1	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2690	15399	28138	1.1	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2817	13440	28080	3.07	6.0E-05	AF053830.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5822	18611	31541	3.61	6.0E-05	Q12960	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GPI35)
5822	18611	31542	3.61	6.0E-05	Q12960	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GPI35)
6309	19081	32066	1.4	6.0E-05	N72839.1	EST_HUMAN	y60g11.1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:246212 5'
6834	19496	32520	0.95	6.0E-05	AA1897890.1	EST_HUMAN	q80a03.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
7983	20678	33803	0.76	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
7983	20678	33804	0.76	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
8342	21035	34172	0.62	6.0E-05	AA150482.1	EST_HUMAN	z108c08.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to repetitive element; contains LTR7 repetitive element;
8347	21040	34177	2.22	6.0E-05	AW896629.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8479	21171	34318	0.63	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9151	21882	35050	1.21	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9151	21882	35051	1.21	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9421	22089	35271	0.85	6.0E-05	T94149.1	EST_HUMAN	y628c12.1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:119062 5'
9621	22274	35462	0.59	6.0E-05	AW627885.1	EST_HUMAN	h37a03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874444 3'
10849	23340	36579	3.06	6.0E-05	R75639.1	EST_HUMAN	y56d08.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;
11502	24103	37415	3.36	6.0E-05	AA044015.1	EST_HUMAN	z158f02.1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12387	25239	30822	14.34	6.0E-05	AW980110.1	EST_HUMAN	MFO-NT0098-250400-001-f09 NT0098 Homo sapiens cDNA
12810	25053		1.4	6.0E-05	BE888403.1	EST_HUMAN	7q28a08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3307768 3'
1382	14129	26802	10.46	6.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241189-040-h11 ST0234 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1855	14593		1.2	5.0E-05	8923391	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55896), mRNA
2551	15266	28001	1.1	5.0E-05	P23249	SWISSPROT	PROTEIN MOV-10
3961	16710	29350	2.41	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5074	17763	30403	0.72	5.0E-05	Q26422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5074	17763	30409	0.72	5.0E-05	Q26422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5438	18237	30951	13.38	5.0E-05	X88856.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
5903	18688	31638	3.75	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCMA09 3'
6078	18855	31822	0.99	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7231	19916		0.87	5.0E-05	AB037084.1	NT	Mus musculus gene for calretinin, exon 1
12175	24810		3.84	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12440	24810		4.72	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2810	13032		3.84	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4449	17185	29809	0.73	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4449	17185	29810	0.73	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4820	17551		1.16	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
4955	17681	30289	0.75	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sense) gene, complete cds
6841	19503	32528	0.74	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
9423	22101		7.57	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
9801	22550	35745	0.47	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
10306	22953	36168	0.59	4.0E-05	P23780	SWISSPROT	ENDONUCLEASE]
10668	23359	36599	4.18	4.0E-05	AW627946.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
12140	24628		1.48	4.0E-05	AW117580.1	EST_HUMAN	element MIR repetitive element:
12789	25041		1.71	4.0E-05	AA417758.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:
665	13441	28082	1.8	3.0E-05	A1248081.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:
1037	13767	28457	0.88	3.0E-05	AW273951.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:
1109	13866	26523	1.01	3.0E-05	BF037898.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:
1109	13866	26524	1.01	3.0E-05	BF037898.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:
3287	16048		0.73	3.0E-05	A1288919.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:
4349	17088	28719	7.98	3.0E-05	BE169211.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:
4349	17088	28720	7.98	3.0E-05	BE169211.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4434	17170	29788	0.94	3.0E-05	AA368678.1	EST_HUMAN	EST78996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4434	17170	29789	0.94	3.0E-05	AA368679.1	EST_HUMAN	EST78996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4550	17285		0.99	3.0E-05	AL168302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4686	17420	30055	1	3.0E-05	P97468	SWISSPROT	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
4785	13441	26082	0.82	3.0E-05	A1248061.1	EST_HUMAN	qf64c10.x1 Soares_fetal_liver_spleen_infls_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element/contains element KER repetitive element;
4791	17522	30144	0.97	3.0E-05	AU126721.1	EST_HUMAN	AU125721 NT2RM4 Homo sapiens cDNA clone NT2RM4002075 5'
5470	18269	31101	1.66	3.0E-05		NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2p), mRNA
6659	19419	32433	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6659	19419	32434	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7799	20494	33616	2.33	3.0E-05	BE733167.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5'
8250	20944	34082	1.47	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Stralagene schizoa brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8791	21483	34630	1.68	3.0E-05	AW770982.1	EST_HUMAN	h194e08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009688 3'
8796	21487	34633	1.23	3.0E-05	6912431	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HV1), mRNA
8799	21491	34638	0.51	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9029	21719		0.58	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9220	21899	35068	1.22	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9563	22216		2.92	3.0E-05	A1769331.1	EST_HUMAN	wg36109.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367208 3'
10433	23079	36303	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10433	23079	36304	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12072	24585		1.77	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromere end
2323	15048	27784	1.09	2.0E-05	A1286021.1	EST_HUMAN	qf68e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2687	15301	28037	2.43	2.0E-05	M13782.1	NT	MER3.b2 MER3 repetitive element;
						NT	Human adenosine deaminase (ADA) gene, complete cds
2718	15426		7.45	2.0E-05	AA180562.1	EST_HUMAN	zq48a12.r1 Stralagene hNT neuron (8937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element/contains element L1 repetitive element;
3134	15898	28544	1.23	2.0E-05	BE066038.1	EST_HUMAN	RC3-BT0319-12020-014-028 BT0319 Homo sapiens cDNA
3343	18102	28784	0.93	2.0E-05	AF184814.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3362	18121	28779	1.22	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3485	18242		0.71	2.0E-05	X95465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3787	18539		0.78	2.0E-05	AL039107.1	EST_HUMAN	DKFZp668064_r1 566 (synonym: hfrd2) Homo sapiens cDNA clone DKFZp668064 5'
4943	17377		1.09	2.0E-05	BE378471.1	EST_HUMAN	601238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
5672	18467	31382	1.92	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5827	18616		0.69	2.0E-05	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
5880	18666	31606	0.76	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
5880	18666	31607	0.76	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6065	18844	31808	0.61	2.0E-05	A1149272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_8to9weeks_2Nb-HP8to9W Homo sapiens cDNA clone IMAGE:1716114 3'
6527	19233	32297	2.26	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element;
6801	19462	32483	3.27	2.0E-05	Y08926.1	NT	mw06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6814	19475	32497	1.12	2.0E-05	A1492980.1	EST_HUMAN	P_falciptarum mRNA for AARP1 protein, partial
6824	19485		9.37	2.0E-05	A1991025.1	EST_HUMAN	qz47b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:002711
7053	19744	32806	1.93	2.0E-05	AF224262.1	NT	002711 PRO-POL-DUTPASE POLYPROTEIN; wu35h07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7053	19744	32807	1.93	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7267	19951		0.83	2.0E-05	AF128847.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7785	20480	33605	1.71	2.0E-05	A1381040.1	EST_HUMAN	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
9020	21710	34862	0.53	2.0E-05	BE244840.1	EST_HUMAN	tc20h05.x1 NCI_CGAP_GL1.1 Homo sapiens cDNA clone IMAGE:2109369 3'
9020	21710	34863	0.53	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9167	21837	35002	0.58	2.0E-05	P49457	SWISSPROT	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9167	21837	35003	0.58	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9823	22474	35677	0.49	2.0E-05	AL163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10035	22693	35900	0.87	2.0E-05	BF055639.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10457	23103	36333	0.54	2.0E-05	AJ131024.1	NT	77f6g08.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
10457	23103	36334	0.54	2.0E-05	AJ131024.1	NT	Homo sapiens olase gene, exon 1-alpha
10499	23135	36362	1.98	2.0E-05	N41751.1	EST_HUMAN	Homo sapiens olase gene, exon 1-alpha
							yw91a06.r1 Soares_placenta_8to9weeks_2Nb-HP8to9W Homo sapiens cDNA clone IMAGE:259570 5'

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10489	23135	36363	1.98	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP6b9W Homo sapiens cDNA clone IMAGE:259570 5'
10541	19485		2.42	2.0E-05	A1991025.1	EST_HUMAN	wu35h07.x1 Soares_Diagrafa_colon_NHOD Homo sapiens cDNA clone IMAGE:2522077 3'
11287	23948	37243	1.33	2.0E-05	A1493285.1	EST_HUMAN	1930h09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN. ;
11287	23948	37244	1.33	2.0E-05	A1493285.1	EST_HUMAN	1930h09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN. ;
11430	23197	36428	2.27	2.0E-05	BE175901.1	EST_HUMAN	RC5-H10592-280300-012-E12 HT0582 Homo sapiens cDNA
12185	25188		4.86	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2 ;
12342	25155		2.27	2.0E-05	AF275648.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12874	25247		1.44	2.0E-05	D16593.1	NT	Human gene for L-histidine decarboxylase, complete cds
2285	14991	27731	3.22	1.0E-05	P27448	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78
2700	15603	28143	1.6	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3641	16394	29034	1.91	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lemito 120 Suppressor of Hairless (Su(H)) gene, partial cds
3793	16545		1.02	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3949	16999	29337	9.2	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4152	16894	29523	1.2	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4244	16985	29608	2.52	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4799	17530	30152	1.81	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
6653	19416	32428	1.22	1.0E-05	AJ246003.1	NT	Homo sapiens Speet gene for speatin protein
6980	19505	32530	2.58	1.0E-05	AA641846.1	EST_HUMAN	ns18g02.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.11 L1 L1 repetitive element ;
6982	19676	32722	3.28	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7671	20341		1.16	1.0E-05	P19474	SWISSPROT	S2 KD RO PROTEIN (SLOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8813	21505		2.24	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8988	21849	34789	3.02	1.0E-05	AA462578.1	EST_HUMAN	z25h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb1.02882 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9187	21857	35022	12.45	1.0E-05	AA236110.1	EST_HUMAN	zs05e11.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element ;
9286	22020	35189	0.62	1.0E-05	AV732190.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFB1H01 5'
9738	22889	35593	0.74	1.0E-05	AW510902.1	EST_HUMAN	hd41a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element ;

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	22389	35594	0.74	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
9816	22467	35989	1.16	1.0E-05	AW281521.1	EST_HUMAN	OFRT1 OFR repetitive element
9816	22467	35970	1.16	1.0E-05	AW281521.1	EST_HUMAN	UHH-B12-agk-a-08-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10084	22732		1.87	1.0E-05	AW468995.1	EST_HUMAN	UHH-B12-agk-a-08-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
							ha07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element
10836	23518	36780	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10836	23518	36761	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11854	24438	37780	1.38	1.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
2078	15387	28129	4.8	9.0E-06	AI683811.1	EST_HUMAN	tt73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'
3092	15857	28498	3.53	9.0E-06	AI218983.1	EST_HUMAN	cg11b08.x1 Soares_placenta_8tc9wacke_2NBHP8b6W Homo sapiens cDNA clone IMAGE:1759191 3'
3597	16350		2.82	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5815	18604	31532	2.61	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6765	19509	32534	0.8	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7340	20021	33099	0.85	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7673	20337	33450	13.94	9.0E-06	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver spleen_inFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element
8363	21056	34197	1.1	9.0E-06	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
8881	21572	34715	2.89	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8881	21572	34716	2.89	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9122	21810	34976	4.3	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10858	23538	36784	3.46	9.0E-06	Q10364	SWISSPROT	POTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2532	16597	27986	1.27	8.0E-06	AW382639.1	EST_HUMAN	RC3-C10283-201199-011-h11 C10283 Homo sapiens cDNA
10430	23076	36298	0.75	8.0E-06	P34083	SWISSPROT	FASGLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10430	23076	36299	0.75	8.0E-06	P34083	SWISSPROT	FASGLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
958	13723		2.89	7.0E-06	AA069729.1	EST_HUMAN	ab90f10.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1419	14167	28851	3.42	7.0E-06	7682177	NT	MER20.11 MER20 repetitive element; Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2876	15643		5.93	7.0E-06	AI368252.1	EST_HUMAN	qwt6g09.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3551	16308		0.92	7.0E-06	AA385542.1	EST_HUMAN	EST199205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5609	18405		5.68	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
5715	18508	31429	1.01	7.0E-06	N98845.1	EST_HUMAN	yy6507.r1 Scores_multiple_sclerosis_2/bhMSP Homo sapiens cDNA clone IMAGE:278412 5'
8888	21380	34524	0.7	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF0881E), mRNA
9800	22451		0.45	7.0E-06	Q61147	SWISSPROT	GERULOPLASMIN PRECURSOR (FERROXIDASE)
11930	28356	30608	2.32	7.0E-06	BF215972.1	EST_HUMAN	60186152F-1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2918	15684	28329	1.28	6.0E-06	BE089189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3680	18433	29076	1.08	6.0E-06	BE089189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4705	15708	28359	1.91	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4710	17442	30074	2.21	6.0E-06	A1040099.1	EST_HUMAN	ox08e02.x1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1665738 3' similar to contains MER8.12 MER8 repetitive element;
5265	18071	30700	1.32	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5324	18127	30787	1.06	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
8756	22407		1.48	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
12755	25016	30979	2.27	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1i subunit (CACNA1I), mRNA
5970	18752	31713	3.27	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6245	19019	31993	2.31	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7134	19821	32887	1.1	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8359	21052	34192	0.53	5.0E-06	AW859972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8359	21052	34189	0.53	5.0E-06	AW859972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10002	22650	35992	6.18	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10410	23058	36273	0.45	5.0E-06	P06881	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12649	24953	30987	2.83	5.0E-06	AI065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
632	13411	28046	6.1	4.0E-06	R16287.1	EST_HUMAN	ye48c03.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element;
826	13596	28286	7.07	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCL_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element L1 repetitive element;

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1311	14059	26733	4.64	4.0E-06	A1334928.1	EST_HUMAN	1b33e09.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1311	14059	26734	4.64	4.0E-06	A1334928.1	EST_HUMAN	1b33e09.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1457	14204	26889	1.8	4.0E-06	BF366612.1	EST_HUMAN	QV2-NT0046-200600-250-107 NT0046 Homo sapiens cDNA
2261	14988	27728	2.17	4.0E-06	AW015401.1	EST_HUMAN	UI-H-BIO-sat-4-05-Q-UI.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3060	15826	28471	0.9	4.0E-06	AF198349.1	NT	Gallus gallus Dacth2 protein (Dacth2) mRNA, complete cds
3874	16624	29262	1.05	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4756	17488	30115	1.89	4.0E-06	A1866939.1	EST_HUMAN	w94c10.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
8397	21090	34225	0.56	4.0E-06	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
8699	21391	34536	3.56	4.0E-06	AF009650.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9607	22260	35446	1.24	4.0E-06	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11427	23194	36425	4.21	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2160	14890	27624	1.75	3.0E-06	AA700562.1	EST_HUMAN	Z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element;
2160	14890	27625	1.76	3.0E-06	AA700562.1	EST_HUMAN	Z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element;
2263	14889		1.44	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2922	15688	28332	1.05	3.0E-06	AA868218.1	EST_HUMAN	ek48g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3259	18021		2.05	3.0E-06	A1857779.1	EST_HUMAN	w122a05.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734
3763	16515	29162	1.13	3.0E-06	BE047094.1	EST_HUMAN	LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
3763	16515	29153	1.13	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCL CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4524	17259	29893	3.74	3.0E-06	X54816.1	NT	hg64d12.x1 NCL CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6068	18847	31811	0.93	3.0E-06	AU159412.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus)
7129	18817		2.43	3.0E-06	P08648	SWISSPROT	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7981	20676	33801	0.83	3.0E-06	BE562964.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8884	21276	34413	0.66	3.0E-06	P07743	SWISSPROT	601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5'
12349	24755		3.84	3.0E-06	AW385282.1	EST_HUMAN	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
197	13010		2.81	2.0E-06	P64369	SWISSPROT	RQ4-LT0001-261198-011-A03 LT0001 Homo sapiens cDNA
1561	14308		4.45	2.0E-06	P21414	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
2376	15098	27838	4.8	2.0E-06	A1672138.1	EST_HUMAN	POLYPROTEIN[CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE] w9d4e03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element;

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2469	15187	27826	2.37	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2571	15285	28023	1.88	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3509	16265	28919	1.12	2.0E-06	AV657555	EST_HUMAN	AV657555 GLG Homo sapiens cDNA clone GLCFDB05 3'
3744	16497	29132	1.59	2.0E-06	AA173518.1	EST_HUMAN	ZP0205.r1 Stratiene ovarian cancer (8937219) Homo sapiens cDNA clone IMAGE:595232 5'
3753	16505	29141	0.82	2.0E-06	AW450215.1	EST_HUMAN	UHH-B13-aky-q-05-0-UL.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3758	16510	29146	1.82	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5988	18779		0.83	2.0E-06	AA974832.1	EST_HUMAN	on34h01.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558809 3' similar to contains Alu repetitive element
6028	18908	31768	0.83	2.0E-06	AI539448.1	EST_HUMAN	te51f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TRQ13537
6348	19118	32108	5.47	2.0E-06	AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
7818	20513		1.63	2.0E-06	AW869223.1	EST_HUMAN	w50b04.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7988	20883	33809	0.57	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0067-120400-002-02 SN0067 Homo sapiens cDNA
8735	21427		0.6	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
8747	21439	34586	1.8	2.0E-06	H82051.1	EST_HUMAN	zh27c11.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TRP70467 P70467 REVERSE TRANSCRIPTASE ;
9116	21804	34969	0.82	2.0E-06	AF003529.1	NT	yis37cd4.r1 Soares ovary tumor N3HOT Homo sapiens cDNA clone IMAGE:236974 5' similar to gb:X74929
9116	21804	34970	0.82	2.0E-06	AF003529.1	NT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9135	21823		0.46	2.0E-06	AI473450.1	EST_HUMAN	Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions
9600	22253	35438	1	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions
9819	22470		0.63	2.0E-06	AV748968.1	EST_HUMAN	518g10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
12251	25357	30609	2.1	2.0E-06	P23249	SWISSPROT	yw66e03.s1 Soares_placenta_8to8weeks_2NHP8to9W Homo sapiens cDNA clone IMAGE:257212 3'
32	12860	25477	2.36	1.0E-06	O76082	SWISSPROT	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
642	13421	26060	2.62	1.0E-06	AF084394.1	NT	PROTEIN MOV-10
1434	14181	26866	1.61	1.0E-06	P08125	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1514	14261	26947	1.87	1.0E-06	AL163278.2	NT	Mus musculus DMMME protein (DMMME) mRNA, complete cds
1564	14311	26997	1.27	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CMZ-8
1564	14311	26998	1.27	1.0E-06	AA034141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1578	14325		1.34	1.0E-06	P27625	SWISSPROT	z08a12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element
						EST_HUMAN	z08a12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element
						SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT

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1987	14723	27443	5.09	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1987	14723	27444	5.09	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4336	17075	28703	12.81	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5208	18016	30638	5.07	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5232	18038	30665	0.83	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5232	18038	30666	0.83	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5389	18189	30881	1.22	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
5706	18500		0.78	1.0E-06	BE08327.1	EST_HUMAN	CMO-BT0281-031189-087-H04 BT0281 Homo sapiens cDNA
6773	19517	32545	6.91	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
7644	25427		0.63	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
7900	20595		0.77	1.0E-06	AA912623.1	EST_HUMAN	cl29c08.s1 Scores_NF_T_OBC_S1 Homo sapiens cDNA
8171	20865	33997	1.2	1.0E-06	A1347010.1	EST_HUMAN	qp54e02.k1 NC1_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926842 3'
8387	21080	34215					q23008.x1 NC1_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1926842 3'
9204	22083	35255	1.31	1.0E-06	A1287878.1	EST_HUMAN	MIR repetitive element
9279	22033	35205	0.94	1.0E-06	N74635.1	EST_HUMAN	za55e01.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:298472 3'
9581	22234	35417	0.55	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9581	22234	35418	4.28	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9627	22280	35470	4.28	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
			4.76	1.0E-06	AA132611.1	EST_HUMAN	zot1e08.r1 Stratiagene colon (#837204) Homo sapiens cDNA clone IMAGE:587174 5'
9688	22340		3.37	1.0E-06	AA448257.1	EST_HUMAN	z044f11.s1 Scores_total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:587174 5'
10385	23031		1.68	1.0E-06	AL163203.2	NT	gb:D28129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11648	24245		3.85	1.0E-06	AW880841.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
11724	24318	37641	1.38	1.0E-06	AA164914.1	EST_HUMAN	zq42c02.s1 Stratiagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632354 3' similar to SW/POL SMSAV P03359 POL POLYPYRROLINE;
11724	24318	37642	1.38	1.0E-06	AA164914.1	EST_HUMAN	zq42c02.s1 Stratiagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632354 3' similar to SW/POL SMSAV P03359 POL POLYPYRROLINE;
12390	14723	27443	1.79	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
12390	14723	27444	1.79	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
351	13150	25790	2.24	9.0E-07	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
351	13150	25791	2.24	9.0E-07	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8306	21000		0.53	9.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11212	23875	37161	2.87	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11733	24326	37650	1.3	9.0E-07	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
4719	17451	30084	3.26	8.0E-07	AI288596.1	EST_HUMAN	q82g07.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4719	17451	30085	3.26	8.0E-07	AI288596.1	EST_HUMAN	q82g07.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5798	18587		9.43	8.0E-07	P21414	SWISSPROT	POLYPROTEIN CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE
7901	20596		9.73	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11622	24219		6.59	8.0E-07	T07770.1	EST_HUMAN	EST056860 Fetal brain, Stratagene (cat#938206) Homo sapiens cDNA clone HFBEN89
11912	24476		8.22	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1858	14596	27312	0.91	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5432	18231	30944	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5432	18231	30945	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1905	14842	27352	2.98	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
2496	15213	27956	4.52	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
3955	16705		1.83	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4P33 INTERGENIC REGION
9040	21730	34885	1.52	6.0E-07	BF001867.1	EST_HUMAN	7g94f07.x1 NCI_CGAP_C018 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L.
11836	24420	37761	1.3	6.0E-07	BE063509.1	EST_HUMAN	CM0-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
12156	25307		2.28	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-260300-121-412 NN1029 Homo sapiens cDNA
318	13121		1.94	5.0E-07	AI831893.1	EST_HUMAN	wf84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1035	13795		4.25	5.0E-07	AA380630.1	EST_HUMAN	EST193615 Supt cells Homo sapiens cDNA 5' end
3028	15794		0.88	5.0E-07	AI831893.1	EST_HUMAN	wf84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
6029	18809	31769	0.9	5.0E-07	U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
6864	19446	32463	1.69	5.0E-07	AI393981.1	EST_HUMAN	Ig06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
6864	19446	32464	1.69	5.0E-07	AI393981.1	EST_HUMAN	Ig06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
7248	19933	33008	17	5.0E-07	AW070885.1	EST_HUMAN	xa31802.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:U15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8173	20867	33959	0.74	5.0E-07	O9WLUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8388	21081		0.82	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10265	22913	36123	4.94	5.0E-07	AI908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10560	23256	36493	1.28	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11500	24101	37413	4.04	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11574	24173		2.52	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12561	25211		3.48	5.0E-07	AW882537.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3981	16729	29364	2.02	4.0E-07	AW009602.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
7078	19769		0.83	4.0E-07	AJ272285.1	NT	we84h05.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697 3'
7167	19854	32923	1.74	4.0E-07	Q92ZV6	SWISSPROT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7167	19854	32924	1.74	4.0E-07	Q92ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7823	20518	33644	0.6	4.0E-07	AL163207.2	NT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8949	21640	34787	5.41	4.0E-07	AW419134.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10027	22675	35890	0.47	4.0E-07	BE901975.1	EST_HUMAN	xy49g11.x1 NCL CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10027	22675	35891	0.47	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959851 5'
10223	22871	36084	0.49	4.0E-07	AL163218.2	NT	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959851 5'
10856	23536	36781	3.14	4.0E-07	AI765528.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C018
10856	23536	36782	3.14	4.0E-07	AI765528.1	EST_HUMAN	w81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11184	23849		1.66	4.0E-07	BE001828.1	EST_HUMAN	w81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
431	13217	25862	9.64	3.0E-07	U19719.1	NT	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
569	13350	25978	2.12	3.0E-07	AJ271735.1	NT	Human microtubule-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced
1353	14101	26776	2.87	3.0E-07	M99149.1	NT	untranslated exons
1622	14369		2.03	3.0E-07	M64857.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2039	14773		1.42	3.0E-07	AA526763.1	EST_HUMAN	Human polymorphic microsatellite DNA
2286	15011	27749	1.83	3.0E-07	M99149.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2472	15190	27930	7.81	3.0E-07	BE005077.1	EST_HUMAN	element; contains L1, L3 L1 repetitive element
2472	15190	27931	7.81	3.0E-07	BE005077.1	EST_HUMAN	Human polymorphic microsatellite DNA
3031	15797	28443	1.16	3.0E-07	T84704.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3157	15920	28566	1.45	3.0E-07	P38739	SWISSPROT	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
4678	17412	30047	7.42	3.0E-07	AV950201.1	EST_HUMAN	yc50112.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111695 5'
4711	17443	30075	0.88	3.0E-07	A197238.1	EST_HUMAN	HYPOPHYSAL 63.8 KD PROTEIN IN GLUT1-RM1 INTERGENIC REGION PRECURSOR
5004	17727	30330	1.3	3.0E-07	T57850.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLOCCD01 3'
5004	17727	30331	1.3	3.0E-07	T57850.1	EST_HUMAN	we86b12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347987 3'
							yc14h09.s1 Strabagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to
							gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
							yc14h09.s1 Strabagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to
							gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

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5580	18377	31290	12.43	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
5583	18689	31610	0.83	3.0E-07	O42280	SWISSPROT	PEPTIDYLARGININE DEIMINASE TYPE ALPHA
6603	19366		5.57	3.0E-07	AA815176.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
7409	20086	33170	3.48	3.0E-07	AW787168.1	EST_HUMAN	cc04c10.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1338890 3'
7561	20231		0.79	3.0E-07	AI591065.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
9028	21718	34872	0.85	3.0E-07	P33240	SWISSPROT	tw28f11.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element;
9028	21718	34873	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
11484	24085		1.45	3.0E-07	BE439409.1	EST_HUMAN	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
11656	24253		1.75	3.0E-07	AF028308.1	NT	HTM1-025F1 HTM1 Homo sapiens cDNA
12791	25043		6.1	3.0E-07	AJ132352.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
27	12855	25471	4.15	2.0E-07	AF282088.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
150	12985	25606	9	2.0E-07	L77569.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
150	12985	25607	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
177	12989	25629	44.15	2.0E-07	U38849.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
731	13505	26160	2.45	2.0E-07	AF003530.1	NT	Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds
731	13505	26161	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
744	13517		0.82	2.0E-07	P11369	SWISSPROT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
922	13688	26353	3.73	2.0E-07	AA223260.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
923	13680	26354	2.15	2.0E-07	T63042.1	EST_HUMAN	z08807.s1 Striatagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:U131860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
1140	13895	26556	1.37	2.0E-07	Q26768	SWISSPROT	yc15g04.s1 Striatagene lung (#637210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1586	14342	27032	2.98	2.0E-07	Q08701	SWISSPROT	J6 AUTOANTIGEN
3676	16428	29070	15.93	2.0E-07	AF125348.1	NT	HYPOTHETICAL 72.5 KD PROTEIN C2E7.10 IN CHROMOSOME I
5059	17778	30395	0.84	2.0E-07	AW070865.1	EST_HUMAN	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
							xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP-C38H2.1 CE00923 PROBABLE RABGAP DOMAINS ;

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5059	17778	30396	0.84	2.0E-07	AW070995.1	EST_HUMAN	xcd5h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP.C38H2.1
5260	18066	30694	1.21	2.0E-07	AW898066.1	EST_HUMAN	CE00923 PROBABLE RABGAP DOMAINS ;
6456	25090	32223	0.81	2.0E-07	AW448968.1	EST_HUMAN	RC3-NN0068-260400-021-g11 NN0068 Homo sapiens cDNA
6565	19330	32337	1.79	2.0E-07	AI208715.1	EST_HUMAN	ULF-BI3-ake-b-01-0-U.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
7568	20238	33342	0.67	2.0E-07	X95159.1	NT	qg58d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8369	21062		4.08	2.0E-07	AV729390.1	EST_HUMAN	H sapiens bica2 gene exon 9
8595	21287	34426	0.97	2.0E-07	AA035198.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
9961	22313		2.8	2.0E-07	AL163303.2	NT	z427g09.s1 Soares_pregnant_uterus_NthIPU Homo sapiens cDNA clone IMAGE:471808 3'
10167	22815	36033	5.41	2.0E-07	AW892507.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10386	23032	38245	0.9	2.0E-07	P00751	SWISSPROT	OM4-NN0003-280300-124-e06 NN0003 Homo sapiens cDNA
10386	23032	38246	0.9	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PBF2)
11871	24945		2.44	2.0E-07	BE153717.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PBF2)
11953	25212		2.39	2.0E-07	AI732462.1	EST_HUMAN	PMO-HT0339-280100-006-H07 HT0339 Homo sapiens cDNA
1080	13838		1.97	1.0E-07	AL163282.2	NT	zn85h11.x6 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element ;
2381	15103	27842	1.11	1.0E-07	P10263	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
2830	14259	28945	2.51	1.0E-07	P09256	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3727	13838		1.29	1.0E-07	AL163282.2	NT	GLYCOPROTEIN GPV
4260	17001	29631	2.76	1.0E-07	AV718662.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
4260	17001	29632	2.76	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4590	17424		0.93	1.0E-07	O75820	SWISSPROT	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
5072	17791	30406	0.93	1.0E-07	AA019181.1	EST_HUMAN	ZINC FINGER PROTEIN 189
6410	19178	32177	0.87	1.0E-07	U82671.2	NT	zn55g02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363026 5'
6768	19512	32537	5.24	1.0E-07	BE047871.1	EST_HUMAN	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6768	19512	32538	5.24	1.0E-07	BE047871.1	EST_HUMAN	IZ43d06.y1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2281339 5'
7392	20071	33150	9.08	1.0E-07	N55081.1	EST_HUMAN	IZ43d06.y1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2281339 5'
7548	20218	33320	0.67	1.0E-07	BF375909.1	EST_HUMAN	yz43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7548	20218	33321	0.67	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7577	20246	33351	1.31	1.0E-07	AL163281.2	NT	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA

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7721	20385	33499	0.84	1.0E-07	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8114	20808	33941	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8114	20808	33942	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8853	21544	34691	2.78	1.0E-07	AA693576.1	EST_HUMAN	z151e10 s1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
9170	21840	35005	0.97	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9517	22170	35353	0.45	1.0E-07	BE327843.1	EST_HUMAN	h128h06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9836	22487	35989	2.77	1.0E-07	BE74524.1	EST_HUMAN	MER18 repetitive element;
9844	22495	35996	1.21	1.0E-07	AA396311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10362	23009		1.28	1.0E-07	AL163282.2	NT	EST189054 Brain IV Homo sapiens cDNA
12212	25188	30810	3.83	1.0E-07	BE048770.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12514	24884		1.87	1.0E-07	X51755.1	NT	h153c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR-O95722 O95722 DJ1163J1.1;
7181	19867	32940	0.84	9.0E-08	AI639362.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
9787	22438	35645	1.88	9.0E-08	AV734818.1	EST_HUMAN	h15b06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080185 3'
11136	23804	37082	1.71	9.0E-08	AI891052.1	EST_HUMAN	AV734819 cDNA Homo sapiens cDNA clone cdABFB06 5'
11668	24263	37587	2.8	9.0E-08	AL163301.2	NT	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
12166	24848		4.44	9.0E-08	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C101
593	15546		3.7	8.0E-08	AI911352.1	EST_HUMAN	Homo sapiens partial sbeeth-1 gene
1026	13788		0.72	8.0E-08	BE785469.1	EST_HUMAN	wd16b05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
3532	16288		1.53	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8638	21330	34474	3.05	8.0E-08	AI752387.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8638	21330	34475	3.05	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9527	22180	35364	2.93	8.0E-08	AW970893.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
10481	23107	36838	0.47	8.0E-08	AF111167.2	NT	EST382776 MAGE resequences, MACK Homo sapiens cDNA
11211	23874		2.1	8.0E-08	AF253417.1	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
78	12904	25542	2.66	7.0E-08	Q02357	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1340	14088	26764	13.91	7.0E-08	X04808.1	NT	ANKRYN 1 (ERYTHROCYTE ANKYRIN)
3553	16318	28965	1.15	7.0E-08	P15305	SWISSPROT	Rat mRNA for ribosomal protein L31
							DYNEIN HEAVY CHAIN (DYHC)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3563	16318	28966	1.15	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10716	23405		1.67	7.0E-08	A1535743.1	EST_HUMAN	cong3.P11.A5 confrm Homo sapiens cDNA 3'
11672	24267	37589	5.17	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12619	16318	28965	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12619	16318	28966	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12690	24975		1.89	7.0E-08	AJ131016.1	NT	Homo sapiens SCL gene locus
798	13570	26230	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
798	13570	26231	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2363	15085	27824	2.97	6.0E-08	BE144398.1	EST_HUMAN	MRO-HT0168-191189-004-g09 HT0168 Homo sapiens cDNA
3058	15824	28469	0.81	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4222	16963	28588	0.98	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7851	20546		0.69	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9227	21906		0.56	6.0E-08	AA827075.1	EST_HUMAN	ob5605.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains
							MER12.b3 MER12 repetitive element ;
11391	23997	37289	2.24	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
11520	24120		1.33	6.0E-08	AL163209.2	NT	ENDONUCLEASE]
83	12809	25547	3.72	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C009
							Homo sapiens chromosome 21 segment HS21C103
2229	14957	27697	1.82	5.0E-08	AA493851.1	EST_HUMAN	rh03b08.s1 NCJ_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive
11914	24477		8.36	5.0E-08	P06681	SWISSPROT	element;
12099	24599	31085	2.54	5.0E-08	AW851878.1	EST_HUMAN	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
1754	14496	27195	0.97	4.0E-08	P25723	SWISSPROT	QV0-CT0225-131089-034-a12 CT0225 Homo sapiens cDNA
1754	14496	27196	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2888	15655		1.09	4.0E-08	AL078581.1	EST_HUMAN	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
3894	16644	29284	1.04	4.0E-08	U82663.1	NT	DKFZp434J0426_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434J0426 5'
6311	18082	32067	1.08	4.0E-08	P52624	SWISSPROT	Homo sapiens shox gene, alternatively spliced products, complete cds
8697	21369	34533	0.63	4.0E-08	O16393	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9037	21727	34881	1.05	4.0E-08	L42571.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
9545	22198		0.71	4.0E-08	P08547	SWISSPROT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
10228	22876		0.68	4.0E-08	A1016342.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							ct78d12.s1 Scores: total: fetus_Nb2HF8_sw Homo sapiens cDNA clone IMAGE:1622803 3'
10284	22932	36147	3.87	4.0E-08	AU050027.1	EST_HUMAN	ar22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1698411 3' similar to contains Alu
							repetitive element; contains element MER22 repetitive element ;

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1847	14585		4.11	2.0E-08	AW270271.1	EST_HUMAN	XP43H1.x1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2545	16280		1.71	2.0E-08	K00216.1	NT	Sheep His-fRNA-GUG
3202	15965	28618	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3202	15965	28619	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3840	16591		1.76	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-503 ST0197 Homo sapiens cDNA
4373	17111		2.48	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element:
4903	17630		2.36	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2819327 3' similar to contains Alu repetitive element:
5549	18348	31255	1.19	2.0E-08	AA813204.1	EST_HUMAN	ab0h11.s1 Soares testis_NHT Homo sapiens cDNA clone 1377189 3'
5742	18534	31457	0.93	2.0E-08	AW088924.1	EST_HUMAN	xd32c04.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3
7903	20598	33728	0.92	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element:
8009	20704	33832	1.35	2.0E-08	AA490121.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS; PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8983	21673		0.9	2.0E-08	AU139978.1	EST_HUMAN	ab02g06.g1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
10416	23062	36281	0.79	2.0E-08	N78097.1	EST_HUMAN	AU139878 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10416	23062	36282	0.79	2.0E-08	N78097.1	EST_HUMAN	YU7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element:
12184	24856		1.54	2.0E-08	AL183284.2	NT	YU7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element:
1499	15571	26531	1.16	1.0E-08	P31792	SWISSPROT	Homo sapiens chromosome 21 segment HS21C084
1768	14510	27211	1.45	1.0E-08	AF125348.1	NT	POL POLYPROTEIN [CONTAINS; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2044	14777		2.31	1.0E-08	BE141059.1	EST_HUMAN	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5512	18310	31211	4.85	1.0E-08	AJ010770.1	NT	PM2-HT0130-150959-001-f12 HT0130 Homo sapiens cDNA
7668	20332	33443	1.26	1.0E-08	P19474	SWISSPROT	Homo sapiens hyperon gene, exons 1-50
7834	20629	33756	0.52	1.0E-08	AL163302.2	NT	52 KD RO PROTEIN (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8028	20723	33855	0.64	1.0E-08	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C102
8028	20723	33856	0.64	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8445	21137	34275	1.94	1.0E-08	AI015304.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9104	21792		0.45	1.0E-08	P09593	SWISSPROT	alpha35a05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9105	21793	34956	0.78	1.0E-08	BE072572.1	EST_HUMAN	S-ANTIGEN PROTEIN PRECURSOR
							PM2-BT0546-210100-004-d02 BT0546 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9866	22518	35712	1.2	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10453	23089	36330	0.77	1.0E-08	P98063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11285	23946	37241	4.14	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12282	24715		2.82	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
4218	16859	29583	4.65	9.0E-09	AL163278.2	NT	Homo sapiens immunoglobulin constant region complex (germline)
4218	16859	29584	4.65	9.0E-09	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
9962	22810		0.52	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
6390	19159		0.62	8.0E-09	AI270615.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7164	19851	32920	7.68	8.0E-09	AI183500.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7899	20594	33726	2.65	8.0E-09	AW900159.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
8887	21578		2.65	8.0E-09	AA938892.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
3593	16346		1.73	7.0E-09	D66942.1	NT	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7802	20497		0.61	7.0E-09	BF108755.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7946	20841		0.82	7.0E-09	AA256200.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
9159	21829	34983	2.91	7.0E-09	L09709.1	NT	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
10083	22731	35946	1.42	7.0E-09	BE254850.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
10244	22892		0.5	7.0E-09	AA058628.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
10571	23266		1.49	7.0E-09	T97950.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2149	14879		0.98	6.0E-09	AL040439.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
4922	17680	30283	3.12	6.0E-09	BE169421.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
5296	18101	30760	11.59	6.0E-09	AW195784.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
8475	21167	34311	0.93	6.0E-09	BE161653.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
9074	21763	34925	1.96	6.0E-09		NT	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
10176	22824		3.76	6.0E-09	AF200923.2	NT	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
10632	23324	36561	1.44	6.0E-09	BF108755.1	EST_HUMAN	ye58a12.b1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'

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11798	24388	37722	1.37	6.0E-09	C01803.1	EST_HUMAN	HUMG50003762 Human adult (K Okubo) Homo sapiens cDNA
1394	14141	26818	3.27	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-Q14-H10 HT0252 Homo sapiens cDNA
1845	14583	27298	1.06	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6316	19087	32071	1.73	5.0E-09	AA359464.1	EST_HUMAN	EST88746 Fetal lung II Homo sapiens cDNA 5' end
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S913S>
6748	17917	30581	0.76	5.0E-09	U66059.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
8484	21176	34321	0.48	5.0E-09	P37071	SWISSPROT	PM2-JM0053-240300-005-c09 UM0053 Homo sapiens cDNA
9995	22843	35855	2.22	5.0E-09	AW799667.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
508	13292		2.12	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
944	13710		2.5	4.0E-09	AL163285.2	NT	Homo sapiens hypothetical protein (AF038169), mRNA
1453	14200	26884	2.52	4.0E-09	9556718	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2016	14751	27479	2.31	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2016	14751	27480	2.31	4.0E-09	AF175325.1	NT	EST158385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2430	15151	27885	6.07	4.0E-09	AA350878.1	EST_HUMAN	zw04c06.r1 Soares NIH-MP, S1 Homo sapiens cDNA clone IMAGE:768298 5'
7746	20442	33565	0.59	4.0E-09	AA495747.1	EST_HUMAN	Yd11a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:68804 3'
8420	21113	34250	0.62	4.0E-09	T64042.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
10779	23482	36704	2.06	4.0E-09	AL163209.2	NT	hm94f10.x1 NCI_CGAP_Lu2 Homo sapiens cDNA clone IMAGE:2443627 3'
11011	23683	36943	1.47	4.0E-09	AB86401.1	EST_HUMAN	z34a12.r1 Soares NIH-MP, S1 Homo sapiens cDNA clone IMAGE:685278 5' similar to gb-L07807
11061	23731		1.53	4.0E-09	AA195142.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
2351	15073	27810	4.77	3.0E-09	BE222239.1	EST_HUMAN	h009a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2557	15271	28006	1.2	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
2656	15366	28104	1.13	3.0E-09	P23249	SWISSPROT	h009a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3323	16083	28733	1.12	3.0E-09	BE222239.1	EST_HUMAN	PROTEIN MOV-10
3371	16130		1.08	3.0E-09	AA44272.1	EST_HUMAN	h009a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
4076	16820		0.7	3.0E-09	X16674.1	NT	MER18 repetitive element;
4392	17129	29761	3.42	3.0E-09	AF175325.1	NT	z54a04.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4476	17211	29836	1.85	3.0E-09	Q8Y3R5	SWISSPROT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
							Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
							258.1 KDA PROTEIN C21ORF5 (KIAA0933)

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7800	20495	33617	1.19	3.0E-09	BE465780.1	EST_HUMAN	h80a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091 O55091 IMPACT PROTEIN. ;
10147	22795	36009	1.7	3.0E-09	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10945	23624	36873	4.8	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
10945	23624	36874	4.8	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
794	13566		2.43	2.0E-09	X16874.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1235	13984	26653	7.99	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1655	14401		7.46	2.0E-09	AL118573.1	EST_HUMAN	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2326	15051	27787	1.1	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0833)
3916	16666	29306	3.01	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5076	17795	30411	0.85	2.0E-09	M23161.1	NT	Human transposon-like element mRNA
5633	18428	31341	0.55	2.0E-09	A004062.1	EST_HUMAN	alpha7b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6056	18838		0.57	2.0E-09	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6682	19599		0.83	2.0E-09	AA357407.1	EST_HUMAN	EST166142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7351	20032	33110	8.4	2.0E-09	AA461430.1	EST_HUMAN	z63h08.r1 Soares_testis_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element
7423	20700	33188	0.68	2.0E-09	W28834.1	EST_HUMAN	52411 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7717	20361	33494	0.62	2.0E-09	AW862126.1	EST_HUMAN	MR1-GT0352-240200-105-b08 C10352 Homo sapiens cDNA
8612	21304	34447	1.78	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11233	23896	37183	1.62	2.0E-09	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C049
12428	13566		22.07	2.0E-09	X16674.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12495	25403		2.41	2.0E-09	AA228070.1	EST_HUMAN	nc11602.1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
12634	24934		1.75	2.0E-09	U82698.1	NT	Homo sapiens exon gene, alternatively spliced products, complete cds
974	13739		0.72	1.0E-09	W78152.1	EST_HUMAN	z479003.s1 Soares_Tetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to gpl02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1087	13945	26503	2.01	1.0E-09	5031924	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1087	13945	26504	2.01	1.0E-09	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1630	14376		1.17	1.0E-09	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2892	15659	28304	1.59	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2926	15692	28336	3.25	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2926	15692	28337	3.25	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3034	15800	28446	0.7	1.0E-09	BE535440.1	EST_HUMAN	601068602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4744	17476		6.4	1.0E-09	AA719297.1	EST_HUMAN	zh35b03.s1 Soares_pineaal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains
5416	18215	30923	0.66	1.0E-09	AL163283.2	NT	Alu repetitive element; contains element MER22 repetitive element ;
5740	18532	31455	1.89	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS21C083
6053	18833	31795	3.13	1.0E-09	P26694	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
8289	20983	34124	0.85	1.0E-09	A188474.1	EST_HUMAN	GIRGUMSPOROZOITE PROTEIN PRECURSOR (CS)
10212	22860		2.92	1.0E-09	AL163283.2	NT	w039b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
11799	24389		1.68	1.0E-09	AL163283.2	NT	MER25.11 MER25 repetitive element ;
12333	25344	30717	2.25	1.0E-09	11418127	NT	Homo sapiens chromosome 21 segment HS21C083
12503	24857		1.35	1.0E-09	T93176.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1286	14036	28707	3.74	9.0E-10	AW867740.1	EST_HUMAN	ye24e05.r1 Stragelene lung (#637210) Homo sapiens cDNA clone IMAGE:118688 5'
2838	15606	28256	4.41	8.0E-10	A1870071.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
6735	19569	32601	4.76	9.0E-10	A1452982.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
142	12857	25599	13.27	8.0E-10	U63630.2	NT	SW-RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ;
3337	18097	28748	0.88	8.0E-10	BE080748.1	EST_HUMAN	iy48609.x1 Soares_NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
4177	16917	28544	3.17	8.0E-10	AA376832.1	EST_HUMAN	TR-000372 000372 PUTATIVE P150. ;
9865	22515		2.44	8.0E-10	U36308.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
685	13460	26107	9.36	7.0E-10	7706225	NT	QV1-BT0531-150200-071-01 BT0531 Homo sapiens cDNA
685	13460	26108	9.36	7.0E-10	Q13342	SWISSPROT	EST189584 Small Intestine I Homo sapiens cDNA 5' end
1618	14365	27055	2.24	7.0E-10	P08548	SWISSPROT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
2013	14748		3.17	7.0E-10	P08548	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
2664	18278		24.23	7.0E-10	P08547	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
3085	15850	28491	2.19	7.0E-10	X00856.1	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
6092	18870	31836	4.18	7.0E-10	AA345220.1	EST_HUMAN	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
7316	19899	33078	1.08	7.0E-10	BF352883.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7556	20226		1.48	7.0E-10	P35084	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7875	20570	33686	1.6	7.0E-10	AF029701.2	NT	H. sapiens DHFR gene, exon 3
7875	20570	33697	1.6	7.0E-10	AF029701.2	NT	EST161247 Gall blackfly II Homo sapiens cDNA 5' end
10209	22857	36073	1.87	7.0E-10	L08895.1	NT	IL3-HT0819-110700-208-D12 HT0819 Homo sapiens cDNA
							DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
							Homo sapiens presenilin-1 gene, exons 1 and 2
							Homo sapiens presenilin-1 gene, exons 1 and 2
							Homo sapiens MAD5/MEF2-family transcription factor (MEF2C) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
893	13662	26327	3.5	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2684	15393	28132	1.21	6.0E-10	AI424405.1	EST_HUMAN	U022607.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4689	17423		2.7	6.0E-10	AW853719.1	EST_HUMAN	RC3-C10254-031099-012-g12 C10254 Homo sapiens cDNA
8692	21374	34518	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1)
8692	21374	34519	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1)
9634	22187	35373	0.46	6.0E-10	P98073	SWISSPROT	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
11950	24503		2.16	6.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGe resequences, MAGL Homo sapiens cDNA
745	13518		7.27	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N219 5'
3468	16224	29878	2.5	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
4931	17659	30289	1	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7222	19907		1.51	5.0E-10	BF105159.1	EST_HUMAN	60182184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9436	22114	35288	1.89	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9436	22114	35289	1.89	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
109	12930		1.17	4.0E-10	AI221083.1	EST_HUMAN	q09080.x1 Soares_placenta_8to9weeks_2NbhP8to9W Homo sapiens cDNA clone IMAGE:1769049 3' similar to contains LTR8.b2 LTR8 repetitive element :
567	13348	25976	0.74	4.0E-10	AA515260.1	EST_HUMAN	nf4a01.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:924648 3'
1989	14725	27446	1.31	4.0E-10	AW594709.1	EST_HUMAN	hg58g03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
2580	15294	28032	3.73	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7076	19767	32831	25.71	4.0E-10	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10095	22743	35957	0.49	4.0E-10	AW293243.1	EST_HUMAN	UI-H-B12-ah-a-07-Q.U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727081 3'
10343	22990	36208	0.89	4.0E-10	AI287342.1	EST_HUMAN	ec63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
895	13663	26329	3.55	3.0E-10	N36113.1	EST_HUMAN	y32708.s1 Soares_melanocyte_2NbhM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.1 L1 repetitive element;
1329	14078		4.72	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
4498	17234	29864	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4498	17234	29865	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5368	18169	30855	1.24	3.0E-10	N60109.1	EST_HUMAN	yz11g08.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:282782 3'
6110	18987	31856	2.52	3.0E-10	P20350	SWISSPROT	RHOMBOD PROTEIN (VEINLET PROTEIN)
6258	19032	32007	3.43	3.0E-10	BE302970.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7660	20324	33432	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7660	20324	33433	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8629	21321	34463	1.2	3.0E-10	H87208.1	EST_HUMAN	ye74b12.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element;
8647	21638	34784	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA
8647	21638	34785	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA
9240	21919		0.58	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphatase hydrolase (FHIT) gene, exon 5
10359	23006		2.37	3.0E-10	T65891.1	EST_HUMAN	ye11e12.r1 Strategene lung (#037210) Homo sapiens cDNA clone IMAGE:80398 5'
10493	23139		1.34	3.0E-10	AA769294.1	EST_HUMAN	nz36g03.s1 NCI_CGAP_GCBT1 Homo sapiens cDNA clone IMAGE:1289908 3'
12584	24907	31003	2.85	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0818-110500-136-E07 HT0818 Homo sapiens cDNA
34	12862	25479	1.67	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
34	12862	25480	1.67	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1890	14627		1.96	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2985	15751		1.04	2.0E-10	BF675047.1	EST_HUMAN	602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5714	18507		2.54	2.0E-10	Q28640	SWISSPROT	(HPRG)
6156	18933	31900	1.37	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7279	19963	33039	6.47	2.0E-10	BE791082.1	EST_HUMAN	601566208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
7912	20607	33737	0.48	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7912	20607	33738	0.48	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9202	21871		0.99	2.0E-10	BF434566.1	EST_HUMAN	7078408.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
11287	23958		1.37	2.0E-10	A1862153.1	EST_HUMAN	la10f12.x1 Soares fetal Testis NB2H-F8_9w Homo sapiens cDNA clone IMAGE:2043895 3'
1498	14245		1.87	1.0E-10	AW867767.1	EST_HUMAN	MRO-SN0038-280300-001-01 SN0038 Homo sapiens cDNA
1602	14348	27037	3.18	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCA11 3'
2586	15300		3.16	1.0E-10	AW852001.1	EST_HUMAN	QV6-CT0225-191189-058-e08 CT0225 Homo sapiens cDNA
3491	16247	28801	0.89	1.0E-10	AW852812.1	EST_HUMAN	QV2-TT0003-161189-013-g10 TT0003 Homo sapiens cDNA
3528	16284		0.7	1.0E-10	AL041885.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3825	16284		1.03	1.0E-10	AL041885.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3986	16744		6.19	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

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4108	16851	29477	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4108	16851	29478	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4113	16856	29484	1.94	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4149	16891		1.84	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5085	17804		1.51	1.0E-10	A1797745.1	EST_HUMAN	we8204.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347815 3' similar to contains MER31.11 MER31 repetitive element;
6720	19635	32678	0.66	1.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7375	20055		0.85	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7583	20251	33357	0.55	1.0E-10	AU128594.1	EST_HUMAN	AU128594 NT2P22 Homo sapiens cDNA clone NT2P2003761 5'
8138	20832	33966	1.04	1.0E-10	AW408990.1	EST_HUMAN	IB_9A4 Fetal brain library Homo sapiens cDNA
8553	21245		1.07	1.0E-10	A1268340.1	EST_HUMAN	qm04e10.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element;
10102	22750		4.01	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.r1 Stratagene neuroepithelium NT2RAM1 937294 Homo sapiens cDNA clone IMAGE:548314 5'
10831	23513	36764	2.65	1.0E-10	AI038280.1	EST_HUMAN	oy85h03.x1 Soares_fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
11896	17913		1.71	1.0E-10	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, P22, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
255	13063	25702	1.59	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2097	14828	27561	6.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_j1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2097	14828	27562	8.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_j1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28795	2.45	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_j1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28796	2.45	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_j1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
4465	17201	28827	1.03	9.0E-11	AA775985.1	EST_HUMAN	ae78f01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5487	18286		3.83	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10054	22702	35919	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
10054	22702	35920	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
12258	24703	31080	3.9	9.0E-11	C16633.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506B08 5'
3114	15879		8.33	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;

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3945	16695	29334	0.7	8.0E-11	AK78617.1	EST_HUMAN	hm54c08.x1 NCI_CGAP_Ki67 Homo sapiens cDNA clone IMAGE:2161936 3'
4022	16768	29398	4.88	8.0E-11	N23712.1	EST_HUMAN	yw48a08.s1 W ekmam Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
6574	19338		0.65	8.0E-11	AW168158.1	EST_HUMAN	xf45h11.x1 NCI_CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11
1430	14177	26862	1.75	7.0E-11	AA330642.1	EST_HUMAN	MER10 repetitive element ; EST34392 Embryo, 6 week 1 Homo sapiens cDNA 5' end
3852	16602	29240	1.03	7.0E-11	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8996	21089	34224	2.05	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10129	22777		1.17	7.0E-11	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
403	13188	25837	7.01	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
403	13188	25838	7.01	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6622	19384	32398	0.67	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filarin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds a
7593	20261	33369	3.65	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8262	20956	34095	7.81	6.0E-11	AV727898.1	EST_HUMAN	AV727898 HTC Homo sapiens cDNA clone HTCCASC06 5'
9213	21892	35059	0.62	6.0E-11	BE063508.1	EST_HUMAN	GM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11	12838	25451	1.49	6.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3359	12838	25451	1.9	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4203	16944	29571	1.36	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6423	19191	32187	1.63	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7430	20107	33194	14.05	5.0E-11	11416799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1380	14127		1.94	4.0E-11	AA436042.1	EST_HUMAN	zu01512.f1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:730559 5'
2793	15498	28238	7.14	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909285 5'
2969	15735	28385	1.16	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4576	17311	29939	0.85	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6384	19153	32153	3.2	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
6903	19641	32686	0.82	4.0E-11	AA42660.1	EST_HUMAN	zv58f10.f1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:757983 5' similar to TR:G1055250
7274	19958		4.5	4.0E-11	AF224689.1	NT	G1055250 PHEROMONE RECEPTOR VN4 ;
9295	21982		1.79	4.0E-11	BE149425.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9562	22215	35402	0.9	4.0E-11	AI609753.1	EST_HUMAN	RC1-HT0256-210100-013-408 HT0256 Homo sapiens cDNA f82912.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2106830 3' similar to WP-ZK353.1 CE00385 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12462	24830	31029	1.47	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1475	14222	26908	2.8	3.0E-11	6079077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4243	16984		1.04	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
940	13707	26372	1.97	2.0E-11	AI150502.1	EST_HUMAN	q38c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13 MER10 repetitive element;
1162	13916	26580	3.99	2.0E-11	R24807.1	EST_HUMAN	y949e12.f1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1162	13916	26581	3.99	2.0E-11	R24807.1	EST_HUMAN	y949e12.f1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1808	14354	27042	4.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3'beta) genes, complete cds
1808	14354	27043	4.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3'beta) genes, complete cds
1812	14359	27048	1.21	2.0E-11	AI126371.1	EST_HUMAN	q51c10.x1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:U02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);contains L1.11 L1' repetitive element;
3191	15954	28607	7.58	2.0E-11	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3320	16080	28730	1.11	2.0E-11	AI478617.1	EST_HUMAN	hm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
3356	18116	28771	0.93	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGLACTOSAMINYLTRANSFERASE) (GALNAC-T1)
3488	16244		1.01	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4408	17146		0.68	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
4567	17302		0.72	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4882	17609		1.77	2.0E-11	BE062568.1	EST_HUMAN	QV2-BT0258-261099-014-e01 BT0258 Homo sapiens cDNA
6044	18824	31785	1.02	2.0E-11	AW877808.1	EST_HUMAN	QV2-PT0073-280300-109-h08 PT0073 Homo sapiens cDNA
6218	18992	31988	1.87	2.0E-11	AA581028.1	EST_HUMAN	nc88h05.f1 NCI_CGAP_G01 Homo sapiens cDNA clone IMAGE:787493 5' similar to SW:PR16_YEAST
7095	19784	32850	0.59	2.0E-11	BF592845.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP18.
7782	20477		0.56	2.0E-11	P37072	SWISSPROT	7797c03.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3442865 3'
8123	21811		1.14	2.0E-11	AF029308.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN COR6
10184	22832	36046	5.44	2.0E-11	Q13606	SWISSPROT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10413	23059	36277	1.12	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10413	23059	36278	1.12	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11056	23726	36997	1.48	2.0E-11	AA035369.1	EST_HUMAN	zkt27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11056	23726	36998	1.48	2.0E-11	AA035369.1	EST_HUMAN	zkt27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11080	23760	37035	1.57	2.0E-11	AA261958.1	EST_HUMAN	zs18b04.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685519 5'
12017	25332		1.54	2.0E-11	AA704195.1	EST_HUMAN	zj77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460824 3'
12048	24567		3.54	2.0E-11	AW842143.1	EST_HUMAN	RQO-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12073	24586	31123	1.87	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12332	24748		2.67	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12479	24840		3.14	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12781	25035		3.37	2.0E-11	11417986	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
661	13437	26078	1.34	1.0E-11	AJ131016.1	NT	Homo sapiens SOL gene locus
1195	13947	26811	3.35	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1485	14732		2.36	1.0E-11	AF115914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2030	14785	27494	1.13	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2122	14853	27582	2.91	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3490	16246	28900	1.2	1.0E-11	BE004315.1	EST_HUMAN	CMO-SN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5249	18055	30883	16.93	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5741	18533	31456	0.63	1.0E-11	BF222646.1	EST_HUMAN	7p57d01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8101	20785	33926	3.15	1.0E-11	4885548	NT	MER10 repetitive element
8480	21172	34317	5.44	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8946	21637	34782	1.89	1.0E-11	BF365119.1	EST_HUMAN	y73d08.r1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:28166 5'
8946	21637	34783	1.89	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NNT149 Homo sapiens cDNA
11257	23919	37212	1.82	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NNT149 Homo sapiens cDNA
9697	22348	35542	1.07	9.0E-12	AL163300.2	NT	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:428597 5'
9697	22348	35543	1.07	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9237	21916		0.63	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
12125	24817		3.91	8.0E-12	AJ271736.1	NT	IL5-B10578-130300-036-G12 B10578 Homo sapiens cDNA
4613	17348	26982	1.16	7.0E-12	Q05904	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2
11322	24013	37316	9.59	7.0E-12	AA704735.1	EST_HUMAN	34 KD SPIGULE MATRIX PROTEIN PRECURSOR (LSM34)
3535	16291		0.71	6.0E-12	AV730554.1	EST_HUMAN	z23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
4314	17053	26878	8.52	6.0E-12	AA732516.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF08 5'
6295	19068	32051	0.77	6.0E-12	AF020503.1	NT	m288f11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8894	21585	34723	1.04	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9374	21949		1.67	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12
1020	13780	26442	3.52	5.0E-12	T06573.1	EST_HUMAN	MER28 repetitive element;
3385	16144	28801	1.61	5.0E-12	BE047778.1	EST_HUMAN	EST04462 Fetal brain, Strategene (cat#636206) Homo sapiens cDNA clone HFB0V33
3713	16466	29104	5.03	5.0E-12	AJ271736.1	NT	z42605.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2281217 5'
5931	18715	31671	6.41	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5931	18715	31672	6.41	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6399	18168	32167	11.33	5.0E-12	AW974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6393	19424	32439	0.94	5.0E-12	AL040739.1	EST_HUMAN	EST386850 IMAGE resequences, MAGN Homo sapiens cDNA
6942	19424	32439	1.16	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1815.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1815 3'
8128	20822	33959	1.33	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1815.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1815 3'
8566	21258		0.55	5.0E-12	AW887037.1	EST_HUMAN	z01g12.s1 Scores_fetal_Nb-H110W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.83 L1 repetitive element;
8893	21584		0.54	5.0E-12	AL079681.1	EST_HUMAN	RC1-OT0088-220300-011-407 OT0088 Homo sapiens cDNA
9006	21686	34847	2.93	5.0E-12	AJ271735.1	NT	DKFZp434J0428.L1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0428 5'
9323	21990	35161	0.96	5.0E-12	P34982	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 1/2
10175	22823		4.45	5.0E-12	AL163303.2	NT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10282	22910	36120	0.76	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C103
10468	23114	36344	0.44	5.0E-12		6978764	Homo sapiens chromosome 21 segment HS21C102
237	13047	25686	4.2	4.0E-12	AA700326.1	EST_HUMAN	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
238	13047	25686	4.03	4.0E-12	AA700328.1	EST_HUMAN	z74g11.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460678 3'
4577	17312	29940	0.8	4.0E-12	AI689984.1	EST_HUMAN	z74g11.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460678 3'
7519	20190		0.72	4.0E-12	BF445140.1	EST_HUMAN	z26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
8141	20835		3.2	4.0E-12	AF109907.1	NT	nad21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3386077 3' similar to contains MER7.b2
8587	12179	34418	0.87	4.0E-12	AB042815.1	NT	MER7 repetitive element;
11019	23691	36954	4.2	4.0E-12	AJ228043.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
12375	24774		2.76	4.0E-12	U78027.1	NT	Bos taurus Mth2 mRNA for mitochondrial carrier homolog 2, complete cds
							Homo sapiens 859 kb contig between AML1 and GBR1 on chromosome 21q22, segment 3/3
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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602	13380	26011	4.27	3.0E-12	AW341683.1	EST_HUMAN	hdf13d01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2908377 3' similar to TR:O14517
602	13380	26012	4.27	3.0E-12	AW341683.1	EST_HUMAN	O14517 SMRP. ;
5084	17803	30421	0.81	3.0E-12	AL163268.2	NT	hdf13d01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2908377 3' similar to TR:O14517
5365	18167	30853	1.52	3.0E-12	AF111168.2	NT	O14517 SMRP. ;
7854	20318	34109	0.63	3.0E-12	AW854328.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C068
8273	20967	34109	0.51	3.0E-12	O35453	SWISSPROT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9004	21694	34844	0.52	3.0E-12	O35453	SWISSPROT	RC3-C70255-031098-011-h02 C70255 Homo sapiens cDNA
10551	23247	36483	3.03	3.0E-12	U37672.1	NT	SERINE PROTEASE HEPSIN
10551	23247	36484	3.03	3.0E-12	U37672.1	NT	SERINE PROTEASE HEPSIN
1549	14395	27084	1.39	2.0E-12	AW802131.1	EST_HUMAN	Human prostate specific antigen gene, 5' flanking region
4094	16836	29462	0.91	2.0E-12	J01884.1	NT	Human prostate specific antigen gene, 5' flanking region
4094	16836	29463	0.91	2.0E-12	J01884.1	NT	Human prostate specific antigen gene, 5' flanking region
4987	17124	30192	2.03	2.0E-12	BE063509.1	EST_HUMAN	IL5-UM0071-120400-065-a05 UM0071 Homo sapiens cDNA
4840	17570	30192	1.18	2.0E-12	O70308	SWISSPROT	Rat U3A small nuclear RNA
4840	17570	30193	1.18	2.0E-12	O70308	SWISSPROT	Rat U3A small nuclear RNA
5169	17978	30491	0.77	2.0E-12	P11369	SWISSPROT	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
6385	19154	32830	2.8	2.0E-12	AW971857.1	EST_HUMAN	TBX15 PROTEIN (T-BOX PROTEIN 15)
7075	19766	32830	3.74	2.0E-12	T08169.1	EST_HUMAN	TBX15 PROTEIN (T-BOX PROTEIN 15)
7244	18928	33005	1.02	2.0E-12	BE173035.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
7558	20228	33331	2.2	2.0E-12	11422228	NT	ENDONUCLEASE
8208	22087		1.84	2.0E-12	AF198864.1	NT	EST383946 IMAGE resequences, MAGL Homo sapiens cDNA
9885	22535		11.12	2.0E-12	BE165980.1	EST_HUMAN	EST06060 Infant Brain, Bemb Soares Homo sapiens cDNA clone HIBBA13 5' end
10412	23058	36276	0.87	2.0E-12	AL334130.1	EST_HUMAN	MRO-HT0559-200400-015-a08 HT0559 Homo sapiens cDNA
12032	24557		2.81	2.0E-12	AL163263.2	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
12223	24680		2.5	2.0E-12	11418248	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
119	12938	25579	2.21	1.0E-12	AW627674.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
1980	14716		1.39	1.0E-12	A1871726.1	EST_HUMAN	qq07f02.x1 Soares_NHMPUL_S1 Homo sapiens cDNA clone IMAGE:1031835 3' similar to TR:Q13538
3067	15833	28476	1.29	1.0E-12	AF000991.1	NT	Q13538 ORF2: FUNCTION UNKNOWN. ;
							Homo sapiens chromosome 21 segment HS21C083
							Homo sapiens auctotransferase-related protein (SULTX3), mRNA
							h90a09.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.t1
							MER18 repetitive element ;
							wm51107.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1
							repetitive element ;
							Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3067	15833	28477	1.29	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y.2 (TTY2) mRNA, partial cds
3855	16805	29242	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3855	16805	29243	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
5877	18663		2.25	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
5850	18732		1.93	1.0E-12	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6438	19206	32202	0.62	1.0E-12	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7016	19708	32764	2.07	1.0E-12	AF198864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7050	19741	32802	11.32	1.0E-12	A1248533.1	EST_HUMAN	qf68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
7050	19741	32803	11.32	1.0E-12	A1248533.1	EST_HUMAN	qf68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
8005	21298	34442	1.16	1.0E-12	AA782323.1	EST_HUMAN	acc26d05.s1 Stratagene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
11273	23834		1.72	1.0E-12	AW468478.1	EST_HUMAN	h38107.x1 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2821317 3' similar to contains element LTR3 repetitive element;
11942	24487	37809	4.54	1.0E-12	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
12150	24637		1.52	1.0E-12	A1738592.1	EST_HUMAN	w331h08.x1 NCI CGAP_Cor16 Homo sapiens cDNA clone IMAGE:2392085 3'
12294	25308		2.92	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
3618	16371		1	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3927	16677	28320	0.96	9.0E-13	AB029600.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9501	22154		2.67	9.0E-13	N69853.1	EST_HUMAN	zaz26b06.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:293651 3'
700	13475	26123	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
700	13475	26124	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1830	14569	27281	2.94	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nabp) and survival motor neuron protein (smn) genes, complete cds
8011	20706	33834	0.76	8.0E-13	A1894388.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8011	20706	33835	0.76	8.0E-13	A1894388.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10046	22694		3.08	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11779	24370	37701	1.87	8.0E-13	U66060.1	NT	Human germ-line T-cell receptor beta chain TCRBV13S1, TCRBV6S9A2T, TCRBV6S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV6S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
7718	20382	33495	0.71	7.0E-13	AI884398.1	EST_HUMAN	wm31h08.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
7718	20382	33496	0.71	7.0E-13	AI884398.1	EST_HUMAN	wm31h08.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
8133	20827		0.58	7.0E-13	Q85155	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN OLF2
12404	24788		3.05	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866613 5'
12617	24923		1.37	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE)(UDP-GALNAC:POLYPEPTIDE, N- ACETYLGLACTOSAMINYLTRANSFERASE)(GALNAC-T1)
2094	14825	27558	6.75	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3316	16076		0.74	5.0E-13	R78338.1	EST_HUMAN	y82704.1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:145758 5'
3392	10151		1.54	5.0E-13	AA435773.1	EST_HUMAN	z77a12.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
6777	19521	32548	0.84	5.0E-13	P08083	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
10767	23451	36693	2.72	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1860	14598		2.23	4.0E-13	AW378814.1	EST_HUMAN	PM2-HT0224-221089-001-e11 HT0224 Homo sapiens cDNA
2402	15180		1.67	4.0E-13	AF003528.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
5499	18297	31105	5.51	4.0E-13	BE189131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7105	19783	32858	1.05	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7512	20183	33277	0.94	4.0E-13	AA431528.1	EST_HUMAN	z776g12.r1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA.;
7620	20286		1.07	4.0E-13	N44281.1	EST_HUMAN	Y33g05.r1 Scores melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32985 A32985 t complex sterility protein - mouse;
8740	21432	34577	1.07	4.0E-13	AL043810.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434A0128 5'
9402	22064	35235	0.45	4.0E-13	AA076907.1	EST_HUMAN	7804H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7804H11
9819	22568	35764	4.94	4.0E-13	AI289831.1	EST_HUMAN	q32a05.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1898845 3' similar to contains Alu repetitive element;
11120	23789	37068	2.09	4.0E-13	AA435818.1	EST_HUMAN	z778g10.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11120	23789	37067	2.09	4.0E-13	AA435818.1	EST_HUMAN	z778g10.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
175	12887		4.94	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
845	13615		1.82	3.0E-13	AA430310.1	EST_HUMAN	z768g08.r1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2370	15092	27831	1.28	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2483	15201		2.47	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2869	15379	28117	2.91	3.0E-13	BF372962.1	EST_HUMAN	CM3-F10100-140700-242-h08 F10100 Homo sapiens cDNA
3182	15945		2.97	3.0E-13	AA745844.1	EST_HUMAN	cd18402.31 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
5452	18251	31140	0.59	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stragene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element;
5452	18251	31141	0.59	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stragene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element;
5902	18687	31635	0.82	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCI_CGAP_Bm28 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139
7783	20478	33603	7.87	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7975	20670	33792	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re- reactive factor
7975	20670	33793	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re- reactive factor
10098	22746	35961	0.72	3.0E-13	AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10575	23270		3.61	3.0E-13	AJ084788.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
10975	23651	36904	3.96	3.0E-13	BE003509.1	EST_HUMAN	CM0-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
11598	24197	37517	2.29	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
145	12960	26602	3.42	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
232	13043	25683	2.06	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1247	13996	26663	7.99	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3005	15771	28419	0.9	2.0E-13	8824119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3005	15771	28420	0.9	2.0E-13	8824119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3275	16036	28688	1.13	2.0E-13	BF431899.1	EST_HUMAN	ncb7805.x1 Sceres_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3498	16254	28908	1.11	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4088	16831		1.34	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6032	18812	31772	4.7	2.0E-13	Q06852	SWISSPROT	
6113	18890		0.98	2.0E-13	X76417.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6717	19632	32675	7.15	2.0E-13	X18912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
6954	19436	32451	0.65	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
6954	19436	32452	0.65	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10355	23002	36219	3.87	2.0E-13	9031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12105	24802		3.48	2.0E-13	AW882155.1	EST_HUMAN	GMO-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
285	13091	25732	1.52	1.0E-13	S74129.1	NT	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
868	13637	26307	5.64	1.0E-13	AJ007973.1	NT	Homo sapiens LGMID2B gene
							H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP2, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1313	14061	26736	1.08	1.0E-13	X87344.1	NT	
2015	14750	27478	2.13	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
4553	17288	29817	1.64	1.0E-13	BF340987.1	EST_HUMAN	THR repetitive element ;
							602038009F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185866 5'
7810	20505	33626	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element contains element MER24 repetitive element ;
7810	20505	33627	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element contains element MER24 repetitive element ;
9990	22636		0.79	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10189	22847	36063	0.53	1.0E-13	AF300701.1	NT	Mus musculus osteosarcoma protein tyrosine phosphatase mRNA, complete cds
11352	24042	37345	11.1	1.0E-13	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
11934	24492		2.26	1.0E-13	AV716377.1	EST_HUMAN	AV716377 DCB Homo sapiens cDNA clone DDBAIE03 5'
12563	24893		2.12	1.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudocentromeric region; segment 1/2
							aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
324	13125	25761	1.81	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
325	13126	25762	3.05	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
2504	15221		3.66	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-409 CT0322 Homo sapiens cDNA
2599	15313	28050	1.18	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2599	15313	28051	1.18	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2758	15463	28206	2.6	9.0E-14	AB038162.1	EST_HUMAN	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3105	15974	28513	3.06	9.0E-14	AW513298.1	EST_HUMAN	x554h05.x1 NCI_CGAP_LH1 Homo sapiens cDNA clone IMAGE:2707833 3'

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3232	13125	25761	0.84	9.0E-14	AA781159.1	EST_HUMAN	g24cd01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19
3776	16530	29169	6.85	9.0E-14	D14547.1	NT	repetitive element;
4707	17439	30071	1.66	9.0E-14	AJ002153.1	NT	Human DNA, SINE repetitive element
3489	16245		1.27	8.0E-14	BE468263.1	EST_HUMAN	Saguius oedipus gene for seminal vesicle secreted protein semenogelin I
3937	16687		2.67	8.0E-14	R76269.1	EST_HUMAN	hz71c09.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
9348	20419	33539	15.04	8.0E-14	X88211.1	NT	y72a03.11 Soares placenta N02HP Homo sapiens cDNA clone IMAGE:144786 3'
9490	22010	35180	3.69	8.0E-14	AA219318.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
11410	24059		1.72	8.0E-14	BE062558.1	EST_HUMAN	z171c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
12302	24727	31056	2.48	8.0E-14	AI688118.1	EST_HUMAN	QV2-BT0258-261093-014-a01 BT0258 Homo sapiens cDNA
1625	15574		4.77	7.0E-14	AW151873.1	EST_HUMAN	xc92a08.x1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:2328143 3'
8818	21510		10.57	7.0E-14	AL163285.2	NT	x167e10.x1 NCI CGAP_G04 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
358	13156	25767	14.14	6.0E-14	AF020503.1	NT	repetitive element;
9722	22373	35572	2.6	6.0E-14	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C085
9722	22373	35573	2.6	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
604	13382	26014	5.46	5.0E-14	Q63120	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4993	17716	30322	1.41	5.0E-14	AW073781.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
5446	18245	31133	5.77	5.0E-14	P08547	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
1101	15560		2.18	4.0E-14	P04928	SWISSPROT	x603605.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
1870	14608	27319	5.9	4.0E-14	AJ007073.1	NT	repetitive element;
3735	16488		0.87	4.0E-14	AA046502.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4259	17000	29630	1.05	4.0E-14	N46328.1	EST_HUMAN	S-ANTIGEN PROTEIN PRECURSOR
7858	20553		0.59	4.0E-14	X87344.1	NT	Homo sapiens LGMD2B gene
12928	25414		7.02	4.0E-14	AI886224.1	EST_HUMAN	z167a03.11 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:487858 5'
930	13697	26361	1.88	3.0E-14	X05468.1	NT	y73c12.s1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:278180 3' similar to contains L1.13 L1 repetitive element;
							H. sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP2, LMP7, TAP7, DOB, DQB2 and RING8, 9, 13 and 14 genes
							wm08cd03.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element
							R.norvegicus mRNA for CP-G2 protein

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4870	17597	30220	0.92	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element.
4873	17600	30222	0.97	3.0E-14	7659864	NT	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA
6635	19397	32411	1.49	3.0E-14	AI420786.1	EST_HUMAN	fa91c12.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR-000519 000519 FATTY ACID AMIDE HYDROLASE.
6635	19397	32412	1.49	3.0E-14	AI420786.1	EST_HUMAN	fa91c12.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR-000519 000519 FATTY ACID AMIDE HYDROLASE.
6744	25099		0.82	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C043
8686	21378	34522	0.87	3.0E-14	N42165.1	EST_HUMAN	Y007b10.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:270523 5'
10914	23584	36840	1.26	3.0E-14	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11201	17597	30220	7.19	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element.
12539	25282		1.08	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
381	13188	25811	3.71	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
381	13188	25812	3.71	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
674	15548	28091	9.05	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2387	15108		1.49	2.0E-14	AW372898.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2467	15185		2.15	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2529	15245	27983	1.19	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2542	15256		1.14	2.0E-14	BE222432.1	EST_HUMAN	h90g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.t1 OFR repetitive element.
2681	15390		0.95	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5437	18236	30950	0.8	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240900-142-D07 UT0072 Homo sapiens cDNA
5533	18331	31236	0.92	2.0E-14	AJ312351.1	EST_HUMAN	la78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.L3 L1 repetitive element.
6634	18429	31342	3.42	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6784	19528		0.81	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-e06 BN0072 Homo sapiens cDNA
6984	19677	32724	0.62	2.0E-14	4585708	EST	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11) mRNA
7185	19871	32845	1.25	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7407	20084	33167	22.12	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7407	20084	33168	22.12	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
9817	22498	35671	0.57	2.0E-14	AJ978795.1	EST_HUMAN	wr59g10.x1 NCI_CGAP_UT1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element.
10317	22694	36181	0.53	2.0E-14	AV741948.1	EST_HUMAN	AV741848 CB Homo sapiens cDNA clone CBFBFBF04 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10679	23370	36812	4.88	2.0E-14	AW139800.1	EST_HUMAN	U1H-B11-adv-a-10-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
11591	24190	37507	1.29	2.0E-14	AW083989.1	EST_HUMAN	xc36102.x1 NCL_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2583363 3' similar to contains MER1.13
12536	25284		2.28	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
1045	13804	26463	1.88	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1385	14132	26805	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1385	14132	26806	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1994	14730	27452	12.44	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2182	14911	27643	4.55	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2409	15130	27866	3.56	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2945	15711	28363	1.79	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3165	15928	28577	5.42	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3165	15928	28577	5.42	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3866	16616	28255	1.67	1.0E-14	AA682994.1	EST_HUMAN	ae89c12.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:871350 3'
4440	17176	29802	1.91	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5719	18511	31432	2.42	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6576	25095	32351	11.5	1.0E-14	11437150	NT	Homo sapiens promilin (mouse)-like 1 (PROML1), mRNA
6576	25095	32352	11.5	1.0E-14	11437150	NT	Homo sapiens promilin (mouse)-like 1 (PROML1), mRNA
11818	15928	28576	3.05	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
11818	15928	28577	3.05	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
1570	14317	27002	2.06	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2170	14899		1.43	9.0E-15	AF198779.1	NT	Homo sapiens transcription factor GCM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
7395	20074	33152	4.51	9.0E-15	P21416	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7915	20610	33740	1.08	9.0E-15	BE003559.1	EST_HUMAN	60167750F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
12718	24991		2.36	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2814	13253		0.91	8.0E-15	BE281482.1	EST_HUMAN	601148632F1 NIH MGC_19 Homo sapiens cDNA clone IMAGE:3184023 5'
7081	19771	32836	1.14	7.0E-15	BF035327.1	EST_HUMAN	60145831F1 NIH MGC_68 Homo sapiens cDNA clone IMAGE:3862096 5'
10334	22981		3.07	7.0E-15	AW241958.1	EST_HUMAN	xn7402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element;
973	13738	26403	8.64	8.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5829	18618	31549	1.02	6.0E-15	X73482.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
5829	18618	31550	1.02	6.0E-15	X73482.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
401	13186	25834	6.63	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2764	15489	28212	1.38	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3461	16217		1.03	5.0E-15	AW296817.1	EST_HUMAN	U1-H-BW0-ajb-g-10-0-U1.s1 NQ_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3'
10574	23269		2.4	5.0E-15	AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE06 5'
418	12829	25442	2.85	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
6567	19332	32339	0.76	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
10994	20392	33505	3.08	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10994	20392	33506	3.08	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4192	16933		7.06	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANFCARDIODILATIN
4872	17599		0.79	3.0E-15	P92485	SWISSPROT	NADH-JBIQUINONE OXIDOREDUCTASE CHAIN 5
6716	19631		1.33	3.0E-15	Q84625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7179	19865	32937	2.9	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7179	19865	32938	2.9	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9825	22476		2.51	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NQ_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1351784 3' similar to contains MER19.H MER19 repetitive element
10694	23395	36625	2.47	3.0E-15	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12310	25315		1.81	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12814	25058		1.35	3.0E-15	AW877214.1	EST_HUMAN	OM4-PT0034-180200-508-a07 PT0034 Homo sapiens cDNA
243	13052	25692	3.6	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25798	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25799	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16256	28910	0.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16256	28911	0.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4049	16784	28423	1.08	2.0E-15	AW238499.1	EST_HUMAN	xp26h01.x1 NCL CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1.13 L1 repetitive element;
4580	17315		2.46	2.0E-15	AI806335.1	EST_HUMAN	wf07f08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q01043 NINEIN.;
6039	18867	31833	0.88	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6089	18887	31834	0.88	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7014	19706		1.5	2.0E-15	AJ400877.1	NT	Homo sapiens ASOL3 gene, OEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7171	19857	32929	2.82	2.0E-15	AA704195.1	EST_HUMAN	z177e03.s1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7294	19977	33054	5.18	2.0E-15	W05064.1	EST_HUMAN	WP.F44F4.8 CE02227 TRANSPOSASE;
8804	21496	34642	2.86	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
8971	21661	34812	1	2.0E-15	AA397758.1	EST_HUMAN	z177g08.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9304	21971	35145	1.23	2.0E-15	AA397758.1	EST_HUMAN	z177g08.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9304	21971	35146	1.23	2.0E-15	AW379465.1	EST_HUMAN	CNM0-HT0244-201099-078-e12 HT0244 Homo sapiens cDNA
10742	23429		5.56	2.0E-15	AJ271735.1	NT	CNM0-HT0244-201099-078-e12 HT0244 Homo sapiens cDNA
12451	25338		2.04	2.0E-15	U82828.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12653	16256	28910	3.34	2.0E-15	AF223391.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12653	16256	28911	3.34	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2777	15482		2.39	1.0E-15	AI689984.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3011	15777	28427	1.35	1.0E-15	BE043584.1	EST_HUMAN	h28h05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
3139	15903	28548	1.29	1.0E-15	P08547	SWISSPROT	h44e02.y1 NCL CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
5138	17866		0.97	1.0E-15	AW021431.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6279	19052	32030	1.74	1.0E-15	T05763.1	EST_HUMAN	d123c08.y1 Morten Fetal Cochlea Homo sapiens cDNA clone IMAGE:2484202 5'
6809	19647		2.12	1.0E-15	BE074217.1	EST_HUMAN	ye40a10.s1 Scores_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MIER6 repetitive element;
8131	20825	33961	0.86	1.0E-15	AL163280.2	NT	QV3-BT0569-270100-074-q05 BT0569 Homo sapiens cDNA
8319	21012	34149	4.56	1.0E-15	AI200976.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8319	21012	34150	4.56	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8937	21628	34770	0.87	1.0E-15	AL163207.2	NT	qf68h06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'

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8940	21631	34774	1.76	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9146	21877	35042	0.87	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9532	22165	35370	0.94	1.0E-15	AA684653.1	EST_HUMAN	oh37cd3.s1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1
10720	23409	36651	3.6	1.0E-15	AF044083.1	NT	repetitive element;
12722	25148	30896	4.72	1.0E-15	A1783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4489	17204	29830	0.98	9.0E-16	4503188	NT	ts31c05.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element;
10815	23595	36841	2.04	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CCAT displacement protein) (CUTL1) mRNA
11696	24291	37815	1.46	9.0E-16	A1244341.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
11696	24291	37815	1.46	9.0E-16	A1244341.1	EST_HUMAN	q178a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
11696	24291	37815	1.46	9.0E-16	A1244341.1	EST_HUMAN	q178a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
5615	18411	31324	0.71	7.0E-16	4885120	NT	q178a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
7241	19928	33001	1.49	7.0E-16	O88807	SWISSPROT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7241	19928	33001	1.49	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
12675	25237		1.98	7.0E-16	T94149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2137	14857		8.38	6.0E-16	AW972811.1	EST_HUMAN	ye2bc12.r1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:119062 5'
1476	14223	26909	1.08	5.0E-16	AJ251154.1	NT	EST384702 MAGE resequences, MAGL Homo sapiens cDNA
2687	15396	28134	2.17	5.0E-16	AA992176.1	EST_HUMAN	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
9854	22602	35806	0.54	5.0E-16	AL163246.2	NT	cd60cd4.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element;
11504	24105	37418	3.6	5.0E-16	BF21768.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
12757	25018		14.19	5.0E-16	11418127	NT	601885734FT NIH MGC_57 Homo sapiens cDNA clone IMAGE:4104128 5'
2233	14961		1.81	4.0E-16	AB001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2378	15100	27839	1.77	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
2378	15100	27840	1.77	4.0E-16	AW797168.1	EST_HUMAN	QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3450	16206	28856	3.58	4.0E-16	Q19653	SWISSPROT	QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
4121	16863	29489	5.02	4.0E-16	BE083875.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GYCOPROTEIN PRECURSOR
4121	16863	29489	5.02	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
7612	20278	33386	46.62	4.0E-16	AL163284.2	NT	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA

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9195	21865	35029	1.04	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
11182	23847	37133	1.51	4.0E-16	AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
11851	24435	37778	1.44	4.0E-16	Q62632	SWISSPROT	FOLLISTATIN-RELATED PROTEIN PRECURSOR
12014	24547		2.04	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12109	24605	31087	2.31	4.0E-16	6912499	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
130	12945	25589	2.03	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
130	12945	25590	2.03	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
453	13239		1.5	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
463	13248		1.5	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1435	14182	26887	1.38	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2975	15741	28388	3.76	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3913	16663	29304	19.63	3.0E-16	T08169.1	EST_HUMAN	EST060600 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
3939	16689		0.95	3.0E-16	U03887.1	NT	Human BXP20 gene
5196	18004		0.96	3.0E-16	AA07723.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5529	18327	31230	1.79	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8556	21248	34387	4.26	3.0E-16	AD028336.1	EST_HUMAN	am98h05.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains
9790	22441		0.89	3.0E-16	BF680617.1	EST_HUMAN	THR.b2 THR repetitive element ;
10019	22867	35883	5.57	3.0E-16	L78810.1	NT	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
961	13717		1.2	2.0E-16	AL163279.2	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
2385	15106		0.91	2.0E-16	AA821761.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
2694	15403		1.06	2.0E-16	J03061.1	NT	af06d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
4157	16897	29528	1.16	2.0E-16	X88211.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4447	17183	28807	0.96	2.0E-16	AI208793.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
5104	17822	30439	0.76	2.0E-16	BE061178.1	EST_HUMAN	qg56f03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639197 3' similar to contains MER29.13
8842	19404	32419	0.99	2.0E-16	Q31126	SWISSPROT	MER29 repetitive element ;
7615	20281	33389	0.75	2.0E-16	AI470723.1	EST_HUMAN	RC3-BT046-131188-003-H12 BT0046 Homo sapiens cDNA
7887	20562	33889	2.14	2.0E-16	AI732837.1	EST_HUMAN	HISTIDINE-RICH PROTEIN KE4
8058	20762	33883	0.57	2.0E-16	BE859026.1	EST_HUMAN	g16e11.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
							MER33 repetitive element ;
							nz47f08.x5 NCI_CGAP_P112 Homo sapiens cDNA clone IMAGE:1290947 similar to TR-O54849 O54849
							HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 ;contains MER7.11 MER7 repetitive element ;
							7f62f09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8058	20752	33894	0.57	2.0E-16	BE58026.1	EST_HUMAN	718209.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8425	21118	34256	0.81	2.0E-16	AW87721.4.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
8425	21118	34257	0.81	2.0E-16	AW87721.4.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
180	12992	25630	1.84	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
373	13198		29.66	1.0E-16	AA628592.1	EST_HUMAN	af39g11.1 st Soares, fetal_fetus_Nb21-F8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to
1963	14699	27414	2.37	1.0E-16	BF327942.1	EST_HUMAN	contains OFR.12 OFR repetitive element ;
5635	18430	31343	0.75	1.0E-16	AF163864.1	NT	QV0-BND148-070700-293-a10 BN0148 Homo sapiens cDNA
6341	19111		27.85	1.0E-16	U45983.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6479	19246	32246	3.39	1.0E-16	Q02779	SWISSPROT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
7453	19111		7.15	1.0E-16	U45983.1	NT	QV2-PT0012-040400-124-a05 PT0012 Homo sapiens cDNA
9183	21853	35018	1.07	1.0E-16	AW875651.1	EST_HUMAN	CM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA
3722	16475	28112	2.11	9.0E-17	AW900048.1	EST_HUMAN	ig22c11.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12
6624	19386		2.2	9.0E-17	A1392984.1	EST_HUMAN	MER28 repetitive element ;
8007	20702		4.75	9.0E-17	AW160257.1	EST_HUMAN	xp49g12.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR
10124	22772		2.47	9.0E-17	AF200719.1	NT	repetitive element ;
997	13757		1.77	8.0E-17	AW880701.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
3872	16822		0.87	8.0E-17	AL163280.2	NT	QV0-OT0032-080300-155-a01 OT0032 Homo sapiens cDNA
5496	25069	31193	3.7	8.0E-17	BE172081.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
7175	19861		1.94	8.0E-17	AV730759.1	EST_HUMAN	MR0-HT0559-080300-003-a04 HT0559 Homo sapiens cDNA
1441	14188		3.44	7.0E-17	6753097	NT	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
5240	18046		3.3	7.0E-17	AF216850.1	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
						NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6598	16351	32365	8.05	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane
198	13011	25653	8	8.0E-17	AW983880.1	EST_HUMAN	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
6221	18995	31971	1.64	8.0E-17	AW662772.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
10190	22838	36053	0.46	6.0E-17	P20138	SWISSPROT	h81d04.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12
412	12823	25436	2.97	5.0E-17	T64110.1	EST_HUMAN	L1 repetitive element ;
7486	20158	33250	2.09	5.0E-17	T81043.1	EST_HUMAN	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP87)
						EST_HUMAN	yc05h08.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:79639 5'
						EST_HUMAN	yc26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
3628	16379	28020	0.69	4.0E-17	AA643697.1	nt66605.e1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058528 3'
9262	22016	35184	1.07	4.0E-17	AW129165.1	x20604.x1 NCI_CGAP_Ku88 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
11475	24076	37396	2.64	4.0E-17	AL163247.2	Homo sapiens chromosome 21 segment HS21C047
12027	24555		1.75	4.0E-17	A079546.1	Q16530 PMS3 MRNA; contains MER10.12 MER10 repetitive element;
1477	14224		1.14	3.0E-17	D14547.1	Human DNA, SINE repetitive element
2091	14822	27664	1.85	3.0E-17	AW119123.1	cd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3188	15951		1.18	3.0E-17	P35410	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3633	16386	29026	1.34	3.0E-17	BE326822.1	hw05004.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
3633	16386	29027	1.34	3.0E-17	BE326822.1	hw05004.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
4970	17695		1.89	3.0E-17	BF511268.1	UHT-B4-adj-c-06-0-0-01.61 NCI_CGAP_Sub58 Homo sapiens cDNA clone IMAGE:3085043 3'
8166	20860	33992	5.16	3.0E-17	N68451.1	zai14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.15 PTR5 repetitive element;
9601	22264	35439	6.58	3.0E-17	AB026868.1	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10279	22927	36140	0.64	3.0E-17	BF327012.1	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10279	22927	36141	0.64	3.0E-17	BF327012.1	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
11994	24532		3.65	3.0E-17	11417966	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
12764	25023		1.44	3.0E-17	AV720204.1	AV720204 GLC Homo sapiens cDNA clone GLC01F08 5'
343	13144	25782	3	2.0E-17	A1270080.1	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
344	13144	25782	2.17	2.0E-17	A1270080.1	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
967	13733		1.84	2.0E-17	AA722932.1	zq81d04.s1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2448	15167	27904	2.21	2.0E-17	Q28983	ZONADHESIN PRECURSOR
2448	15167	27905	2.21	2.0E-17	Q28983	ZONADHESIN PRECURSOR
2930	15696	28343	6.64	2.0E-17	P12036	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5252	18087	30745	1.88	2.0E-17	M27885.1	Mus musculus ultra high sulfur keratin gene, complete cds
5282	18087	30746	1.88	2.0E-17	M27885.1	Mus musculus ultra high sulfur keratin gene, complete cds
6171	18948		2.04	2.0E-17	AF055006.1	Homo sapiens MHC class 1 region
6398	19167		1.16	2.0E-17	AL134881.1	DKF76782J0610.1 762 (synonym: hma2) Homo sapiens cDNA clone DKF76782J0610 5'
7882	20677	33802	1.12	2.0E-17	Q95158	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3

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8356	21049	34188	1	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin
9769	22420	35628	2.81	2.0E-17	BE299888.1	EST_HUMAN	800944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860615 5'
9804	22455	35637	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9804	22455	35658	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10159	22807	36025	4.82	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10278	22926	36138	0.73	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10278	22926	36139	0.73	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10307	22954	36180	0.49	2.0E-17	A1798902.1	EST_HUMAN	w694b04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10307	22954	36170	0.49	2.0E-17	A1798902.1	EST_HUMAN	w694b04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
733	13507	26164	3.68	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1703	14446		1.26	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
1761	14503	27204	2.73	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2109	14840	27571	2.35	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2335	15059	27795	2.08	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3554	16309		1.3	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4116	16858		7.37	1.0E-17	R09942.1	EST_HUMAN	Y30607.1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:128388 5'
6366	19136		0.69	1.0E-17	AW468488.1	EST_HUMAN	h636e05.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2821312 3' similar to contains Alu repetitive element/contains LTR8.1 LTR8 repetitive element
6555	19320	32327	2.04	1.0E-17	A1185642.1	EST_HUMAN	q665b05.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6555	19320	32328	2.04	1.0E-17	A1185642.1	EST_HUMAN	q665b05.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6989	19682	32730	0.93	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8490	21182	34324	1.33	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101299-072-407 BT0263 Homo sapiens cDNA
9907	22556	35751	0.88	1.0E-17	AW996538.1	EST_HUMAN	QV3-BN0046-220300-129-510 BN0046 Homo sapiens cDNA
11394	24000	37304	2.09	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
11732	24325	37649	2.47	1.0E-17	AA453647.1	EST_HUMAN	z48f05.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:796489 3' similar to TR:G1263081
2474	15192	27932	0.95	9.0E-18	AA174078.1	EST_HUMAN	G1263081 MARINER TRANSPOSASE
6398	22060		3.31	9.0E-18	AL472167.1	EST_HUMAN	z418g12.s1 Stragene fetal retina 837202 Homo sapiens cDNA clone IMAGE:609862 3'
3766	16518	29150	1.52	8.0E-18	4758977	NT	[988403.x1 Scores_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
							Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
							xx10b04.x1 NCL_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
339	13140	25776	16.92	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);

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339	13140	25777	16.92	7.0E-18	AW316976.1	EST_HUMAN	xx10604.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
7343	20024	33100	1.33	7.0E-18	AW887542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0081-170300-011-403 OT0081 Homo sapiens cDNA
12492	13140	25776	3.41	7.0E-18	AW316976.1	EST_HUMAN	xx10604.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
12492	13140	25777	3.41	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xx10604.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3289	16050	28688	1	6.0E-18	X71791.2	NT	RIBOSOMAL PROTEIN L4 (HUMAN); Rattus norvegicus perleil Gdn/Pr-1 gene for glia-derived neslin/protease nexin 1, enhancer region
4698	17432		3.02	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGase C) (TGC)
8148	20842		2.84	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nucleosome chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8246	20940	34077	0.72	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11079	23749	37024	1.61	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11300	23960	37260	1.74	6.0E-18	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12241	24622	31076	3.29	6.0E-18	U87929.1	NT	Human acortitase hydrolase (ACO2) gene, exon 4
1125	13881	28541	21.7	5.0E-18	AI280214.1	EST_HUMAN	qnf5g11.x1 Soares_placenta_8609weeks_2NbtHP8b9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element
5047	17766	30384	0.98	5.0E-18	D61517.1	EST_HUMAN	HUM411F058 Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-411F05
5191	17999	30622	1.2	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
8620	21312	34454	6.25	5.0E-18	BE143312.1	EST_HUMAN	MRO-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
10899	23579	36828	3.47	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
10896	23579	36828	3.47	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12386	24770		3.4	5.0E-18	AW887182.1	EST_HUMAN	MR1-SN0035-000400-001-g11 SN0035 Homo sapiens cDNA
12695	24978		4.16	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
121	12939	25580	1.37	4.0E-18	BED44076.1	EST_HUMAN	h038h04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
121	12938	25581	1.37	4.0E-18	BED44076.1	EST_HUMAN	h038h04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
1711	14454	27163	1.19	4.0E-18	AA821814.1	EST_HUMAN	h024f11.s1 NCI_CGAP_C010 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
1882	14619		1.12	4.0E-18	AI736592.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); w03h08.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:2392065 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2198	14927	27662	1.33	4.0E-18	Q08430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTTRANSFERASE (N- ACETYLGLUCOSAMINYLTTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
2198	14927	27663	1.33	4.0E-18	Q08430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTTRANSFERASE (N- ACETYLGLUCOSAMINYLTTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
3772	18524	29162	0.88	4.0E-18	A1581586.1	EST_HUMAN	ar93b06.x1 Barshead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
5279	18084	30740	2.24	4.0E-18	A1017585.1	EST_HUMAN	cu23e06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5279	18084	30741	2.24	4.0E-18	A1017585.1	EST_HUMAN	cu23e06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
7745	20441		0.63	4.0E-18	AA748811.1	EST_HUMAN	nv64e08.s1 NCL_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:1266938 similar to contains L1 L2 L1 repetitive element;
10927	23607	36858	8.76	4.0E-18	AA371807.1	EST_HUMAN	EST183633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
829	13599	26270	1.68	3.0E-18	AA814196.1	EST_HUMAN	cb23h11.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
908	13676	26340	3.47	3.0E-18	BE089634.1	EST_HUMAN	P-46782 40S RIBOSOMAL PROTEIN S5.;
3931	16681	29322	1.47	3.0E-18	AL163247.2	NT	CMO-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA Homo sapiens chromosome 21 segment HS21C047
6730	19564	32596	5.64	3.0E-18	BE001671.1	EST_HUMAN	PMO-BN0081-100300-001-008 BN0081 Homo sapiens cDNA
10844	23528	36769	1.81	3.0E-18	BF218850.1	EST_HUMAN	601884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
12497	24852		6.14	3.0E-18	AW022015.1	EST_HUMAN	d31h12.y1 Marton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'
244	13053	25693	4.42	2.0E-18	AW836820.1	EST_HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
1130	13888		62.93	2.0E-18	BE256097.1	EST_HUMAN	601114362F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
5328	18129		3.19	2.0E-18	AA868610.1	EST_HUMAN	ak53a07.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577
5419	18218	30927	3.68	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM TQ31, COMPLETE SEQUENCE.;
5419	18218	30928	3.68	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5788	18578		1.68	2.0E-18	BF347226.1	EST_HUMAN	Human DNA, SINE repetitive element
6073	18852	31817	0.77	2.0E-18	X80459.1	NT	602021164F1 NCL_CGAP_Bn067 Homo sapiens cDNA clone IMAGE:4156670 5'
6073	18852	31818	0.77	2.0E-18	X80459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6185	18962	31835	1.04	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6228	19000	31977	5.18	2.0E-18	AW685953.1	EST_HUMAN	IL3-HT0819-220700-222-C12 HT0819 Homo sapiens cDNA
7336	20018	33096	0.81	2.0E-18	AA457619.1	EST_HUMAN	h194g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER19.12 MER19 repetitive element;
8047	20741	33873	0.47	2.0E-18	BE439524.1	EST_HUMAN	aa89d11.11 Striatogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77;
						EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9947	22595	35798	1.88	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12 MER10 repetitive element;
9947	22595	35799	1.88	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12 MER10 repetitive element;
10894	23574	36824	2	2.0E-18	AW470791.1	EST_HUMAN	ha33d06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element;
11736	24328	37653	3.91	2.0E-18	AW151299.1	EST_HUMAN	xg47e09.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element;
12174	13886		1.45	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
4382	17119		1.02	1.0E-18	T95406.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
5271	18077	30707	3.63	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLC/DKE11 3'
5483	18282	31180	2.94	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5483	18282	31181	2.94	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6363	19133	32128	1.53	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8341	21034	34171	1.43	1.0E-18	AI148288.1	EST_HUMAN	oz69d09.x1 Soares, senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1690593 3' similar to contains L1.t1 L1 repetitive element;
9799	22450	35853	4.22	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Ror1 gene, and sodium phosphate transporter (NPT3) gene, complete cds
12130	24621	31092	4.23	1.0E-18	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
532	13316	25952	5.34	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
533	13316	25952	3.24	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
7747	20443		4.47	9.0E-19	F08698.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8588	21280	34419	2.54	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8598	21280	34420	2.54	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11072	23742	37016	4.82	9.0E-19	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11901	13316	25952	1.88	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1026	13766		1.25	8.0E-19	AW974902.1	EST_HUMAN	EST387007 IMAGE resequences, MAGN Homo sapiens cDNA
4372	17110		1.04	8.0E-19	F08648	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8048	20742	33874	0.92	8.0E-19	BE158936.1	EST_HUMAN	MR0-HT0404-210200-001-g06 HT0404 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	14970	27708	1.51	7.0E-19	4758139	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
6384	19134	32128	2.34	7.0E-19	A082090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7199	19885	32959	0.9	7.0E-19	P26444	SWISSPROT	BETA CRYSTALLIN A2
9911	22560	35756	0.51	7.0E-19	A1344951.1	EST_HUMAN	U01c08.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2052302 3'
12036	25397		2.05	7.0E-19	AA705684.1	EST_HUMAN	Z160301.s1 Soares fetal_liver_apleer_TNLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3781	16513		1.34	6.0E-19	AW852930.1	EST_HUMAN	PM0-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4430	17168	29795	1.36	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4430	17168	29796	1.36	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4747	17479		1.3	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4987	17692	30301	1.04	6.0E-19	AL120817.1	EST_HUMAN	DKFZp762F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192 5'
5787	18558	31485	5.36	6.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
10324	22971	36191	1.03	5.0E-19	AJ297698.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11525	24125	37431	7.45	5.0E-19	AW183725.1	EST_HUMAN	X87b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element;
541	13324	25956	1.66	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2689	16398	28136	1.02	4.0E-19	BF687362.1	EST_HUMAN	902130910F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4287874 5'
5311	18115	30773	0.97	4.0E-19	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3833	16584	29219	1.04	3.0E-19	Q28897	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3833	16584	29220	1.04	3.0E-19	Q28897	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4253	16984	29622	0.99	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4253	16984	29623	0.98	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4413	17150	29777	1.12	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5198	18006		0.84	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7283	19966		2.79	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9359	20430	33548	1.15	3.0E-19	X89685.1	NT	M.musculus mRNA for TPO33 protein
12264	24709		23.34	3.0E-19	AF165520.1	NT	Homo sapiens photoboln I protein (PBI) mRNA, complete cds
2565	15279	28017	21.33	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4411	17148		1.03	2.0E-19	A1311783.1	EST_HUMAN	qq01e02.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386
5963	18745	31706	0.67	2.0E-19	AV731382.1	EST_HUMAN	POLENV GENE;
							AV731382 HTF Homo sapiens cDNA clone HTFAZC08 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7238	19923	32968	0.93	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8228	20922	34061	8.08	2.0E-19	AA012854.1	EST_HUMAN	Zs34c08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
9809	22460	35686	0.88	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
11829	24413	37750	1.33	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-04 BT0333 Homo sapiens cDNA
11829	24413	37751	1.33	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-04 BT0333 Homo sapiens cDNA
469	13255		1.87	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2161	14891	27626	1.58	1.0E-19	H30795.1	EST_HUMAN	yo79g07.r1 Soares adult brain N2b4HR55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2723	15430		2.37	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2851	15619		4.95	1.0E-19	4758977	NT	Human gene for Ah-receptor, exon 7-9
3396	16154	28906	1.2	1.0E-19	AA834967.1	EST_HUMAN	aj49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
5983	18784	31728	2.38	1.0E-19	U12186.1	NT	MER37 repetitive element;
6114	25419		0.83	1.0E-19	AA595527.1	EST_HUMAN	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
7528	20199	33293	0.86	1.0E-19	U08813.1	NT	nh22d03.s1 NCJ CGAP_P1 Homo sapiens cDNA clone IMAGE:953093 similar to contains L1.t1 L1 repetitive element;
7528	20199	33294	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
7895	25118		0.83	1.0E-19	AF200719.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
8349	21042	34179	1.75	1.0E-19	M64657.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
8640	21332		2.64	1.0E-19	T99920.1	EST_HUMAN	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
8649	22301		0.46	1.0E-19	U60822.1	NT	ye72b02.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
10087	22735	35950	23.03	1.0E-19	AW812259.1	EST_HUMAN	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10087	22745	35960	1.48	1.0E-19	N44631.1	EST_HUMAN	RCO-ST0174-191069-031-605 ST0174 Homo sapiens cDNA
11760	24351	37693	1.55	1.0E-19	U93163.1	NT	ye31e06.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:272872 5'
6549	19314	32319	2.59	8.0E-20	7657286	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
6549	19314	32320	2.58	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7418	20095	33180	1.34	8.0E-20	A1221371.1	EST_HUMAN	Mus musculus keratin-associated protein 8-1 (Krtap8-1), mRNA
7418	20095	33181	1.34	8.0E-20	A1221371.1	EST_HUMAN	gg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3270	16031	28682	1.41	7.0E-20	BF328455.1	EST_HUMAN	gg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
6898	17972	30529	6.29	7.0E-20	AL138120.1	EST_HUMAN	PM4-AN0088-050900-003-604 AN0088 Homo sapiens cDNA
8394	21087	34222	12.48	7.0E-20	AA557657.1	EST_HUMAN	DKFZp547D092.r1 547 (synonym: hbn1) Homo sapiens cDNA clone DKFZp547D092 5'
							nl46c04.s1 NCI CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28.b2
							MER28 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8394	21087	34223	12.48	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_P74 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
11714	24308		1.95	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3543	16298	28949	3.52	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4239	16980	29605	3.33	6.0E-20	BE622434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4556	17291		1.18	5.0E-20	AV725123.1	EST_HUMAN	AV726123 HTC Homo sapiens cDNA clone HTCBTA01 5'
7015	19707	32763	1.07	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
7846	20541	33668	5.28	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Scores: fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
7846	20541	33669	5.28	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Scores: fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
8002	20697	33825	0.7	5.0E-20	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8734	21426	34572	2.54	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
8734	21426	34573	2.54	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9345	20416		0.94	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
1616	14363	27054	1.34	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5562	18359		0.8	4.0E-20	Q99880	SWISSPROT	HISTONE H2B C (H2B/C)
7826	20521		5.15	4.0E-20	AI874352.1	EST_HUMAN	tz94g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2283396 3'
10396	23042	36259	1.33	4.0E-20	AW937466.1	EST_HUMAN	OV3-DT0043-060200-080-c04 DT0043 Homo sapiens cDNA
2135	14865	27595	1.02	3.0E-20	U03888.1	NT	Human BXP21 gene
4185	16926	29557	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4582	17317	29944	1.05	3.0E-20	AA037616.1	EST_HUMAN	zk36b12.s1 Scores: pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
8833	21525		2.95	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10219	22667	36078	0.63	3.0E-20	BF185264.1	EST_HUMAN	601843661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5'
10561	23257		1.87	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
11496	24097	37408	1.5	3.0E-20	AI284244.1	EST_HUMAN	q70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1884803 3' similar to contains Alu repetitive element;
11496	24097	37409	1.5	3.0E-20	AI284244.1	EST_HUMAN	q70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1884803 3' similar to contains Alu repetitive element;
12051	24569	31118	2.65	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
811	13582		3.12	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.;

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1089	13847	26505	3.37	2.0E-20	AA516335.1	EST_HUMAN	ng99h08.s1 NC1_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
1089	13847	26506	3.37	2.0E-20	AA516335.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN. ; ng99h08.s1 NC1_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
2820	13582		2.38	2.0E-20	AW303868.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN. ; xr24e10.x1 NC1_CGAP_Lip4 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RS5_MOUSE
4893	17620	30238	4.97	2.0E-20	Q28983	SWISSPROT	P97461 40S RIBOSOMAL PROTEIN S5. ;
4893	17620	30239	4.97	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5067	17786		5.98	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
8017	20712	33843	0.81	2.0E-20	AA309457.1	EST_HUMAN	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
9089	21778	34942	8.6	2.0E-20	D10083.1	NT	EST180326 Liver III Homo sapiens cDNA 5' end
9089	21778	34943	8.6	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12426	25141	30895	2.03	2.0E-20	H55371.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
12815	25057		1.39	2.0E-20	11437152	NT	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
2007	15525	27488	3.71	1.0E-20	AA281961.1	EST_HUMAN	Homo sapiens heparin-binding growth factor binding protein (HBP17) mRNA
4406	17143	28772	1	1.0E-20	BF115158.1	EST_HUMAN	Z11408.r1 NC1_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
6794	19538	32566	0.75	1.0E-20	AF049567.1	EST_HUMAN	hr84b06.x1 NC1_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
9061	21750	34908	2.04	1.0E-20	11418491	NT	repetitive element ; AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
11541	24141	37450	2.62	1.0E-20	AF223391.1	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCN1) mRNA
12171	24651		1.73	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2913	15679		0.98	9.0E-21	AJ003514.1	EST_HUMAN	nc60g08.r1 NC1_CGAP_P11 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1
11904	24469		2.52	9.0E-21	AW888189.1	EST_HUMAN	repetitive element ; AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1p12-8J21
8711	21403		2.15	8.0E-21	AW874891.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
11526	24126	37432	3.52	8.0E-21	AA809411.1	EST_HUMAN	b530e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN
12084	24578		4.49	8.0E-21	O21330	SWISSPROT	Q85169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ; cb7f06.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338835 3'
2061	14793	27518	1.62	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2061	14793	27519	1.62	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
3689	18442	28083	0.89	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
4228	16989		5.68	7.0E-21	AA049502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
							2k67a06.r1 Soares_pregnant_uterus_NB-IPU Homo sapiens cDNA clone IMAGE:487858 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6340	19110	32100	0.79	7.0E-21	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8287	20981	34121	1.53	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
8576	21288	34407	10.76	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10013	22661	35877	0.96	7.0E-21	AW856922.1	EST_HUMAN	RCO-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA
10594	23288	36525	2.19	7.0E-21	AA723404.1	EST_HUMAN	ag73403.s1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:398881 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR13 OFR repetitive element ;
11234	23897	37184	1.75	7.0E-21	7706868	NT	Homo sapiens PTD013 protein (PTD013), mRNA
4083	16827	29454	0.83	6.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9034	21724		0.6	6.0E-21	BE162737.1	EST_HUMAN	PM1-HIT0454-080100-002-h09 HIT0454 Homo sapiens cDNA
9303	13870	26334	0.7	5.0E-21	5602031	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4330	17069	29697	2.91	5.0E-21	BE968839.1	EST_HUMAN	60164987F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4749	17481	30112	5.56	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
6665	19582		0.9	5.0E-21	AW440894.1	EST_HUMAN	he05e10.x1 NCI_CGAP_CVL1 Homo sapiens cDNA clone IMAGE:2918154 3'
6917	19654	32700	0.86	5.0E-21	BE565505.1	EST_HUMAN	7f83d11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.11 OFR repetitive element ;
10474	23120	36349	0.44	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
10474	23120	36350	0.44	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
11986	24527		2.83	5.0E-21	AA393574.1	EST_HUMAN	z172c04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1727	14469	27168	1.81	4.0E-21	AA970713.1	EST_HUMAN	cc86a08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA ; contains OFR.11 OFR repetitive element ;
6772	19516	32544	3.27	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
9680	22332	35527	0.83	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9705	22366	36562	0.7	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
1829	14568	27280	0.94	3.0E-21	AA218891.1	EST_HUMAN	zq15006.s1 Straigene fetal retina 937202 Homo sapiens cDNA clone IMAGE:628771 3'
2272	14968	27736	1.24	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3076	15943	28485	4.31	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5412	18211	30919	0.88	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5412	18211	30920	0.88	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5

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5652	18447		0.65	3.0E-21	AV661044.1	EST_HUMAN	AV661044 GLC Homo sapiens cDNA clone GLC0A10 3'
6086	18864		2.3	3.0E-21	BF184739.1	EST_HUMAN	601844485F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
6959	19451	32469	7.69	3.0E-21	BF361093.1	EST_HUMAN	RC1-OT0083-100800-018-g08 OT0083 Homo sapiens cDNA
9592	22245	35429	1.15	3.0E-21	AW887760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12533	25327	30714	2.88	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
141	12956		17.18	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
914	13681	26342	1.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
914	13681	26343	1.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1192	13944		2.75	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
2644	15354	28098	1.98	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2644	15354	28099	1.98	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5396	18196	30890	1.64	2.0E-21	AI624582.1	EST_HUMAN	ts30R03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5489	18288	31184	0.88	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN ;
5489	18288	31185	0.88	2.0E-21	AA027211.1	EST_HUMAN	z997a12.1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8170	20864	33986	0.5	2.0E-21	AJ010770.1	NT	z997a12.1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8261	20955	34094	6.16	2.0E-21	BE141785.1	EST_HUMAN	Homo sapiens hypoxanthine gene, exons 1-50
8722	21414	34557	3.74	2.0E-21	AU136779.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
10991	23665		1.55	2.0E-21	BE350127.1	EST_HUMAN	AU136779 PLACET Homo sapiens cDNA clone PLACE1005052 5'
11289	23950	37246	1.3	2.0E-21	BE973829.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29 b3
11289	23950	37247	1.3	2.0E-21	BE973829.1	EST_HUMAN	MER29 repetitive element ;
12272	24712		9.87	2.0E-21	AF176815.1	NT	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1233	13982	26652	1.6	1.0E-21	AA557657.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1381	14128		2.82	1.0E-21	AI801284.1	EST_HUMAN	Homo sapiens putative B-hydroxyglutamine DNA glycosylase gene, complete cds
6396	19165		2.74	1.0E-21	AL079762.1	EST_HUMAN	n46c04.x1 NCI_CGAP_P74 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29 b2
7092	19781	32847	6.6	1.0E-21	AI223104.1	EST_HUMAN	MER29 repetitive element ;
10484	23130		1.07	1.0E-21	57300338	NT	MER29 repetitive element ;
4377	17114	29747	5.65	9.0E-22	AI702438.1	EST_HUMAN	ar88d12.x1 Barstead codon HP_LRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
8502	21194	34336	1.27	9.0E-22	AL163201.2	NT	DKF2p4340830_r1 434 (synonym: hss3) Homo sapiens cDNA clone DKF2p4340830 5'
8502	21194	34337	1.27	9.0E-22	AL163201.2	NT	qg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M84241 QM
							PROTEIN (HUMAN);
							Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							tz94a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
							NEUTRAL PROTEASE LARGE SUBUNIT ;
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens chromosome 21 segment HS21C001

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10691	23392	36822	2.63	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSGCG05 5'
11707	24302	37627	1.34	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
929	13696		5.55	8.0E-22	BE144748.1	EST_HUMAN	CMO-H10179-281099-078-H05 HT10179 Homo sapiens cDNA
7797	20492		3.72	8.0E-22	AA046502.1	EST_HUMAN	Z672606.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
650	13428	29097	5.92	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4250	16981	29616	2.21	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4977	17700	30307	0.99	7.0E-22	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8590	21282		1.38	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
8731	21423	34568	3.56	7.0E-22	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stragelene (cat#838208) Homo sapiens cDNA clone HFBCF07
9502	22155	35335	2.04	7.0E-22	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
4038	16783	29413	0.98	6.0E-22	AA405040.1	EST_HUMAN	zu65d10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742887 5'
8140	20834		1.33	6.0E-22	AW028123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2542812 3'
6424	19192	32188	3.76	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10217	22865	36077	7.83	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12499	24854		2.22	5.0E-22	BF478611.1	EST_HUMAN	naa27d06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3627	16390		0.85	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8004	20699	33827	0.45	4.0E-22	AV703223.1	EST_HUMAN	AV703223 ADB Homo sapiens cDNA clone ADBAUET12 5'
8312	25428		3.11	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10823	23316	36556	2.47	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085434 5'
12657	24957		2.06	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
939	13706		1.59	3.0E-22	A1469679.1	EST_HUMAN	hm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156811 3' similar to gb:L16893 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN)/contains L1.11 L1 repetitive element;
2575	15289	28026	0.92	3.0E-22	A1859038.1	EST_HUMAN	wf68b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN
3682	16415		1.46	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21.;
						NT	Human chromosomal protein HMG1 related gene
4748	17480	30111	2.6	3.0E-22	A1090125.1	EST_HUMAN	qb26c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697560 3' similar to contains MER1212 MER12 repetitive element;
8129	20823		0.8	3.0E-22	BE159613.1	EST_HUMAN	QV0-H10368-090200-098-f12 HT0368 Homo sapiens cDNA
8134	20828	33963	2.46	3.0E-22	BE089841.1	EST_HUMAN	RC5-B10707-150300-021-H10 BT0707 Homo sapiens cDNA
8258	20952	34088	0.97	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
8258	20952	34089	0.97	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
1846	14681		2.29	2.0E-22	N24942.1	EST_HUMAN	ix73d05.s1 Soares_melanocyte_ZN1bHM Homo sapiens cDNA clone IMAGE:267389 3'
2526	15242	27981	2.15	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR

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3414	16172	28621	4.41	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4200	16941	29567	1.17	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA
5761	25075	31478	1.18	2.0E-22	W39456.1	EST_HUMAN	zxc2001.1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to
6084	18862	31828	3.58	2.0E-22	BF092116.1	EST_HUMAN	(b-X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
9602	22255	35440	1.53	2.0E-22	AI276922.1	EST_HUMAN	RC0-TN0078-150900-025-h12 TN0078 Homo sapiens cDNA
9696	22347	35540	0.69	2.0E-22	AA715315.1	EST_HUMAN	q17h06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878289 3' similar to contains
9698	22347	35541	0.69	2.0E-22	AA715315.1	EST_HUMAN	MER28.i3 MER28 repetitive element;
11761	24352	37684	1.68	2.0E-22	AW418980.1	EST_HUMAN	m04h11.s1 NCL_OGAP_Py22 Homo sapiens cDNA clone IMAGE:1219269 3'
11872	24946	30983	3.71	2.0E-22	AL163280.2	NT	m04h11.s1 NCL_OGAP_Py22 Homo sapiens cDNA clone IMAGE:1219269 3'
1871	14609	27320	1.79	1.0E-22	AW865517.1	EST_HUMAN	haz4f04.x1 NCL_OGAP_Kid1 Homo sapiens cDNA clone IMAGE:2874655 3'
2588	15302	28038	1.1	1.0E-22	U50871.1	NT	Homo sapiens chromosome 21 segment HS21C080
3405	16163	28814	1.37	1.0E-22	D14547.1	NT	PM4-SN0020-010400-008-h02 SN0020 Homo sapiens cDNA
7641	20306	33415	0.89	1.0E-22	BE094667.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
10451	23097	36328	0.79	1.0E-22	AI365435.1	EST_HUMAN	Human DNA, SINE repetitive element
10451	23097	36328	0.79	1.0E-22	AI365435.1	EST_HUMAN	MRO-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
12704	24984	28959	5.89	9.0E-23	AF198349.1	NT	qz09b07.x1 NCL_OGAP_GLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER28.b2
3305	16065	30895	4.16	7.0E-23	5031952	NT	MER29 repetitive element;
10968	23642	3427	1.72	6.0E-23	AF199333.1	NT	qz09b07.x1 NCL_OGAP_GLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER28.b2
4235	16976	28601	1.39	6.0E-23	AL163249.2	NT	MER29 repetitive element;
12005	24540	31105	1.5	6.0E-23	AF224669.1	NT	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
12005	24540	31106	1.5	6.0E-23	AF224669.1	NT	Gallus gallus Dect2 protein (Dect2) mRNA, complete cds
12192	24663	31067	3.28	6.0E-23	AI208130.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAWC07 3'
5358	18160	30844	4.09	5.0E-23	U82671.2	NT	Homo sapiens Ndc56 (D. melanogaster)-like protein (NOT56L) mRNA
							Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
							Homo sapiens chromosome 21 segment HS21C049
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							(UBE2D3) genes, complete cds
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							(UBE2D3) genes, complete cds
							qg56c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to
							SW:MMV10_MOUSE_P23249 PROTEIN MOV-10;
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12
							(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin
							(CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6145	25086	31893	3.93	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7337	25086	31893	3.37	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6347	19117	32106	1.34	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6347	19117	32107	1.34	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7738	20434	33556	4.1	3.0E-23	AA130165.1	EST_HUMAN	z155g09.r1 Soares_pregnant_lutetus_Nbl-HPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element ;
9148	21879	35045	2.96	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
9148	21879	35046	2.96	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
10215	22863	26068	1.18	3.0E-23	AW897927.1	EST_HUMAN	RC3-NN0066-270400-011-h01 NN0066 Homo sapiens cDNA
651	13429	26068	4.25	2.0E-23	AJ289880.1	NT	Homo sapiens KIA00851 gene (partial), X13 gene and LZTFL1 gene
1120	15520		3.87	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2798	15503	28243	1.98	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2798	15503	28244	1.98	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3364	16123		1.46	2.0E-23	AJ201458.1	EST_HUMAN	q873f11.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
3705	18458		3.35	2.0E-23	BE166980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3958	16707	28346	3.65	2.0E-23	H59931.1	EST_HUMAN	y16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
3958	16707	28347	3.65	2.0E-23	H59931.1	EST_HUMAN	y16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7772	20468		4.3	2.0E-23	AF280107.1	NT	Homo sapiens chromosome 21 segment HS21C103
8742	21434	34579	1.21	2.0E-23	AL163303.2	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
11991	24530		2.45	2.0E-23	M32658.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12508	24860		2.87	2.0E-23	AF009660.1	NT	Homo sapiens chromosome 21 segment HS21C052
4492	17228	28857	1.1	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C010
4714	17446		5.59	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6620	18382		3.28	1.0E-23	BE378471.1	EST_HUMAN	6012364.5F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR6.12
8254	20948	34085	4.6	1.0E-23	AA448097.1	EST_HUMAN	z162c08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:3608653 5'
10570	23265	36503	2.05	1.0E-23	BE409843.1	EST_HUMAN	PTR5 repetitive element ;
10570	23265	36504	2.05	1.0E-23	BE409843.1	EST_HUMAN	601301782F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
							601301782F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
							ab75a08.s1 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:852768 3' similar to TR:E19822 E19822 CA PROTEIN. ;
539	13322		1.84	9.0E-24	AA663213.1	EST_HUMAN	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
6357	19127	32121	1.53	8.0E-24	11422027	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3853	16603		1.49	7.0E-24	AW6937954.1	EST_HUMAN	QV0-DT0047-170200-122-e06 DT0047 Homo sapiens cDNA
5087	17806		0.95	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311.1_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434A2311 5'
10536	23233		1.33	7.0E-24	AW303317.1	EST_HUMAN	xy17003.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element;
690	13465		2.72	6.0E-24	AB001421.1	NT	Macaca fascicularis mRNA for Testis-Specific Protein Y (TSPY), complete cds
818	13569	26256	11.74	6.0E-24	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C049
3953	16703	29342	7.9	5.0E-24	AJ229043.1	NT	Homo sapiens 858 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
7657	20321	33430	0.58	5.0E-24	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
11595	24194	37513	1.45	5.0E-24	AW514229.1	EST_HUMAN	hd24b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810413 3' similar to TR-094851
5840	18628	31563	3.85	4.0E-24	AA594178.1	EST_HUMAN	O94851 KIAA0750 PROTEIN;
8581	21273	34411	1.35	4.0E-24	AW81371.1	EST_HUMAN	nm31h05.3' NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085528 3' similar to SW-POL_MLVRK P31795 POL POLYPROTEIN;
11133	23801	37078	1.95	4.0E-24	BE544822.1	EST_HUMAN	RC3-ST0197-130100-014-f06 ST0197 Homo sapiens cDNA
12361	24765	31082	4.89	4.0E-24	AB029016.1	NT	RC3-ST0197-130100-014-f06 ST0197 Homo sapiens cDNA clone IMAGE:3464488 5'
12595	24951	30986	1.77	4.0E-24	11418318	NT	Homo sapiens mRNA for KIAA1083 protein, partial cds
8322	21015		2.85	3.0E-24	AW614871.1	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
8377	21070		1.57	3.0E-24	AW962076.1	EST_HUMAN	h88c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MER29.b2 MER29 repetitive element;
9365	21940	35114	4.33	3.0E-24	AL163252.2	NT	EST374148 IMAGE resequences, MAGO Homo sapiens cDNA
12438	24808	31045	1.41	3.0E-24	BF12762.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
2346	15069	27806	2.72	2.0E-24	AA167539.1	EST_HUMAN	80181049F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
3779	16531		1.01	2.0E-24	AW898189.1	EST_HUMAN	zp11109.r1 Striatogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:509161 5'
7374	20054	33135	0.81	2.0E-24	AF086824.1	NT	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
7379	20059	33138	0.65	2.0E-24	AJ003536.1	EST_HUMAN	Mus musculus rho/rac-interacting citron kinase (Ork) mRNA, complete cds
8639	21331	34476	3.28	2.0E-24	AL119158.1	EST_HUMAN	AJ003538 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MIP12-5H13
8676	21368		0.98	2.0E-24	H69214.1	EST_HUMAN	DKFZp781L1712.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781L1712 5'
9754	22405	35611	0.94	2.0E-24	AJ521759.1	EST_HUMAN	yr52b09.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER29 repetitive element;
9754	22405	35611	0.94	2.0E-24	AJ521759.1	EST_HUMAN	h77609.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
11825	24409	37744	1.31	2.0E-24	AW868552.1	EST_HUMAN	h77609.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
11825	24409	37745	1.31	2.0E-24	AW868552.1	EST_HUMAN	MR1-SN0063-040500-001-a06 SN0063 Homo sapiens cDNA
12281	25377		7.44	2.0E-24	M28877.1	NT	MR1-SN0063-040500-001-a06 SN0063 Homo sapiens cDNA
							Human O family dispersed repeat element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1691	14435	27131	2.68	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51646), mRNA
2679	15388		1.63	1.0E-24	AW820184.1	EST_HUMAN	QVO-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
3020	15786	28433	1.49	1.0E-24	D86423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4237	16978		1.71	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
7447	20123	33214	4.32	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7630	20296	33404	0.81	1.0E-24	BE144526.1	EST_HUMAN	MRO-HT0166-271199-005-d09 HT0166 Homo sapiens cDNA
7845	20540	33667	2.09	1.0E-24	AW901164.1	EST_HUMAN	CMO-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA
11699	24294	37619	1.31	9.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
4939	17667	30275	2.33	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8117	20811	33946	6.59	7.0E-25	AA468646.1	EST_HUMAN	MER1 repetitive element ;
11701	24296	37622	3.26	7.0E-25	AA583540.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to contains THR.b2 THR repetitive element ;
6893	17969		4.9	6.0E-25	W87623.1	EST_HUMAN	m25f06.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST
7622	20288	33397	8.34	6.0E-25	7305360	NT	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
1647	14393	27083	1.18	5.0E-25	AW850271.1	EST_HUMAN	zh65h07.r1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416889 5'
11286	23947	37242	2.44	5.0E-25	AW879107.1	EST_HUMAN	Mus musculus otogelin (Otag), mRNA
1429	14176	26861	2.25	4.0E-25	T98107.1	EST_HUMAN	IL3-CT021B-161189-031-D04 CT0219 Homo sapiens cDNA
3397	16155		3.04	4.0E-25	AW887671.1	EST_HUMAN	EST391217 MAGE resequences, MAGP Homo sapiens cDNA
4282	17021		2.93	4.0E-25	BE170957.1	EST_HUMAN	ye66f04.r1 Soares fetal liver spleen_1NFLS_Homo sapiens cDNA clone IMAGE:121783 5'
3314	16074	28724	3.98	3.0E-25	8923321	NT	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
3314	16074	28725	3.98	3.0E-25	8923321	NT	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
4837	17568	30190	0.75	3.0E-25	P26622	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
6518	19284	32288	0.6	3.0E-25	AA603590.1	EST_HUMAN	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
8235	20829	34065	4.86	3.0E-25	AL163210.2	NT	np27b02.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gbM61866 ZINC FINGER PROTEIN 85 (HUMAN);
10959	23635	36886	1.99	3.0E-25	AA579013.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1328	14075	26749	2.94	2.0E-25	5032158	NT	nf30h10.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.H L1 repetitive element ;
2308	15031	27768	6.42	2.0E-25	BE888016.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2835	15259	27997	3.67	2.0E-25	P17008	SWISSPROT	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
4167	16907	29535	1.76	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4167	16907	29536	1.76	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9665	22317	35514	1.94	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
355	13153	25794	1.03	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0313 5'
1228	13976		2.02	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
2435	15156	27890	1.03	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4906	17537	30160	2.84	1.0E-25	BE162737.1	EST_HUMAN	PM1HT0454-080100-002-009 HT0454 Homo sapiens cDNA
							zq48606.s1 Stragene HNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains Alu repetitive element;
8472	19239		0.79	1.0E-25	AA189080.1	EST_HUMAN	nt54h11.s1 NCI CGAP_Ki68 Homo sapiens cDNA clone IMAGE:1087749 3'
6899	25100	32657	3.14	1.0E-25	AA582980.1	EST_HUMAN	z96g04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.13 PTR5 repetitive element;
7814	20509	33633	4.03	1.0E-25	AA709079.1	EST_HUMAN	R ratius RY2G5 mRNA for a potential ligand-binding protein
9446	22123	35302	0.75	1.0E-25	X60660.1	NT	R ratius RY2G5 mRNA for a potential ligand-binding protein
9446	22123	35303	0.75	1.0E-25	X60660.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
10890	23570	36821	3.06	1.0E-25	U63163.1	NT	Human lambda-de-immunoglobulin constant region complex (germline)
12768	25024		2.18	1.0E-25	X51755.1	NT	Homo sapiens chromosome 21 segment HS21C018
2487	15204	27945	1.41	9.0E-26	AL163218.2	NT	Human DNA, SINE repetitive element
5607	18403		1.99	8.0E-26	D14547.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1571	14318	27003	1.72	7.0E-26	AF003528.1	NT	H. sapiens DNA for endogenous retroviral like element
3962	18711	29351	1.23	7.0E-26	X89211.1	NT	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908386 3'
4138	18880	29508	2.27	7.0E-26	AW340183.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
5551	18348	31257	0.62	7.0E-26	AL163202.2	NT	zn30d08.r1 Stragene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gpM14398 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
11669	24264		8.45	7.0E-26	AA115895.1	EST_HUMAN	EST366628 MAGE resequences, MAGC Homo sapiens cDNA
12547	24885		1.64	7.0E-26	AW954559.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
2222	14950	27689	2.04	6.0E-26	AF029308.1	NT	z952h04.r1 Stragene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:645271 5'
3341	16700	28752	0.95	6.0E-26	AA208131.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
10432	23078	36301	0.68	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10432	23078	36302	0.68	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11663	24278	37600	2.03	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1154	13909	26572	3.61	6.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;

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1164	13909	26573	3.61	5.0E-26	AI708235.1	EST_HUMAN	as38408.x1 Barstead aceta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 OE03371;
1535	14282		1.4	4.0E-26	AA329548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' and
9812	21979		3.72	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10558	23254	36491	2.75	4.0E-26	BE268187.1	EST_HUMAN	501191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
1753	14495	27194	1.21	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1996	14732	27454	1.31	3.0E-26	AL045855.2	EST_HUMAN	DKFZp4341066.1 1434 (synonym: hies3) Homo sapiens cDNA clone DKFZp4341066 5'
2025	14760		3.15	3.0E-26	AA115895.1	EST_HUMAN	zn30d08.11 Striatogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5'
							similar to gbm14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
							zn30f10.11 Striatogene colon (#937204) Homo sapiens cDNA clone IMAGE:589427 5' similar to TR:G685374
3760	16512	29148	1.04	3.0E-26	AA152464.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR;
3760	16512	29149	1.04	3.0E-26	AA152464.1	EST_HUMAN	zn30f10.11 Striatogene colon (#937204) Homo sapiens cDNA clone IMAGE:589427 5' similar to TR:G685374
6811	19472	32495	1.78	3.0E-26	BF245458.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR;
10928	23319	37468	1.42	3.0E-26	AF036405.1	NT	601894863F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
11559	24158	37469	1.83	3.0E-26	AW875651.1	EST_HUMAN	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
11558	24158	37469	1.83	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-005 PT0012 Homo sapiens cDNA
11602	24201	37523	6.56	3.0E-26	AA583173.1	EST_HUMAN	QV2-PT0012-040400-124-005 PT0012 Homo sapiens cDNA
11858	24442	37783	1.36	3.0E-26	AF228925.1	NT	nr37d05.s1 NCL_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1
							OFR repetitive element;
							Mus musculus harmonin isoform b3 (Ush1c) mRNA, complete cds, alternatively spliced
12724	24995		2.52	3.0E-26	AW073434.1	EST_HUMAN	za57509.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2570873 3' similar to contains MER30.11
666	13442	26083	6.76	2.0E-26	AL163282.2	NT	MER30 repetitive element;
1861	14599		3.07	2.0E-26	AL038069.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
3225	15988	28642	5.89	2.0E-26	X86894.1	NT	DKFZp568L171.s1 568 (synonym: hifd2) Homo sapiens cDNA clone DKFZp568L171 3'
5147	17866		1.09	2.0E-26	AF073482.1	NT	Mmusculus mRNA for astrocytic phosphoprotein, PEA-15
10653	23344		2.7	2.0E-26	D87675.1	NT	Homo sapiens myotubularin related protein 7 mRNA, partial cds
							Homo sapiens DNA for amyloid precursor protein, complete cds
							hs89a01.x1 NCL_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu
11180	23846	37132	3	2.0E-26	AI801412.1	EST_HUMAN	repetitive element contains element MER20 MER20 repetitive element;
11395	24001		2.45	2.0E-26	AF055066.1	NT	Homo sapiens MHC class 1 region
12108	24603		1.57	2.0E-26	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
133	12948	25591	5.18	1.0E-26	BE170371.1	EST_HUMAN	QV44-H70538-020300-123-a02 HT0538 Homo sapiens cDNA
2040	14774	27503	1.37	1.0E-26	AL039363.2	EST_HUMAN	DKFZp434H1910.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H1910 5'
2693	15402		9.04	1.0E-26	AF281085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8740	19574		3.05	1.0E-26	BE165890.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10809	23492		2.21	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146 J1 566 (synonym: hfkx2) Homo sapiens cDNA clone DKFZp566C2146 5'
12348	25395		3.53	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22-45 5'
7484	20156		1.11	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9203	22082		4.14	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
11875	24454		5.72	9.0E-27	BF445556.1	EST_HUMAN	naa03c07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3253044 3' similar to contains OFR.t1 OFR repetitive element;
10	12837	25450	3.83	8.0E-27	AI831462.1	EST_HUMAN	wf49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
544	13327		4.33	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1395	14142	26818	59.39	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb-K00558
1395	14142	26820	59.39	8.0E-27	AW162737.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
2164	14893	27629	1.37	8.0E-27	AW864776.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb-K00558
3180	15943	28594	1.81	8.0E-27	P12236	SWISSPROT	TUBULIN ALPHA-1 CHAIN (HUMAN);
3348	18107	28762	0.81	8.0E-27	AF181897.1	NT	PM2-SN0018-220300-002-e07 SN0018 Homo sapiens cDNA
5808	18404	31317	1.02	8.0E-27	AV732214.1	EST_HUMAN	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ANT 3)
6981	17957		2.53	8.0E-27	BE926560.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
6947	19429	32444	2.29	8.0E-27	N84970.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 5'
9109	21797	34961	1.51	8.0E-27	AW857579.1	EST_HUMAN	MR4-BT0398-250800-204-d08 BT0398 Homo sapiens cDNA
9109	21797	34962	1.51	8.0E-27	AW857579.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to
668	13444		1.23	7.0E-27	Z70664.1	NT	REPEATITIVE ELEMENT L1
5030	17750		2.25	7.0E-27	AW628172.1	EST_HUMAN	CM1-C10315-091299-063-d07 CT0315 Homo sapiens cDNA
8758	21448		1.19	7.0E-27	D86894.1	NT	CM1-C10315-091299-063-d07 CT0315 Homo sapiens cDNA
10650	23341		4.26	7.0E-27	AJ271735.1	NT	Human endogenous retroviral element HC2
12484	24843		2.12	7.0E-27	AV723965.1	EST_HUMAN	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:076040
10827	23320	36558	2.75	6.0E-27	M26697.1	NT	O76040 ORF2 FUNCTION UNKNOWN;
11804	24394	37728	1.57	6.0E-27	U93163.1	NT	Human mRNA for KIAA0231 gene, partial cds
							Homo sapiens Xq pseudautosomal region; segment 1/2
							AV723965 HTB Homo sapiens cDNA clone HTBAHE02 5'
							Human nuclear protein (B23) mRNA, complete cds
							Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds

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10137	22785	35996	2.82	5.0E-27	BF668614.1	EST_HUMAN	602121.491F1 NIH_MGC.58 Homo sapiens cDNA clone IMAGE:4278527 5'
10137	22785	35997	2.82	5.0E-27	BF668614.1	EST_HUMAN	602121.491F1 NIH_MGC.58 Homo sapiens cDNA clone IMAGE:4278527 5'
6645	19407	32421	1.65	4.0E-27	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
7840	20535		1.07	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7883	20578		1.54	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9644	22296	35491	0.7	4.0E-27	AW890959.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11604	24203	37525	1.98	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2034	14769	27499	4.81	3.0E-27	X80698.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4238	16979	29604	1.06	3.0E-27	BE071924.1	EST_HUMAN	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
5262	18068	30697	6.24	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
7698	20361	33475	0.63	3.0E-27	BE870351.1	EST_HUMAN	7e33f02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9205	22084	35256	2.93	3.0E-27	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC.68 Homo sapiens cDNA clone IMAGE:3862086 5'
40	12868	25487	14.84	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1888	14625		5.12	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI CGAP_PT11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3107	15872		10.39	2.0E-27	AW629172.1	EST_HUMAN	h151M12.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:076040
3218	15981	28632	1.96	2.0E-27	AF111167.2	NT	076040 ORF2: FUNCTION UNKNOWN.;
3218	15981	28633	1.96	2.0E-27	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4009	16755	28385	1.36	2.0E-27	AF000388.1	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6577	19340	32353	0.61	2.0E-27	H02655.1	EST_HUMAN	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
7989	20684	33910	1.65	2.0E-27	AI868347.1	EST_HUMAN	y86601.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
9169	21839		2.3	2.0E-27	AA551527.1	EST_HUMAN	SP:HMGC_MOUSE Q02591 HOMEOBOX PROTEIN ;
9691	22342	35536	0.76	2.0E-27	X00658.1	NT	wf28g07.x1 NCI CGAP_UT Homo sapiens cDNA clone IMAGE:2428288 3'
9835	22583	35782	1.28	2.0E-27	M78590.1	EST_HUMAN	nh08h05.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1
9835	22583	35783	1.28	2.0E-27	M78590.1	EST_HUMAN	repetitive element ;
10875	23555	36802	4.11	2.0E-27	AU121885.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
11469	14625		3.31	2.0E-27	AA565345.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
426	13212		1.51	1.0E-27	AL163248.2	NT	EST00738 Fetal brain, Striatum (cat#036206) Homo sapiens cDNA clone HFBCF07
							EST00738 Fetal brain, Striatum (cat#036206) Homo sapiens cDNA clone HFBCF07
							AU121885 MAMMA1 Homo sapiens cDNA clone MAMMA1000748 5'
							nk01b10.s1 NCI CGAP_PT11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
							ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							Homo sapiens chromosome 21 segment HS21C048

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976	13741	26404	1.34	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4061	16806		0.98	1.0E-27	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MIER29 b3
6449	19217	32215	6.26	1.0E-27	6005855	NT	MER29 repetitive element;
6771	19515	32542	1.96	1.0E-27	F30158.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6771	19515	32543	1.96	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8508	21200	34346	0.98	1.0E-27	AB007923.1	NT	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8884	21575		2.26	1.0E-27	BE078780.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
9622	22275	35463	2.65	1.0E-27	D87449.1	NT	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
11704	24298	37625	3.51	1.0E-27	AF111093.1	NT	Human mRNA for KIAA0260 gene, partial cds
137	12851		2.94	9.0E-28	BE348399.1	EST_HUMAN	Bos taurus latrophilin 3 splice variant b2b mRNA, complete cds
303	13107	25747	3.31	9.0E-28	AU126260.1	EST_HUMAN	hwt7c11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
10289	22937	36150	0.83	9.0E-28	AA174078.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313 ;
11951	24504		4.85	9.0E-28	BF377859.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
12266	25245		2.48	8.0E-28	AW157571.1	EST_HUMAN	zp18g12.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609892 3'
1158	13913	26576	7.89	7.0E-28	AU142750.1	EST_HUMAN	GM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
11142	23809	37089	3.36	7.0E-28	11417866	NT	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
11910	24474		2.78	7.0E-28	AV735348.1	EST_HUMAN	TR:Q09302 Q09302 KIAA0555 PROTEIN ; contains element MER22 repetitive element ;
8917	21509		0.97	6.0E-28	AF016052.1	NT	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
12526	24873		2.35	6.0E-28	AA504562.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
310	13114		4.19	5.0E-28	A1921003.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone GBFAKA12 5'
3990	16738	28372	1.44	5.0E-28	R79762.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
2831	15343	28087	1.68	4.0E-28	AW195066.1	EST_HUMAN	aa60403.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu
2976	15742	28389	0.78	4.0E-28	4506316	NT	repetitive element contains element PTR5 repetitive element ;
3106	15871	28511	2.52	4.0E-28	BE409100.1	EST_HUMAN	w018c07.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1
7230	19915	32688	1.93	4.0E-28	A1198941.1	EST_HUMAN	THR repetitive element ;
							y89710.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:146443 5'
							xr33c09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN
							Q08379 GOLGIN-95 ;
							Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
							601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
							q08f10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
							REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);

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10774	28457		3.08	4.0E-28	AF023008.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10828	23608		17.24	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
10950	19915	32988	4.75	4.0E-28	A198941.1	EST_HUMAN	qf6810.x1 Soares, testis NIH-Homo sapiens cDNA clone IMAGE:1755018 3' similar to gb:U19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12312	24734		1.84	4.0E-28	AW854244.1	EST_HUMAN	RC3-CT0254-240400-210-f12 CT0254 Homo sapiens cDNA
1260	14009		2.88	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5051	17770		1.05	3.0E-28	AF009880.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8728	21418	34562	1.89	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-008 HT0713 Homo sapiens cDNA
10853	23533	36778	2.09	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
12344	24751		3.62	3.0E-28	A1831991.1	EST_HUMAN	Homo sapiens MHC class 1 region
87	12813	28551	10.6	2.0E-28	BE062167.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element/contains element HGR repetitive element ;
1023	13783	26444	0.86	2.0E-28	4501812	NT	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1142	13897	26558	16.03	2.0E-28	Y11107.3	NT	Homo sapiens a disintegrin and metalloprotease domain 23 (ADAM23) mRNA
2481	15189	27839	2.1	2.0E-28	A1348634.1	EST_HUMAN	Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41 Homo sapiens x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element ;
6215	18989	31986	1.33	2.0E-28	BF224402.1	EST_HUMAN	h76c03.x1 NCI_CGAP_Ku11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element ;
6238	19012		5.07	2.0E-28	BF212905.1	EST_HUMAN	601814786F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048761 5'
7943	20638	33766	0.71	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9484	22137		5.54	2.0E-28	AW972305.1	EST_HUMAN	EST384384 IMAGE resequences, MAGI Homo sapiens cDNA
11614	24212	37536	1.84	2.0E-28	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12322	24741		2.22	2.0E-28	H06378.1	EST_HUMAN	y79c08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
1461	14208	26895	2.84	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2217	14845	27685	2.37	1.0E-28	BF333238.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
7759	20455		3.2	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63081), mRNA
7817	20612		3.3	1.0E-28	8822763	NT	Homo sapiens hypothetical protein FLJ10688 (FLJ10688), mRNA
9178	21848	35014	4.84	1.0E-28	AA308744.1	EST_HUMAN	EST178615 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end similar to similar to retroviral LTR
9776	22427	35633	8.73	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9776	22427	35634	8.73	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA

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10422	23068		0.63	1.0E-28	AU149356.1	EST_HUMAN	AU149356 NT2RM4 Homo sapiens cDNA clone NT2RM4002146 3'
11915	24478		7.79	1.0E-28	AA054182.1	EST_HUMAN	z651c01.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
12651	25143		1.88	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12749	25346	30603	3.18	9.0E-29	AW663867.1	EST_HUMAN	h178g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976266 3'
12436	24806		3.32	8.0E-28	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1598	14344	27034	1.37	7.0E-29	AW968447.1	EST_HUMAN	EST178521 IMAGE resequenced, MAGI Homo sapiens cDNA
12784	25045		7.13	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
581	13361	25989	16.66	6.0E-28	AJ936748.1	EST_HUMAN	wp69b01.x1 NCL_GCAP_Bm25 Homo sapiens cDNA clone IMAGE:2466885 3' similar to TR:015475
12201	24669		8.09	8.0E-28	BE940438.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN; contains LTR7.b1 LTR7 repetitive element;
12286	24717		1.72	6.0E-29	BF569097.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
8630	21322		6.36	6.0E-28	AW887541.1	EST_HUMAN	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
3228	19889		1.84	4.0E-28	AJ752367.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
5919	18704		7.91	4.0E-28	BE164830.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
7979	20674	33797	0.55	4.0E-28	AJ678101.1	EST_HUMAN	QV1-H10471-280300-121-a05 H10471 Homo sapiens cDNA
7979	20674	33798	0.55	4.0E-28	AJ678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8644	21336	34480	6.21	4.0E-28	J04988.1	NT	MER29.12 MER29 repetitive element;
4381	17118	29751	1.4	3.0E-28	AB042287.1	NT	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
4684	17418	30054	1.07	3.0E-28	BF333236.1	EST_HUMAN	Human 90 kD heat shock protein gene, complete cds
5841	18829	31564	1.18	3.0E-28	BE314018.1	EST_HUMAN	Homo sapiens PTS gene for 6-pyruvoylseraldolase synthase, complete cds
8632	21324	34465	2.87	3.0E-28	D38044.1	NT	QV1-BT0821-120800-360-b03 BT0821 Homo sapiens cDNA
9200	21869	35034	1.69	3.0E-28	AW303317.1	EST_HUMAN	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3608527 5'
9431	22109		1.87	3.0E-28	AL163246.2	NT	Human gene for A1H-receptor, exon 7-9
9659	22509		0.61	3.0E-28	BE350127.1	EST_HUMAN	xv1703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
11235	23898	37185	1.47	3.0E-28	AA403053.1	EST_HUMAN	repetitive element; contains MER19.12 MER19 repetitive element;
12102	24600		1.53	3.0E-28	D63882.1	NT	Homo sapiens chromosome 21 segment HS21C046
12789	23376		7.53	3.0E-28	AA016177.1	EST_HUMAN	h108g01.x1 NCL_GCAP_X1a13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
480	13265	25900	1.72	2.0E-28	AF084869.1	NT	MER29 repetitive element;
							z62b01.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335769
							G1335769 GAG-POL POLYPROTEIN.;
							Human HaLM15 mRNA for HaLM15, complete cds
							z632e09.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360712 3'
							Homo sapiens envelope protein RIC-6 (env) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
480	13285	25901	1.72	2.0E-29	AF084889.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
1523	14270	26955	6.62	2.0E-29	A1963604.1	EST_HUMAN	w65d10.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN;
1523	14270	26956	6.62	2.0E-29	A1963604.1	EST_HUMAN	w65d10.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN;
4246	16987	29610	1.63	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5735	18527	31449	0.99	2.0E-29	A082459.1	EST_HUMAN	os71e04.x1 NCL CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1 repetitive element;
6087	18865	31830	1.48	2.0E-29	A1806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element;
7459	18865	31830	1.36	2.0E-29	A1806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element;
7676	20571	33698	1.16	2.0E-29	BE867157.1	EST_HUMAN	601442206F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846848 5'
8477	21169	34313	0.63	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
8477	21169	34314	0.63	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
9408	22070	35241	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9408	22070	35242	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10139	22787	35999	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10139	22787	36000	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10877	23557	36804	1.31	2.0E-29	BF025947.1	EST_HUMAN	601669934F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3852833 5'
11459	24063		2.04	2.0E-29	11426108	NT	Homo sapiens splicing factor similar to dnal (SPF31), mRNA
11499	24100		1.73	2.0E-29	AW880701.1	EST_HUMAN	QV0-QT0032-080300-155-001 OT0032 Homo sapiens cDNA
8691	21383	34527	7.37	1.0E-29	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
10518	23164	36391	0.85	1.0E-29	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
6487	19254	32255	2.97	9.0E-30	AA761215.1	EST_HUMAN	n20c07.e1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element;
11992	24531		1.76	9.0E-30	11422745	NT	Homo sapiens zinc finger regulated transporter-like (ZIRTL), mRNA
6227	19001		8.94	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8168	20862	33994	3.72	8.0E-30	AA388873.1	EST_HUMAN	EST197317 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
8563	21275	34412	3.1	8.0E-30	AI557072.1	EST_HUMAN	PT2.1_13_B11.r.tumor2 Homo sapiens cDNA 3'
1505	14251		1.03	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1766	14508	27209	1.73	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3185	15948	28598	2.3	6.0E-30	BE080028.1	EST_HUMAN	QV0-BN0147-200400-214-f12 BN0147 Homo sapiens cDNA
10437	23083	36310	0.48	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen sc20-10 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12769	17897		3.38	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3994	16742	26376	26.19	5.0E-30	AI386992.1	EST_HUMAN	igb2g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
5159	25176		5.44	5.0E-30	U87931.1	NT	Human eonitrate hydratase (ACO2) gene, exon 7
10802	23485		1.95	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11103	23773	37047	2.47	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11103	23773	37048	2.47	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2139	14869	27599	1.72	4.0E-30	AW837471.1	EST_HUMAN	QV3-DT0043-090200-080-008 DT0043 Homo sapiens cDNA
2139	14869	27600	1.72	4.0E-30	AW837471.1	EST_HUMAN	QV3-DT0043-090200-080-008 DT0043 Homo sapiens cDNA
6756	17925	30560	0.63	4.0E-30	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8803	21495	34641	2.82	4.0E-30	AW812488.1	EST_HUMAN	ENDONUCLEASE
1129	13885		2.11	3.0E-30	A338551.1	EST_HUMAN	GM1-ST0181-091199-035-008 ST0181 Homo sapiens cDNA
3740	16493	29128	0.93	3.0E-30	AF128893.1	NT	qf83c05.x1 Scores: total_fetus_Nb2HF9_6w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element;
7852	20547		0.58	3.0E-30	AF078779.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
8385	21078		0.48	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10333	22980	36200	1.7	3.0E-30	BE350127.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10465	23111	36342	0.53	3.0E-30	AB032969.1	NT	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3 MER29 repetitive element;
10465	23111	36343	0.53	3.0E-30	AB032969.1	NT	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3 MER29 repetitive element;
11168	23835	37116	2.48	3.0E-30	P34056	SWISSPROT	Homo sapiens mRNA for KIAA1143 protein, partial cds
660	13436	26077	0.92	2.0E-30	AW857316.1	EST_HUMAN	Homo sapiens mRNA for KIAA1143 protein, partial cds
1062	13820		3.11	2.0E-30	F08688.1	EST_HUMAN	TRANSCRIPTION FACTOR AP-2
1482	14209	28896	5.31	2.0E-30	BE175877.1	EST_HUMAN	GM0-CT0307-310100-158-M03 CT0307 Homo sapiens cDNA
2720	15427	28165	8	2.0E-30	BE765232.1	EST_HUMAN	HS223F051 normalized infant brain cDNA Homo sapiens cDNA
2920	15686	28331	6.39	2.0E-30	AF114156.1	NT	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
3769	16521	29160	2.26	2.0E-30	AW206581.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
4727	17459	30095	1.51	2.0E-30	BE288945.1	EST_HUMAN	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
4727	17459	30096	1.51	2.0E-30	BE288945.1	EST_HUMAN	UI-H-B11-af-c-12-Q-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
6660	19420	32435	0.55	2.0E-30	BF306337.1	EST_HUMAN	60111860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
8375	21068	34208	0.45	2.0E-30	AA019103.1	EST_HUMAN	60111860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
8435	21128	34265	4.66	2.0E-30	C18939.1	EST_HUMAN	601893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138893 5'
							zs68c10.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:363186 5'
							C18939 Human placenta cDNA (TF-ujwara) Homo sapiens cDNA clone GEN-570 C01 5'

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8533	21225	34366	3.61	2.0E-30	BE670617.1	EST_HUMAN	7c37c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8533	21225	34367	3.61	2.0E-30	BE670617.1	EST_HUMAN	7c37c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8897	22547	35741	3.62	2.0E-30	AW971568.1	EST_HUMAN	EST383667 MAGI2 resequences, MAGI2 Homo sapiens cDNA ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
9882	22630	35839	7.37	2.0E-30	AW470791.1	EST_HUMAN	C18839 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-570C01 5'
280	13087	25729	18.33	1.0E-30	C18839.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
525	13309	25942	2.34	1.0E-30	AW468897.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
699	13474	26122	2.62	1.0E-30	AL163203.2	NT	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
2209	14937	27675	7.16	1.0E-30	AA664377.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
2464	15182	27921	2.01	1.0E-30	BF347728.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
3050	15816	28461	0.94	1.0E-30	AA315045.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
7824	20290	33399	2.46	1.0E-30	BF183230.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
12581	25268		6.95	1.0E-30	H55593.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
3748	16501	29135	0.81	9.0E-31	T73025.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
3748	16501	29136	0.81	9.0E-31	T73025.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
8223	20917	34053	0.81	9.0E-31	R18214.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
8223	20917	34054	0.81	9.0E-31	R18214.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
8522	21214		1.63	9.0E-31	Z38293.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
8524	21216	34359	0.48	9.0E-31	AF078779.1	NT	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
1054	13813	26473	2.41	8.0E-31		NT	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
2414	15135		4.6	8.0E-31	AL163208.2	NT	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
4861	17590	30213	1.43	8.0E-31	P23275	SWISSPROT	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
4861	17590	30214	1.43	8.0E-31	P23275	SWISSPROT	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
2674	15383	28123	3.29	7.0E-31	BE326517.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
2674	15383	28124	3.29	7.0E-31	BE326517.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
8300	20964	34130	0.96	7.0E-31	AF208541.1	NT	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
8300	20964	34131	0.96	7.0E-31	AF208541.1	NT	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;

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9166	21838		0.94	7.0E-31	BE408811.1	EST_HUMAN	601304129F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12434	24805	31044	2.26	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3667	16420		2.66	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8053	20747		4.37	6.0E-31	AF055066.1	NT	Homo sapiens MHC class 1 region
8228	20923	34062	0.66	6.0E-31	BE350127.1	EST_HUMAN	ht09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
12169	25195		1.96	6.0E-31	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
187	13000	25840	3.58	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
187	13000	25841	3.58	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8344	21037		0.73	5.0E-31	BF056640.1	EST_HUMAN	7k06f04.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT; contains L1.11 L1 repetitive element;
592	13362		5.18	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1806	14352	27040	0.91	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-LUDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
1810	14550		1.57	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2792	15497		1.23	4.0E-31	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETIMAR) mRNA
12205	24872		1.86	4.0E-31	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12457	24828		1.86	4.0E-31	11430273	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
7239	18924	32998	12.23	3.0E-31	4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8) mRNA
7393	20072	33151	1.28	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8081	20755		2	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
9479	22132	35312	3.7	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10498	23144	36371	0.54	3.0E-31	AA421242.1	EST_HUMAN	zu08d04.t1 Soares_basis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
10527	23224	36459	2.04	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
11101	23771		3.65	3.0E-31	BF035327.1	EST_HUMAN	601459531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
12819	25059		1.68	3.0E-31	AB037683.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
1910	14647	27358	1.37	2.0E-31	AW838171.1	EST_HUMAN	QV24.T0051-280300-111403 L10051 Homo sapiens cDNA
2211	14839	27677	1.09	2.0E-31	AI393388.1	EST_HUMAN	tg44g05.x1 Soares_NFL.T.GBC.S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2339	15062	27800	1.69	2.0E-31	AL119245.1	EST_HUMAN	DKFZp781G1513_11761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781G1513 5'
2442	15161	27898	4.01	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5193	18001	30824	0.81	2.0E-31	AW444486.1	EST_HUMAN	UHH-B13-akb-4-09-UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'
5624	18421	31334	3.57	2.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER29.B3 MER29 repetitive element ;
8975	21865		2.05	2.0E-31	AA877784.1	EST_HUMAN	m0804.s1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
9107	21795	34959	3.84	2.0E-31	7681535	NT	Homo sapiens B9 protein (B9), mRNA
9806	22457	35661	0.94	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
9806	22457	35662	0.94	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
9806	22457	35662	0.94	2.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3688310 5'
9875	22623	35829	2.35	2.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3688310 5'
9875	22623	35830	2.35	2.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3688310 5'
12144	24632		1.56	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12279	25413		1.75	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
15	12842	25458	11.08	1.0E-31	U63183.1	NT	(IMAGE-B1) genes, complete cds
1658	14404	27092	1.35	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1658	14404	27093	1.35	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1658	14404	27094	1.35	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4592	17327	28952	1.15	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547B235 5'
4592	17327	28953	1.15	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547B235 5'
5210	18018	30840	3.79	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-15/289-028-a08_1 ST0220 Homo sapiens cDNA
6042	18822	31782	2.2	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite cb1 repeat region
7189	19875	32948	1	1.0E-31	AF128145.1	NT	Bos laurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
10136	22784	35965	0.51	1.0E-31	U63183.1	NT	(IMAGE-B1) genes, complete cds
10833	23515	36757	2.7	1.0E-31	AI086434.1	EST_HUMAN	q21h03.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN ;
11830	24414	37752	1.48	1.0E-31	U68081.1	NT	Human gemline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB rels, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBV1S1, TCRBV1S2,>
6542	19307	32312	2.38	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
7492	20184		0.86	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2070	14802	27530	2.48	8.0E-32	AI056770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5394	18194	30887	0.97	8.0E-32	AW967214.1	EST_HUMAN	RC2-BN0048-200300-015-004 BN0048 Homo sapiens cDNA
4807	17538	30161	0.98	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
12122	24614		8.19	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphion and neighbouring non-amplified region
2735	15442	28180	1.01	6.0E-32	A1478104.1	EST_HUMAN	hm34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159984 3' similar to contains MER29.13
7266	19950		1.47	6.0E-32	BE888016.1	EST_HUMAN	MER28 repetitive element;
1011	13771	26431	16.78	5.0E-32	AF116627.1	NT	601511630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
910	13677		1.76	4.0E-32	AL163246.2	NT	Homo sapiens PRO1181 mRNA, complete cds
5148	17867		0.91	4.0E-32	A1985593.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
7503	20174	33266	2.94	4.0E-32	11432574	NT	MER18 repetitive element;
7503	20174	33267	2.94	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8257	20951		1.2	4.0E-32	BE064410.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
443	13229	25872	3.7	3.0E-32	Y17293.1	NT	RC4-BT0311-141189-011-R06 BT0311 Homo sapiens cDNA
1437	14184	26870	8.08	3.0E-32	AV731500.1	EST_HUMAN	Homo sapiens FLI-1 gene, partial
9294	21961	35135	8.38	3.0E-32	AV758634.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK07 5'
9294	21961	35136	8.38	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
10843	23525	36768	3.57	3.0E-32	AA77621.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
12146	24634		3.51	3.0E-32	BE279086.1	EST_HUMAN	295607.s1 Soares_fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element;
12507	17899	30586	2.97	3.0E-32	5174574	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12507	17899	30587	2.97	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
12656	24956		2.27	3.0E-32	BE279086.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
6158	18935	31902	0.81	2.0E-32	M35418.1	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6387	19156	32155	5.32	2.0E-32	Z38133.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6387	19156	32156	5.32	2.0E-32	Z38133.1	NT	H.sapiens mRNA for myosin
8176	20870	34003	2.26	2.0E-32	AA114294.1	EST_HUMAN	H.sapiens mRNA for myosin
8176	20870	34004	2.26	2.0E-32	AA114294.1	EST_HUMAN	zn86-c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
11859	24443	37784	2.98	2.0E-32	T18962.1	EST_HUMAN	zn86-c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
12763	25022	30961	2.42	2.0E-32	AV738449.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b12056
							AV738449 CB Homo sapiens cDNA clone CBFBIA08 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12763	25022	30982	2.42	2.0E-32	AV736448.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFIA08 5'
3090	15855		1.67	1.0E-32	BE743298.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
6955	19437	32453	7.02	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8494	21186	34328	8.08	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
3474	16230		4.58	9.0E-33	BE327112.1	EST_HUMAN	hw7c05.x1 NCL_CGAP_LU24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:088539 088539 WW DOMAIN BINDING PROTEIN 11;
6326	19096		4.05	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8687	21379	34523	1.95	9.0E-33	BF347228.1	EST_HUMAN	602021184F1 NCL_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4156870 5'
10701	23392		5.22	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
58	12887	25517	3.14	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
58	12887	25518	3.14	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2158	14888	27622	2.29	7.0E-33	AI590116.1	EST_HUMAN	hw2b09.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element;
2655	15365		6.45	7.0E-33	AV730056.1	EST_HUMAN	AV730088 HTF Homo sapiens cDNA clone HTFAVE08 5'
3236	15988		9.3	7.0E-33	AW971307.1	EST_HUMAN	EST383398 IMAGE resequences, MAGI, Homo sapiens cDNA
8845	21537		1.56	7.0E-33	X54890.1	NT	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphatase) (EC 3.1.3.48)
10732	23419	36660	2.41	7.0E-33	BF347228.1	EST_HUMAN	602021184F1 NCL_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4156870 5'
11213	23876	37162	1.83	7.0E-33	AW971568.1	EST_HUMAN	EST383657 IMAGE resequences, MAGI, Homo sapiens cDNA
12127	24619	31090	4.34	7.0E-33	AA801418.1	EST_HUMAN	hw16h01.s1 NCL_CGAP_P1e1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.1 L1 repetitive element;
3720	16473		0.94	8.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5976	18768	31720	0.96	8.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
5976	18768	31721	0.96	8.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8478	21170	34315	9.33	8.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8603	21295	34438	3.09	8.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
8910	22559	35754	1.12	8.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
9910	22559	35755	1.12	8.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1770	14512		1.46	5.0E-33	BF373515.1	EST_HUMAN	QV1-F10169-100700-271-e02 FT0169 Homo sapiens cDNA
1874	14612		1.19	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1891	14828	27337	1.43	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1891	14828	27338	1.43	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2270	14996		1.29	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C086
10148	22796	36010	0.8	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10148	22796	36011	0.8	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
1106	13863		2.16	4.0E-33	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C007
2121	14852	27581	1.64	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2419	15140		2.02	4.0E-33	AA626821.1	EST_HUMAN	ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element ;
2547	15262	27999	4.16	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4450	17188	29811	2.15	4.0E-33	AW263349.1	EST_HUMAN	U1-H-B12-ah1-c-03-Q-U1 st NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5318	18122	30779	24.73	4.0E-33	AA053053.1	EST_HUMAN	z171a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671_mna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6299	19072	32057	0.87	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6299	19072	32058	0.87	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1067	13825		5.5	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_K1413 Homo sapiens cDNA clone IMAGE:3146286 3' similar to contains MER28.b3 MER28 repetitive element ;
1068	13825		3.89	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_K1413 Homo sapiens cDNA clone IMAGE:3146286 3' similar to contains MER28.b3 MER28 repetitive element ;
2451	15595		0.92	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLCBCF09 3'
10338	22985	36203	1.04	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR-Q13579 Q13579 MARINER TRANSPOSASE ;
102	12843		3.21	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Scores_fetal_heart_NthH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 OFR repetitive element ;
4385	17122		5.39	2.0E-33	BE159039.1	EST_HUMAN	MRO-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
4925	17653	30285	28.91	2.0E-33	AA626883.1	EST_HUMAN	ab51g11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5033	17753	30365	2.75	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5033	17753	30366	2.75	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6329	18099	32087	1.81	2.0E-33	AI277492.1	EST_HUMAN	qb66d01.x1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
8998	21698		2.18	2.0E-33	AI052256.1	EST_HUMAN	cc21d03.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1875973 3' similar to gb:M29536 TRANSITIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
10513	23159	36384	1.48	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
10513	23159	36385	1.48	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
11046	23716	36985	1.26	2.0E-33	AA453847.1	EST_HUMAN	z48f05.a1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:795489 3' similar to TR-G1263081 G1263081 MARINER TRANSPOSASE ;

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8	12835		1.16	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5156	17873	30485	2.46	1.0E-33	4502566	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
5501	18299	31198	0.58	1.0E-33	AF189420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
7307	19990	33087	1.04	1.0E-33	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
8920	25432		0.84	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11292	23953	37251	1.83	1.0E-33	AW996818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
11663	24259	37581	3.32	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12407	24790		2.21	1.0E-33	A1927191.1	EST_HUMAN	w088c06.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:24624103'
12570	12835		4.07	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12602	24914	31005	1.41	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
12780	25034		1.61	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2168	14697	27631	0.96	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
7689	20353	33468	0.86	8.0E-34	BE068882.1	EST_HUMAN	MR4-BT0399-200101001-001-H03 BT0398 Homo sapiens cDNA
1426	14173	26858	2.27	7.0E-34	T70845.1	EST_HUMAN	yJ15e05.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108320 5'
9900	14173	26858	0.56	7.0E-34	T70845.1	EST_HUMAN	yJ15e06.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108320 5'
12191	24662		3.05	7.0E-34	H12896.1	EST_HUMAN	yJ14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
458	13243	25884	2.3	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
458	13243	25885	2.3	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
12011	24544	31107	2.13	6.0E-34	U03686.1	NT	Mus musculus DAB/2J hair-specific (hac1-1) gene
1873	14611		2.9	5.0E-34	7706500	NT	Homo sapiens Npw38-bhding protein NpwBP (LOC51729), mRNA
5002	17725	30328	3.61	5.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP55) mRNA, complete cds
8765	21457	34607	1.37	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10550	23248	38482	2.24	5.0E-34	AB037858.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11219	23882		1.79	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1991	14727	27449	1.84	4.0E-34	A1804687.1	EST_HUMAN	1994c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2249194 3'
5770	18561	31488	0.64	4.0E-34	AA861773.1	EST_HUMAN	81G5c01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407836 3'
8936	21627	34769	1.26	4.0E-34	BF209178.1	EST_HUMAN	601874950F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
6138	18916	31886	0.78	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11100	23770		3.14	3.0E-34	BF035327.1	EST_HUMAN	60145853 IF1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
8850	21541	34887	1.16	2.0E-34	A1678101.1	EST_HUMAN	w335g09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER28 repetitive element;

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8850	21541	34888	1.16	2.0E-34	A1678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
11113	23783	37057	1.34	2.0E-34	P51805	SWISSPROT	MER28.12 MER29 repetitive element
11113	23783	37058	1.34	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1494	14241	26928	6.53	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3683	16416	29055	1.32	1.0E-34	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4051	16796	29425	0.97	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4051	16796	29426	0.97	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4446	17182		3.44	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-H08 BT0508 Homo sapiens cDNA
6047	18827	31788	2.05	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
6047	18827	31789	2.05	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
9225	21904	35078	0.45	1.0E-34	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F6
9596	22249	35434	7.1	1.0E-34	AL036835.1	EST_HUMAN	DKFZp564A1563.1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564A1563 5'
11138	23805	37083	1.39	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11138	23805	37084	1.39	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11153	23820	37100	1.82	1.0E-34	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12372	25350		1.65	1.0E-34	AA807097.1	EST_HUMAN	cc31ct11.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203
12583	24949		4.22	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FL14 PRECURSOR (HUMAN);
3636	16389	28028	1.2	9.0E-35	AW663302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
218	13029		7.71	8.0E-35	6031190	NT	h77b08.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2968787 5'
1730	14472	27171	3.43	8.0E-35	BF589937.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
1730	14472	27172	3.43	8.0E-35	BF589937.1	EST_HUMAN	na33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912
4814	17545	30170	2.69	8.0E-35	BF183195.1	EST_HUMAN	075912 DIACYLGLYCEROL KINASE IOTA;
10588	23283	36522	2.42	8.0E-35	BE783480.1	EST_HUMAN	na33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:4040324 5'
12119	24811		3.95	8.0E-35	BF568282.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
6393	19162	32163	2.05	7.0E-35	11425417	NT	601238468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
1391	14138	26815	1.83	6.0E-35	AA757115.1	EST_HUMAN	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300860 3'
1960	14686	27409	2.09	8.0E-35	6005975	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
4030	16775	29406	0.84	6.0E-35	AW297191.1	EST_HUMAN	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone '3069397 3'
							Homo sapiens zinc finger protein 208 (ZNF208), mRNA
							UI-H-BW0-ajd-d-09-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7798	20493	33615	3.84	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8610	21302	34445	0.93	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
8610	21302	34446	0.93	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
9565	22218	35403	0.86	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0368 gene, partial cds
9803	22454	35656	3.17	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
1704	14447	27146	1.36	5.0E-35	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2787	15492	28232	1.07	5.0E-35	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
3008	15775	28424	1.7	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4376	17113	29746	1.7	5.0E-35	AF023268.1	NT	Homo sapiens cdk2 kinase (CLK2), protein1, cdk1, glucocorticoid-induced serine/threonine kinase (GSK3), and metaxin genes, complete cds; metaxin pseudogene and glucocorticoid-induced serine/threonine kinase (GSK3) gene, partial cds
8084	20778		3.99	5.0E-35	BE890992.1	EST_HUMAN	601431884F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8109	20803	33936	2.35	5.0E-35	A1208765.1	EST_HUMAN	qg38a015.x1 Soares Testis, NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
8109	20803	33937	2.35	5.0E-35	A1208765.1	EST_HUMAN	qg38a015.x1 Soares Testis, NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
11130	23798		2.46	5.0E-35	AA001788.1	EST_HUMAN	zh84f12.r1 Soares fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:428015 5'
1413	14161	26845	16.86	4.0E-35	BE257907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1811	14551	27265	4.87	4.0E-35	H91193.1	EST_HUMAN	y488a07.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTRS repetitive element ;
4753	17485		0.72	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7108	19796		1.81	4.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NC1_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
8416	21109	34248	8.88	4.0E-35	AL046596.1	EST_HUMAN	DKFZp434L148.r1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp434L148 5'
11728	24322	37646	1.38	4.0E-35	AW303317.1	EST_HUMAN	xv1763.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element ;
1573	14320	27006	7.78	3.0E-35	BE268182.1	EST_HUMAN	601126260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2330	15055		1.5	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5256	18062	30690	31.47	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3665381 3' similar to TR:Q9QZH7
5256	18062	30691	31.47	3.0E-35	BF433100.1	EST_HUMAN	Q9QZH7 F-BOX PROTEIN FBL2. ; 7n25a08.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3665381 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9388	22050		1.42	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10074	22722	35939	1.12	3.0E-35	AW003063.1	EST_HUMAN	wr03a05.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10286 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE.]; K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
106	15535	25567	1.88	2.0E-35	N88965.1	EST_HUMAN	REPETITIVE ELEMENT
1165	13919	26582	1.55	2.0E-35	T11909.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
2215	14943	27883	5.73	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gab2, complete cds
3306	16068	28714	1.12	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3306	16068	28715	1.12	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3545	16300		0.94	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3890	16840	29279	0.78	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3890	16840	29280	0.78	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4621	17356		2.57	2.0E-35	H49239.1	EST_HUMAN	Yt19a12.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
5486	18294	31192	2.7	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-198-b04 BT0701 Homo sapiens cDNA
7004	19696	32749	0.95	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7004	19696	32750	0.95	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7775	20471	33593	0.45	2.0E-35	AV723718.1	EST_HUMAN	AV723718 HTB Homo sapiens cDNA clone HTBAYA10 5'
7775	20471	33594	0.45	2.0E-35	AV723718.1	EST_HUMAN	AV723718 HTB Homo sapiens cDNA clone HTBAYA10 5'
10697	23388	36826	2.24	2.0E-35	X59417.1	NT	H. sapiens PROS-27 mRNA
11817	18294	31192	1.28	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-198-b04 BT0701 Homo sapiens cDNA
11889	16066	28714	1.72	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11889	16066	28715	1.72	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12062	24577	31120	1.36	2.0E-35	BE904978.1	EST_HUMAN	601498774FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12062	24577	31121	1.36	2.0E-35	BE904978.1	EST_HUMAN	601498774FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12572	24900		5.96	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
12689	15535	25567	1.56	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
45	12874	25496	6.81	1.0E-35	AA631949.1	EST_HUMAN	REPETITIVE ELEMENT
45	12874	25497	6.81	1.0E-35	AA631949.1	EST_HUMAN	fmfcr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
735	19509	26165	19.5	1.0E-35	AW388473.1	EST_HUMAN	fmfcr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1

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735	13509	26166	18.5	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA
889	13658		1.3	1.0E-35	T87947.1	EST_HUMAN	y83a01.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:116762 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2644	15258	27986	1.68	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2770	15475	28217	1.09	1.0E-35	BE350127.1	EST_HUMAN	h108q01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28 b3 MER29 repetitive element ;
2770	15475	28218	1.09	1.0E-35	BE350127.1	EST_HUMAN	h108q01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28 b3 MER29 repetitive element ;
3140	15804	28549	1.81	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCCEB1L) mRNA
3161	15924	28570	3.3	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEP08 3'
3161	15924	28571	3.3	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEP08 3'
4388	17125	29756	3.93	1.0E-35	7656905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
4388	17125	29757	3.93	1.0E-35	7656905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
5423	18222	30934	1.41	1.0E-35	11526238	NT	Homo sapiens chromatin assembly factor 1, subunit B (p80) (CHAF1B), mRNA
7383	20063	33141	0.86	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
7541	20211	33311	1.18	1.0E-35	11418002	NT	Homo sapiens KIAA0845 gene product (KIAA0845), mRNA
9442	25125	35297	2.16	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAGE3 Homo sapiens cDNA clone PLACE3000382 3'
9442	25125	35298	2.16	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAGE3 Homo sapiens cDNA clone PLACE3000382 3'
10477	23123	36352	0.7	1.0E-35	BF589594.1	EST_HUMAN	naa08a08.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341 O31341 BETA-GALACTOSIDASE ;
10477	23123	36353	0.7	1.0E-35	BF589594.1	EST_HUMAN	naa08a08.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341 O31341 BETA-GALACTOSIDASE ;
11758	24348	37680	1.46	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
11758	24349	37681	1.46	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
11768	24359		1.91	1.0E-35	AI525119.1	EST_HUMAN	promme-7.D01.7 bvtumor Homo sapiens cDNA 5'
11917	25313		1.37	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12121	24613		1.83	1.0E-35	11418110	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
12471	24837		2.13	1.0E-35	BE792832.1	EST_HUMAN	60158483F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938885 5'
9129	21817	34983	0.56	8.0E-36	AA349480.1	EST_HUMAN	EST54898 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
2831	15697	28344	1.1	7.0E-36	AW857579.1	EST_HUMAN	CM1-CT0315-091288-053-407 CT0315 Homo sapiens cDNA
3116	15881		3.84	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7554	20224	33327	5.92	7.0E-36	U06872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
7554	20224	33328	5.92	7.0E-36	U06872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN

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1998	14734	27456	2	6.0E-36	7706822	NT	Homo sapiens nhlh2 (NINJ2), mRNA
2418	15139		5.58	6.0E-36	AB035346.1	NT	Homo sapiens TOL9 gene, exon 12
3630	16383	28023	0.71	6.0E-36	BF515101.1	EST_HUMAN	U1H-BW1-ant-c-12.0.U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5248	18054	30682	3.54	6.0E-36	AI435169.1	EST_HUMAN	tr83b06.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb:IM1849 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7009	19701	32756	3.57	6.0E-36	AW780143.1	EST_HUMAN	h06h02.x1 NCI_CGAP_Cot4 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52292 IMPORTIN ALPHA-2 SUBUNIT ;
8550	21242	34385	2.33	6.0E-36	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
10125	22773		0.51	6.0E-36	C16827.1	EST_HUMAN	C16827 Clontech human aorta polyA+ mRNA (p5572) Homo sapiens cDNA clone GEN-535C11 5'
11536	24136	37443	3.11	6.0E-36	AI380499.1	EST_HUMAN	tr95c09.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2 MER9 repetitive element ;
134	12949	25592	10.74	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2755	15460	28202	5.75	5.0E-36	BE388436.1	EST_HUMAN	801285507F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3599	16352	28991	1.45	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4736	17468	30104	2.15	5.0E-36	5729729	NT	Homo sapiens AP15-like 1 (AP15L1), mRNA
4736	17468	30105	2.15	5.0E-36	5729729	NT	Homo sapiens AP15-like 1 (AP15L1), mRNA
7686	20360	33494	0.61	5.0E-36	11076227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
11887	12849	25592	3.53	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12168	24650	31103	3.45	5.0E-36	11417862	NT	Homo sapiens calcitriol binding protein 1 (KIAA0330), mRNA
1203	13955	26819	1.69	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1423	14170	26856	1.03	4.0E-36	P10266	SWISSPROT	
1640	14386	27074	1.61	4.0E-36	BE382574.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3626386 5'
2219	14947		2.13	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3349	16108	28763	0.82	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3349	16108	28764	0.82	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5629	18425		0.84	4.0E-36	R84023.1	EST_HUMAN	Y1805.r1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:139713 5'
5964	18746	31707	2.33	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
7553	20223	33326	1.63	4.0E-36	M33320.1	NT	Human platelet Glycoprotein Iib (GP1Ib) gene, exons 2-28
8453	21145	34285	1.62	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8453	21145	34286	1.62	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10909	23589	36835	2.84	4.0E-36	AA400370.1	EST_HUMAN	z08c10.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
12183	24655		2.09	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFA1C2), mRNA
12227	25199		7.3	4.0E-36	AV753628.1	EST_HUMAN	AV753628 TP Homo sapiens cDNA clone TPGABH01 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12798	25047		1.44	4.0E-36	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
880	13455	28100	2.58	3.0E-36	AF099810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
1484	14231	26917	1.32	3.0E-36	AF110238.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1484	14231	26918	1.32	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2297	15022	27757	1.21	3.0E-36	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4467	17203	28929	5.88	3.0E-36	10181139	NT	Mus musculus Junctophilin 1 (Jp1-pending), mRNA
11050	23720	36991	1.59	3.0E-36	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
3167	15930	28578	2.38	2.0E-36	BE259287.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
4904	17631	30246	5.45	2.0E-36	AW880376.1	EST_HUMAN	QVQ-OT0030-240300-174-H04 OT0030 Homo sapiens cDNA
5398	18198	30892	3.1	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
5758	18550	31471	3.95	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBB128 5' end
6481	18248	32248	12.22	2.0E-36	T68629.1	EST_HUMAN	Yc4407.1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
9288	21955	35128	1.07	2.0E-36	BF512794.1	EST_HUMAN	UIH-BW 1-aru-a-11-0-U1.a1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9449	21999	35172	0.79	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
865	13634	26304	0.79	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
2141	14871	27603	1	1.0E-36	BE409310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2189	14928	27604	1	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-H07 HT0217 Homo sapiens cDNA
3339	16099	27604	1.36	1.0E-36	BF673761.1	EST_HUMAN	RC1-HT0217-131189-021-H07 HT0217 Homo sapiens cDNA
5810	18599	31527	1.16	1.0E-36	AF156962.1	NT	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
			1.28	1.0E-36	4827084	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6090	18888		4.19	1.0E-36	AI887714.1	EST_HUMAN	Homo sapiens GC8 Homo sapiens cDNA clone IMAGE:2307882 3' similar to contains Alu repetitive element
6286	18069	32052	1.21	1.0E-36	R25012.1	EST_HUMAN	y636g10.1 Scores Infant brain INIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6286	18068	32053	1.21	1.0E-36	R25012.1	EST_HUMAN	y636g10.1 Scores Infant brain INIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6582	18345	32359	0.73	1.0E-36	AL120542.1	EST_HUMAN	SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
7326	20009	33087	0.85	1.0E-36	11428108	NT	DKFZp761A229.1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A229 5'
7326	20009	33088	0.85	1.0E-36	11428108	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7860	20555	33679	5.13	1.0E-36	AA148034.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7860	20555	33680	5.13	1.0E-36	AA148034.1	EST_HUMAN	z051a12.1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:580398 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
7952	20647	33770	1.34	1.0E-36	AA420467.1	nc60608.t1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745670
7952	20647	33771	1.34	1.0E-36	AA420467.1	nc60608.t1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745670
8079	20773	33902	0.61	1.0E-36	AU141688.1	AU141688 THYR01 Homo sapiens cDNA clone THYR01001033 5'
8079	20773	33903	0.61	1.0E-36	AU141688.1	AU141688 THYR01 Homo sapiens cDNA clone THYR01001033 5'
8927	21618	34762	2.71	1.0E-36	AW103658.1	xs82507.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10014	22662	35878	3.88	1.0E-36	BF364169.1	QV3-NN1023-010600-198-H01 NN1023 Homo sapiens cDNA
10226	22874	36086	0.56	1.0E-36	AW855868.1	RC3-CT0278-040500-017-e10 CT0278 Homo sapiens cDNA
10226	22874	36087	0.56	1.0E-36	AW855868.1	RC3-CT0278-040500-017-e10 CT0278 Homo sapiens cDNA
10867	23547	36795	3.3	1.0E-36	AW897636.1	GM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11354	24044	37347	4.17	1.0E-36	AW504143.1	UI-HF-BN0-ale-c-03-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
11393	23999	37302	1.45	1.0E-36	AB05536.1	RC-BT091-210199-110 BT091 Homo sapiens cDNA
11393	23999	37303	1.45	1.0E-36	AB05536.1	RC-BT091-210199-110 BT091 Homo sapiens cDNA
12080	24576		3.81	1.0E-36	11418177	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12501	24655		3.03	1.0E-36	AL163213.2	Homo sapiens chromosome 21 segment HS21C013
12747	25011		3.23	1.0E-36	AF202723.1	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7281	18965	33042	2.12	9.0E-37	AW009277.1	ws80607.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
7281	18965	33043	2.12	9.0E-37	AW009277.1	ws80607.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
12309	24733		1.35	9.0E-37	W22618.1	73D4 Human retina cDNA Tsp508L-cleaved sublibrary Homo sapiens cDNA not directional
3350	16109	28765	0.99	8.0E-37	4757979	Homo sapiens chimerin (chimerin) 2 (CHN2) mRNA
5168	17977		1.58	8.0E-37	BE698077.1	GM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA
5738	18530	31451	3.75	8.0E-37	BE350127.1	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5738	18530	31452	3.75	8.0E-37	BE350127.1	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5787	18578	31507	8.24	8.0E-37	AW840840.1	MER29 repetitive element;
7784	20478	33804	6.22	8.0E-37	X87344.1	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
1282	14011		3.03	7.0E-37	AL042800.1	Hi.sapiens DNA, DMB, HLA-Z1, JPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1738	14480	27179	0.97	7.0E-37	AF111167.2	DKFZp434E0422_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0422 5'
1738	14480	27180	0.97	7.0E-37	AF111167.2	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10657	23348	36585	8.69	7.0E-37	AB17700.1	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene

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10811	23494	38729	2.25	7.0E-37	AI538702.1	EST_HUMAN	hm87g03.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element ;
8338	21031	34188	1.34	6.0E-37	AF169689.1	NT	Homo sapiens protocadherin alpha 10 alternate isoform (PODH-alpha10) mRNA, complete cds
12824	24829		2.94	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 urea-B4 domain protein 2 (SUN2) mRNA, partial cds
6002	18783	31744	3.9	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6002	18783	31745	3.9	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8654	21346	34490	0.9	5.0E-37	AV750211.1	EST_HUMAN	AV750211 NPC Homo sapiens cDNA clone NPC8GH09 5'
10837	23519		4	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
12055	24572		6.86	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2423	15144	27877	2.12	4.0E-37	AA702794.1	EST_HUMAN	z990404.at Soares_fetal_liver_spleen_1INFL_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6194	18970	31945	0.61	4.0E-37	AW784502.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9296	21935	35109	0.74	4.0E-37	AA843806.1	EST_HUMAN	ak09a02.s1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2010	14745	27472	3.2	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2010	14745	27473	3.2	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2965	15731		3.15	3.0E-37	AW961150.1	EST_HUMAN	EST373222 MAGe resequences, MAGF Homo sapiens cDNA
6774	18565	31494	0.92	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone IMAGE:2373898 3' similar to TR:Q19537
7455	20129	33221	0.71	3.0E-37	AI749952.1	EST_HUMAN	al34c05.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373898 3' similar to TR:Q19537
372	13197	25842	0.68	2.0E-37	D89790.1	NT	Q13537 SIMILAR TO POGO ELEMENT ;
372	13197	25843	0.68	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1058	13816	28477	2.64	2.0E-37	AU131202.1	EST_HUMAN	Homo sapiens mRNA for AML1, complete cds
1058	13816	28478	2.64	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1856	14892	27405	1.67	2.0E-37	AL163247.2	NT	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
3873	16623	29261	4.78	2.0E-37		NT	Homo sapiens chromosome 21 segment HS21C047
4988	17693		0.93	2.0E-37	AL163284.2	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
5304	18108		0.66	2.0E-37	BF038327.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
6561	19328	32333	3.46	2.0E-37	AA346720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
7895	20590	33720	0.46	2.0E-37	BE537764.1	EST_HUMAN	601458331F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
7895	20590	33721	0.46	2.0E-37	BE537764.1	EST_HUMAN	601087534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
7937	20632	33759	2.88	2.0E-37	BF204032.1	EST_HUMAN	601087534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
11549	24148	37459	11.22	2.0E-37	AF176013.1	NT	601889157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111408 5'
12784	25037		3.54	2.0E-37		NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
2081	14813	27546	4.93	1.0E-37	AL163281.2	NT	Homo sapiens pectadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA

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3192	15955		1.06	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-018-h03 CT0347 Homo sapiens cDNA
3943	16893	29332	0.72	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4888	17615	30234	2.35	1.0E-37	BF371719.1	EST_HUMAN	QV6-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
5914	18699		0.94	1.0E-37	7305360	NT	Mus musculus oligodendrocyte (Olig), mRNA
8113	20807	33940	1.25	1.0E-37	BE546032.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
							zp21b02.1 Stralagene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:610059 5' similar to
							contains L1.12 L1 repetitive element;
8634	21326	34468	2.67	1.0E-37	AA171406.1	EST_HUMAN	Human somatic cytochrome c (HCT) processed pseudogene, complete cds
10597	23291	36529	2.96	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HCT) processed pseudogene, complete cds
12363	24766		2.81	1.0E-37	BE771814.1	EST_HUMAN	OM3-FT0086-140700-243-d07 FT0086 Homo sapiens cDNA
5690	18483	31402	2	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
1200	13952	26616	2.02	8.0E-38	BF346221.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2502	15219	27962	1.8	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NC1_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4153992 5'
12420	13952	26616	1.6	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4197	16938	29563	0.73	7.0E-38	H19092.1	EST_HUMAN	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
5039	17758		1.31	7.0E-38	AF287263.1	NT	601456722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5'
3037	15803	28450	1.2	8.0E-38	BF033033.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5502	18300	31199	1.6	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5502	18300	31200	1.6	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7226	19913	32886	0.57	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
11918	24480		2.57	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12395	24783	31038	12.78	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P204, complete cds
12767	25161	30900	1.7	6.0E-38	AB002059.1	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
710	13484	26133	1.38	5.0E-38	AW971819.1	EST_HUMAN	EST383308 IMAGE resequences, MAGL Homo sapiens cDNA
2455	15173	27912	0.99	5.0E-38	AJ237740.1	NT	Homo sapiens RIBLIR gene (partial), exon 8
3849	16446	29086	0.85	5.0E-38	7549804	NT	Homo sapiens delodinate, iodotyrosine, type II (DIO2), transcript variant 2, mRNA
3917	16867	29307	0.92	5.0E-38	T83107.1	EST_HUMAN	yd40407.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110749 5' similar to
							SP-OLF3_MOUSE P23275 OLFATORY RECEPTOR ;
3917	16867	29308	0.92	5.0E-38	T83107.1	EST_HUMAN	yd40407.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110749 5' similar to
8930	19666	32712	1.48	5.0E-38	BE871610.1	EST_HUMAN	SP-OLF3_MOUSE P23275 OLFATORY RECEPTOR ;
116	12936	25575	4.56	4.0E-38	Z25466.1	NT	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
116	12936	25576	4.59	4.0E-38	Z25466.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2093	14824		5.25	3.0E-38	AF003530.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
3684	16437		2.19	3.0E-38	7549807	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions

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3836	16587	29224	1.76	3.0E-38	P5338	SWISSPROT	SSU72 PROTEIN
3836	16587	29225	1.76	3.0E-38	P5338	SWISSPROT	SSU72 PROTEIN
4574	17309		1.47	3.0E-38	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6655	25097	32430	8.11	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7144	19831	32900	0.56	3.0E-38	AW302461.1	EST_HUMAN	xc04401.x1 NCI_CGAP_Brm53 Homo sapiens cDNA clone IMAGE:2827009 3'
7488	20160	33252	8.26	3.0E-38	BF373694.1	EST_HUMAN	CM3-FT0181-140700-241-407 FT0181 Homo sapiens cDNA
8548	21240	34383	2.1	3.0E-38	H85494.1	EST_HUMAN	y68804.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:249775 5'
8548	21240	34384	2.1	3.0E-38	H85494.1	EST_HUMAN	y68804.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:249775 5'
9872	22522		2.24	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12630	17896	30488	1.65	3.0E-38	11435947	NT	Homo sapiens chromosome 21 segment HS21C048
49	12878	25504	1.4	2.0E-38	AL163248.2	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1358	14106	26781	2.99	2.0E-38	5902097	NT	zw30d01.11 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
1641	14387	27075	2.21	2.0E-38	AA437353.1	EST_HUMAN	SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1641	14387	27076	2.21	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.11 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
2408	15129	27865	1.45	2.0E-38	W76571.1	EST_HUMAN	SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
5632	18427	31339	0.69	2.0E-38	Z26634.2	NT	z66609.11 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:345664 5'
5632	18427	31340	0.69	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7619	20285	33395	1.46	2.0E-38	AV721103.1	EST_HUMAN	Homo sapiens mRNA for ankyrin B (440 kDa)
8382	21075		4.38	2.0E-38	BE165980.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8793	21485	34631	0.56	2.0E-38	FO6450.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8864	21555	34700	2.04	2.0E-38	AF069755.1	NT	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
9121	21809		1.06	2.0E-38	BE22256.1	EST_HUMAN	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
10346	22993	36212	1.71	2.0E-38	D63479.2	NT	hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710
11200	23885	37151	1.37	2.0E-38	AA595480.1	EST_HUMAN	GUO POLYPROTEIN ;
11200	23885	37152	1.37	2.0E-38	AA595480.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11472	24073	37382	5.79	2.0E-38	BE1712760.1	EST_HUMAN	nc34g03.s1 NCI_CGAP_P23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
11638	24235	37557	3.52	2.0E-38	AF190501.1	NT	E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE ;
							nc34g03.s1 NCI_CGAP_P23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
							E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE ;
							QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA
							Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11638	24235	37558	3.52	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11971	24517		3.05	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAHX07 5'
11973	24518		2.06	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12260	24705	31081	6.45	2.0E-38	H55941.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
12323	24742		1.43	2.0E-38	S74903.1	NT	E1 beta-pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
12777	25031		3.76	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1071	13829		2.55	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.1 Scores Testis_NHT Homo sapiens cDNA clone IMAGE:742639 5' similar to contains element
1982	14728	27450	2.53	1.0E-38	4885288	NT	MER19 repetitive element;
2012	14747	27475	1.11	1.0E-38	7681969	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2489	15216	27860	2.34	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4290	17029	29655	1.23	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4558	17263	29921	1	1.0E-38	8922543	NT	Homo sapiens chromosome 21 segment HS21C003
5937	18719	31877	4.71	1.0E-38	7305360	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5937	18719	31878	4.71	1.0E-38	7305360	NT	Mus musculus otogelin (Obog), mRNA
7304	19987	33063	3.15	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9051	21740	34898	0.71	1.0E-38	11422260	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9310	21977	35150	6.13	1.0E-38	BE350127.1	EST_HUMAN	h009p01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.63
10301	22948	36163	0.58	1.0E-38	R18512.1	EST_HUMAN	MER29 repetitive element;
11588	24187	37503	1.28	1.0E-38	7662109	NT	yf98b08.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30488 5'
12118	25140		2.2	1.0E-38	AL163204.2	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
53	12882	26510	15.3	8.0E-39	4502312	NT	Homo sapiens chromosome 21 segment HS21C084
1373	14121	26796	1.45	8.0E-39	4758229	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1821	14560		1.27	8.0E-39	AJ823404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
2087	14819	27550	5.79	7.0E-39	AL163227.2	NT	wh3f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
10711	23400	36639	2.24	8.0E-39	BF331826.1	EST_HUMAN	POL PROTEIN;
12698	24978		1.66	8.0E-39	BE970394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
987	13750	26412	1.57	5.0E-39	AF003528.1	NT	QV1-BT0631-040800-357402 BT0631 Homo sapiens cDNA
							7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6
							CE00828;
							Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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2984	15750	28397	8.62	5.0E-39	A1750154.1	EST_HUMAN	at3804.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
12410	24793		2.04	5.0E-39	11420289	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ,contains LTR7.11 LTR7 repetitive element ;
537	13320	25954	6.78	4.0E-39	AB015610.1	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
3559	16314	28961	0.97	4.0E-39	AL163210.2	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
7974	20669	33791	1.27	4.0E-39	AA632948.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
9228	21907	35078	0.56	4.0E-39	D84116.1	NT	as82q04.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
9228	21907	35078	0.56	4.0E-39	D84116.1	NT	OFR.b1 OFR repetitive element ;
12427	24802		4.47	4.0E-39	11418177	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12534	24878		2.71	4.0E-39	BE836452.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
46	12875	25498	14.86	3.0E-39	AA631949.1	EST_HUMAN	QV0-FN0063-260600-278-c08 FN0063 Homo sapiens cDNA
46	12875	25499	14.86	3.0E-39	AA631949.1	EST_HUMAN	frf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
46	12875	25500	14.86	3.0E-39	AA631949.1	EST_HUMAN	frf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11963	24511	37257	4.35	3.0E-39	A1084557.1	EST_HUMAN	frf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11963	24511	37258	4.35	3.0E-39	A1084557.1	EST_HUMAN	ox83a10.s1 Soares_NHMPV_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
12006	24541		5.82	3.0E-39	H37803.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
877	13646		5.8	2.0E-39	BE409203.1	EST_HUMAN	yp51c08.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:190954 3'
892	13681		14.08	2.0E-39	A1525119.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1009	13769		4.2	2.0E-39	AF000573.1	NT	promine-7.D01.r b1 tumor Homo sapiens cDNA 5'
1520	14287		11.91	2.0E-39	AW372318.1	EST_HUMAN	Homo sapiens homogenisate 1,2-dioxigenase gene, complete cds
1866	14702	27419	3.28	2.0E-39	AA720574.1	EST_HUMAN	PM0-BT0340-211259-003-002 BT0340 Homo sapiens cDNA
2834	16346	28089	1.84	2.0E-39	AL163246.2	NT	nw21g02.s1 NCJ_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4370	17108	29743	1.48	2.0E-39	BF370207.1	EST_HUMAN	THR repetitive element ;
5403	18203	30907	4.21	2.0E-39	AA508880.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
7269	19653	33028	2.36	2.0E-39	AA080867.1	EST_HUMAN	RC4-FN0037-290700-011-e10 FN0037 Homo sapiens cDNA
7431	20108	33195	0.72	2.0E-39	AL163202.2	NT	ng86103.s1 NCJ_CGAP_P16 Homo sapiens cDNA clone IMAGE:941693
7431	20108	33196	0.72	2.0E-39	AL163202.2	NT	zn08102.11 Striatagene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:548651 5'
8209	20903	34038	0.67	2.0E-39	AF078779.1	NT	Homo sapiens chromosome 21 segment HS21C002
8394	22056		0.55	2.0E-39	AA984531.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
							Rattus norvegicus putative four repeat ion channel mRNA, complete cds
							am88c11.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630198 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9526	22179		0.73	2.0E-39	AF686660.1	EST_HUMAN	tu35e03.x1 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:2253052 3'
11409	24058	37385	2.97	2.0E-39	D86984.1	NT	Human mRNA for KIAA0209 gene, partial cds
1503	14249	26336	3.71	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1503	14249	26337	3.71	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1521	14268	26952	4.24	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4098	16841	29467	0.7	1.0E-39	11430303	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
4098	16841	29468	0.7	1.0E-39	11430303	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
4612	17347	29980	2.5	1.0E-39	AW951995.1	EST_HUMAN	EST384065 MAGE resequences, MAGB Homo sapiens cDNA
4612	17347	29981	2.5	1.0E-39	AW951995.1	EST_HUMAN	EST384065 MAGE resequences, MAGB Homo sapiens cDNA
4634	17388	30021	8.86	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
5274	18079	30735	1.02	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5274	18079	30736	1.02	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5542	18339	31246	1.97	1.0E-39	T80878.1	EST_HUMAN	Alu repetitive element, contains LTR1 repetitive element ;
5578	18375	31287	4.84	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5578	18375	31288	4.84	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6727	19561		1.57	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7264	19948	33025	1.8	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8482	21154	34297	1.03	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K3 PRECURSOR (RNAse K6)
12357	24761		1.34	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
542	13325	25957	1.68	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1213	13963	26629	15.14	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1213	13963	26630	15.14	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1432	14179	26865	6.54	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3765	16517	26155	0.97	9.0E-40	4503784	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3956	17878	29343	3.99	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3036	15802	28449	0.84	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 Hela cDNA Library/Homo sapiens cDNA clone 7H15A04
3903	16653		3.35	8.0E-40	BE39654.1	EST_HUMAN	901288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
7616	20282	33390	2.03	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds

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7616	20282	33391	2.03	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
10813	23496	36732	2.27	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2730	15437	28174	8.41	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2730	15437	28175	8.41	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
5849	18636		2.24	6.0E-40	BE504769.1	EST_HUMAN	h240g01.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:3210480 3'
6055	18835	32522	1.11	6.0E-40	7661989	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
6836	19498	32523	3.56	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
9877	22527	35722	10.25	6.0E-40	AV653028.1	EST_HUMAN	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
9877	22527	35723	10.25	6.0E-40	AV653028.1	EST_HUMAN	Homo sapiens GLC Homo sapiens cDNA clone GLCDGF04 3'
1869	14607	27318	1.78	4.0E-40	AI699005.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2101	14832		2.27	4.0E-40	AF003528.1	NT	h91501.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL. PROTEIN. ;
4356	17094	28729	9.08	4.0E-40	7662117	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7786	20481	33606	0.5	4.0E-40	AU127831.1	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7890	20585	33714	6.22	4.0E-40	AA742809.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8953	21644	34793	5.17	4.0E-40	BE009416.1	EST_HUMAN	nv34e10.r1 NCL CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
8953	21644	34794	5.17	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10616	23309	36548	3.03	4.0E-40	AW841585.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
4111	16854	28481	1.02	3.0E-40	AI925949.1	EST_HUMAN	RC1-CN0017-120200-012-e04 GN0017 Homo sapiens cDNA
6543	18308	32313	7.02	3.0E-40	11417342	NT	wh1207.x1 NCL CGAP_K0111 Homo sapiens cDNA clone IMAGE:2380549 3'
8280	20974	34115	3.62	3.0E-40	5454167	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8868	21559	34704	1.25	3.0E-40	AF078779.1	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9111	21799	34963	1.42	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11232	23895	37182	8.36	3.0E-40	6003813	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11563	24162	37473	2.23	3.0E-40	AW118799.1	EST_HUMAN	Homo sapiens serine threonine protein kinase (NDR), mRNA
317	13120		8.63	2.0E-40	AI223036.1	EST_HUMAN	xd96h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804 Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS ;
							q952h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'

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777	13549		1.61	2.0E-40	AW303888.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
1818	14557		0.82	2.0E-40	AV731601.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S5 ;
1927	14663	27375	1.58	2.0E-40		NT	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1927	14663	27376	1.58	2.0E-40		NT	Homo sapiens prolesome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2064	14796	27522	1.21	2.0E-40	AI988562.1	EST_HUMAN	Homo sapiens prolesome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2166	14895	27630	2.48	2.0E-40	5453592.1	EST_HUMAN	wf90a11.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91829 Q91829
2695	15404		1.44	2.0E-40	BE275932.1	EST_HUMAN	ZINC FINGER PROTEIN ;
3123	15888	28529	4.28	2.0E-40	5453592.1	EST_HUMAN	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4843	17573	30197	1.66	2.0E-40	AL163280.2	NT	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
4843	17573	30198	1.68	2.0E-40	AA225989.1	EST_HUMAN	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
863	13632		1.78	1.0E-40	BF036881.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2627	15339	28083	0.93	1.0E-40		EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2692	15401		1.34	1.0E-40	BE018348.1	EST_HUMAN	nc09a09.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2741	15447	28185	1.18	1.0E-40	BF541030.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
2741	15447	28186	1.18	1.0E-40	BF541030.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
3292	16053		1.27	1.0E-40	4507142	NT	SYNTAXIN 17 ;
4571	17306	29934	4.52	1.0E-40	4508012	NT	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
6161	18938	31907	0.75	1.0E-40	W92708.1	EST_HUMAN	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
6161	18938	31908	0.75	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens sorting nexin 3 (SNX3) mRNA
6987	19680	32727	1.77	1.0E-40	AA573201.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6987	19680	32728	1.77	1.0E-40	AA573201.1	EST_HUMAN	zh79f11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7133	19820	32866	0.69	1.0E-40	P26508	SWISSPROT	zh79f11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
10834	23516	36758	8.34	1.0E-40	AU146345.1	EST_HUMAN	zh79f11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
11694	24289	37612	1.89	1.0E-40	AA614255.1	EST_HUMAN	h42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
11694	24289	37613	1.89	1.0E-40	AA614255.1	EST_HUMAN	h42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
12376	25274		10.09	1.0E-40	BF334112.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]
7822	20517	33643	1.62	8.0E-41	AL163203.2	NT	AU146345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
							np09h03.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:1115861 similar to TR:G1138406
							G1138406 KIAA0173 PROTEIN ;
							np09h03.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:1115861 similar to TR:G1138406
							G1138406 KIAA0173 PROTEIN ;
							MR2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C003

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
809	15553	26246	1.24	7.0E-41	A934384.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
809	15553	26247	1.24	7.0E-41	A934384.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
4609	17344	29976	0.92	7.0E-41	BE388592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
4609	17344	29977	0.92	7.0E-41	BE388592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
5183	17991	30507	1.2	7.0E-41	11545770	NT	Homo sapiens hypodermic protein FLJ13188 (FLJ13188), mRNA
5918	18703	31656	3.49	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6260	19034	32009	0.61	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
6895	17971	30528	0.88	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11411	24060	37366	2.23	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
11631	24228	37552	1.73	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12782	25271		4.35	7.0E-41	11417972	NT	Homo sapiens pascadillo (zetafish) homolog 1, containing BRCT domain (PES1), mRNA
274	13061	25724	1.19	6.0E-41	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2104	14835	27569	2.04	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4433	17169	29797	0.91	6.0E-41	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682877 5'
7871	20566	33692	1.44	6.0E-41	BF513783.1	EST_HUMAN	UHH-BW1-amp-b-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
1795	14535	27244	1.11	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:79628 3'
4087	16830		1.07	5.0E-41	4885638	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6452	19220		2.26	5.0E-41	BE067042.1	EST_HUMAN	PMA-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
382	13169		2.42	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1076	13834	26492	1.26	4.0E-41	AU118344.1	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005563 5'
1388	14135	26810	15.51	4.0E-41	A1027117.1	EST_HUMAN	ow45e06.s1 Soares_parityrdd_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1849794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE ; contains LTR5.b1 LTR5 repetitive element ;
1388	14135	26811	15.51	4.0E-41	A1027117.1	EST_HUMAN	ow45e06.s1 Soares_parityrdd_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1849794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE ; contains LTR5.b1 LTR5 repetitive element ;
1403	14150	26830	1.88	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1632	14378	27065	6.08	4.0E-41	A1500408.1	EST_HUMAN	trn96c04.x1 NCI_CGAP_Brr25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element ;
2891	15658	28302	3.55	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2891	15658	28303	3.55	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4124	16866	29493	2.24	4.0E-41	XG2685.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6416	19184		1.41	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
6583	22246	35430	7.24	4.0E-41	BF304683.1	EST_HUMAN	601988096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11671	24256		11.07	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAAC07 5'
12646	25164		1.63	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
12727	24998	30971	1.69	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
927	13894	26358	2.68	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deaminase type II, complete cds
4301	17040	29667	2.45	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6404	18204	30908	7.78	3.0E-41	X87689.1	NT	H. sapiens mRNA for putative p64 CLCP protein
6288	19061	32043	1.59	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7159	18846	32916	0.71	3.0E-41	AA356168.1	EST_HUMAN	EST64883 Jurkat T-cells VI Homo sapiens cDNA 5' end
11730	24323	37647	1.26	3.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11924	24465		1.52	3.0E-41	AA609768.1	EST_HUMAN	af1710.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'
12456	24825		1.48	3.0E-41	BF128922.1	EST_HUMAN	601762840F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026081 5'
1817	14299	26987	5.17	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1951	14686	27399	1.84	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2216	14944	27684	1.54	2.0E-41	D86662.1	NT	Human mRNA for KIAA0207 gene, complete cds
2264	14990	27730	3.34	2.0E-41	X89631.1	NT	G. gorilla DNA for ZNF80 gene homolog
2831	14298	26987	4.65	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3321	18081	28731	1.41	2.0E-41	AA449549.1	EST_HUMAN	z408b04.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:785839 5'
4579	17314	29942	1.17	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4579	17314	29943	1.17	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
5141	17659	30475	0.9	2.0E-41	AW236547.1	EST_HUMAN	xm47706.x1 NCI_CGAP_GG8 Homo sapiens cDNA clone IMAGE:2687363 3' similar to TR:O70343 O70343
6530	19296	32300	0.76	2.0E-41	4504778	NT	PPAR GAMMA COACTIVATOR 1:
7572	20241	33346	8.08	2.0E-41	AF038404.1	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
7967	20682	33786	1.45	2.0E-41	M69944.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
7967	20682	33787	1.45	2.0E-41	M69944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
7986	20680	33818	1.12	2.0E-41	AA328265.1	EST_HUMAN	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8874	21565	34710	1.61	2.0E-41	P52742	SWISSPROT	EST31723 Embryo, 12 week I Homo sapiens cDNA 5' end
9317	21984	35155	0.52	2.0E-41	11417118	NT	ZINC FINGER PROTEIN 135
9317	21984	35156	0.52	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11468	24071	37379	2.76	2.0E-41	AA372637.1	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
3201	15964	28616	1.05	1.0E-41	BE869735.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3201	15964	28617	1.05	1.0E-41	BE869735.1	EST_HUMAN	801445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4529	17284	28897	14.08	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
6749	17918	30582	0.66	1.0E-41	H99079.1	EST_HUMAN	Y18503.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:262061 3'
9318	21985	35157	1.69	1.0E-41	A1217868.1	EST_HUMAN	q75c10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
11111	23781	37056	1.66	1.0E-41	AW847812.1	EST_HUMAN	IL3-CT0213-190200-040-F09 CT0213 Homo sapiens cDNA
12054	24571		2.81	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8418	21111		1.14	9.0E-42	BE178191.1	EST_HUMAN	RCO-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
9072	21781	34922	3.49	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9072	21761	34923	3.49	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
450	13238	25875	7.71	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2102	14833	27587	0.92	8.0E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12093	25277		4.4	8.0E-42	AA493896.1	EST_HUMAN	h07602.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA ;
12111	25154		1.56	8.0E-42	AW088062.1	EST_HUMAN	xc97a04.x1 NCI_CGAP_Brt35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.12
911	13678		2.58	7.0E-42	AL163285.2	NT	OFR repetitive element ;
9143	21874	35039	1.57	7.0E-42	A1204358.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
11126	23795	37071	1.3	7.0E-42	AA568592.1	EST_HUMAN	qf58g12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
11126	23795	37072	1.3	7.0E-42	AA568592.1	EST_HUMAN	m23g07.s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:914652
1848	14586	27289	3.21	6.0E-42	AF012872.1	NT	m23g07.s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:914652
1848	14586	27300	3.21	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2287	15012		3.55	6.0E-42	AW238556.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
5381	18181	30871	1.63	6.0E-42	AB028690.1	NT	xp28f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.H1 L1 repetitive element ;
5630	18181	30871	1.45	6.0E-42	AB028690.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
132	12947	25859	7.53	5.0E-42	AJ271735.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
428	13214		1.41	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
474	13260		2.57	5.0E-42	5730038	NT	h021e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
475	13261		2.74	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6587	19350	32363	1.04	5.0E-42	11433083	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6587	19350	32364	1.04	5.0E-42	11433083	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E8-associated protein, Angelman syndrome) (UBE3A), mRNA
6587	19350	32364	1.04	5.0E-42	11433083	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E8-associated protein, Angelman syndrome) (UBE3A), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6704	19619	32662	3.12	5.0E-42	11417857	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7101	19789	32854	1.59	5.0E-42	AF071569.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7711	20375	33489	0.57	5.0E-42	4826977	NT	Homo sapiens reelin (RELN) mRNA
8677	21369	34515	3.55	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10920	23600	36849	2.44	5.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
736	13510	26167	5.09	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
736	13510	26168	5.09	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
1044	13803	26462	3.46	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4171	18911	29541	1.22	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4202	16943	29570	1.07	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4223	16964	29589	4.15	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4543	17278	29909	15.12	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
10545	23241	36475	1.56	4.0E-42	AW818630.1	EST_HUMAN	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
10545	23241	36476	1.56	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11389	23995	37297	1.5	4.0E-42	BF035327.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
1466	14213	26902	2.81	2.0E-42	BF376834.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
2413	15134		2.92	2.0E-42	AW898344.1	EST_HUMAN	RCQ-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2425	15146	27879	2.22	2.0E-42	AW250059.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
5670	18465	31379	7.8	2.0E-42	AW955368.1	EST_HUMAN	2819293 3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
5670	18465	31380	7.8	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGC resequences, MAGC Homo sapiens cDNA
6654	19416	32429	1.46	2.0E-42	AI052586.1	EST_HUMAN	EST367438 MAGC resequences, MAGC Homo sapiens cDNA
9741	22392	35596	1.32	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:1653417 3'
9955	22603	35807	0.88	2.0E-42	P81649	SWISSPROT	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
9955	22603	35808	0.88	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
11742	24334	37660	1.37	2.0E-42	AL163248.2	NT	RIBONUCLEASE K3 (RNASE K3)
717	13490	26143	1.21	1.0E-42	X57147.1	NT	Homo sapiens chromosome 21 segment HS21C046
1019	13779	26441	1.1	1.0E-42	AW295809.1	EST_HUMAN	Human endogenous retrovirus pHLE.1 (ERV9)
1079	13837	26485	1.18	1.0E-42	AJ251818.1	NT	U1-H-B11-afh-e-04-Q-UJ.s1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1079	13837	26496	1.18	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1220	15563	26841	16.49	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homodog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1220	15563	26842	16.49	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homodog mRNA, nuclear gene encoding mitochondrial protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1696	14439	27137	1.13	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2546	15261	27998	1.63	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2964	15730	28380	10.26	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3695	16449	29088	2.6	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3905	16655	29296	1.17	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21G067
4221	16962	29587	1.92	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21G080
4554	17289	29918	0.75	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-e03 ST0197 Homo sapiens cDNA
4697	17431	30062	1.88	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4697	17431	30063	1.88	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4728	17460	30097	6.02	1.0E-42	4506758	NT	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
5044	17763	30378	1.08	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
5044	17763	30379	1.08	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
9986	22834	35844	4.03	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
637	13416	26052	19.69	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
637	13416	26053	19.69	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
684	13459	26104	6.03	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
684	13459	26105	6.03	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
684	13459	26106	6.03	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5612	18408	31321	0.76	8.0E-43	H13952.1	EST_HUMAN	y08e1.1.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3632	16385	29025	6.42	7.0E-43	AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2822251 5'
8667	21359		4.09	7.0E-43	A1936748.1	EST_HUMAN	wp68b01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN, contains LTR.b1 LTR7 repetitive element:
1321	14070		10.45	6.0E-43	AA491890.1	EST_HUMAN	ne72d06.s1 NCI_CGAP_Ewt1 Homo sapiens cDNA clone IMAGE:909803 similar to gbL05095 60S
2600	15314		2.25	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
6219	18993	31968	2.24	6.0E-43	9955973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
6808	19469	32492	2.09	6.0E-43	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810881 3' similar to contains MER1.13 MER1 MER1 repetitive element:
9751	22402	35607	2.16	6.0E-43	AA185154.1	EST_HUMAN	z35d06.r1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G529641
11044	22714		2.55	6.0E-43	AL119158.1	EST_HUMAN	G529641 DB1, COMPLETE CDS, contains element PTR7 repetitive element:
138	12953		2.64	5.0E-43	AL163213.2	NT	DKFZp61L1712_r1 761 (synonym: hamp2) Homo sapiens cDNA clone DKFZp61L1712 5'

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480	13275	25909	4.55	5.0E-43	AA382780.1	EST_HUMAN	EST196033 Testis 1 Homo sapiens cDNA 5' end
2850	15618	28264	1.52	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC08 5'
6213	19463	32484	1.17	5.0E-43	AI613509.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260452 3'
6802	19463	32484	0.72	5.0E-43	AI613509.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260452 3'
8778	21470		0.46	5.0E-43	H74277.1	EST_HUMAN	y449g12.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:229510 5'
9248	21927	35098	0.47	5.0E-43	AA044450.1	EST_HUMAN	zk55a02.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:486698 5' similar to gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
9248	21927	35099	0.47	5.0E-43	AA044450.1	EST_HUMAN	zk55a02.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:486698 5' similar to gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
9264	22018	35186	4.44	5.0E-43	AA465288.1	EST_HUMAN	ab33608.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
10297	22944	36158	2.31	5.0E-43	AI733244.1	EST_HUMAN	cc52c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P80591 P80591 PV14 GENE ;
10335	22982	36201	1.21	5.0E-43	AL049110.1	EST_HUMAN	DKFZp434D0119 r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119
10663	23354	36593	5.29	5.0E-43	AW7863007.1	EST_HUMAN	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
10891	23571	36822	1.84	5.0E-43	W28011.1	EST_HUMAN	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
952	15519	26383	5.9	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6176	17987	30502	1.02	4.0E-43	AI056338.1	EST_HUMAN	oy47h03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1669013 3'
6276	19049	32026	0.7	4.0E-43	6996009	NT	Homo sapiens glycyl-IRNA synthetase (GARS), mRNA
7030	19722		2.32	4.0E-43	11416793	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
8077	20771	33900	5.21	4.0E-43	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.i3 MER10 repetitive element ;
8077	20771	33901	5.21	4.0E-43	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.i3 MER10 repetitive element ;
10213	22861	36074	1.23	4.0E-43	6005967	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
11275	23836	37228	1.68	4.0E-43	T77380.1	EST_HUMAN	y472h10.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:113827 5'
12030	24556		3.05	4.0E-43	R20950.1	EST_HUMAN	y06b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ;
1191	13943		4.59	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1690	14434	27130	2.07	3.0E-43	X97868.1	NT	H.sapiens gene encoding La autoantigen
3558	16313	28960	1.31	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, (leukemic cell line SKH1), mRNA Mutant, 5638 nt]
4258	16969	28629	1.04	3.0E-43	AA548154.1	EST_HUMAN	nk55d06.s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419

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5803	18593	31518	0.72	3.0E-43	D34813.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6264	19038	32013	2.24	3.0E-43	7305360	NT	Mus musculus obogelin (Olog), mRNA
6264	19038	32014	2.24	3.0E-43	7305360	NT	Mus musculus obogelin (Olog), mRNA
6626	19380	32404	4.29	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8063	20757		8.38	3.0E-43	AA458824.1	EST_HUMAN	aa88f11.s1 Stragene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element
8719	21411	34554	1.87	3.0E-43	7681721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
9764	22415	35822	0.56	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC83848), mRNA
178	12991		7.67	2.0E-43	AI190764.1	EST_HUMAN	q61c09.x1 Soares_testis_NHT-Homo sapiens cDNA clone IMAGE:1733988 3' similar to contains P.T.R7.13 P.T.R7 P.T.R7 repetitive element
6383	19152	32151	1.13	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCL_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element
6383	19152	32152	1.13	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCL_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element
7176	19862	32833	1.32	2.0E-43	AW207390.1	EST_HUMAN	U1H.B11-efr-a-09-0-U1 s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8207	20901		5.59	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11156	23823		4.94	2.0E-43	T03007.1	EST_HUMAN	FB1G5 Fetal brain, Stragene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1645	14391	27080	2.94	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1645	14391	27081	2.94	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1700	14443	27142	1.57	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2727	15434	28170	3.85	1.0E-43	BF348283.1	EST_HUMAN	60202313F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4157698 5'
5325	18128	30788	0.74	1.0E-43	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6514	19279	32280	8.45	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6514	19279	32281	8.45	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6870	17947	30542	1.36	1.0E-43	R19751.1	EST_HUMAN	y940601.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP-BD38_MOUSE P28656 BRAIN PROTEIN DN38
7833	20528	33655	1.13	1.0E-43	AF175265.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
7965	20680		4.03	1.0E-43	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFAZT1) gene, partial cds
8738	21428	34574	25.49	1.0E-43	AW963676.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
10189	22837	36052	0.68	1.0E-43	AW563228.1	EST_HUMAN	EST365298 MAGE resequences, MAG8 Homo sapiens cDNA
10884	23564	36812	8.11	1.0E-43	AI984961.1	EST_HUMAN	w67801.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
11338	24028	37332	4.78	1.0E-43	11424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
11975	24520		3.04	1.0E-43	AL137984.1	EST_HUMAN	DKFZp761D1015_1 761 (synonym: hmy2) Homo sapiens cDNA clone DKFZp761D1015 5'
12253	24889	31079	1.88	1.0E-43	AI875418.1	EST_HUMAN	w669504.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313776 3'

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12469	24835	31032	3.41	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
870	13639	26309	8.23	8.0E-44	A1222985.1	EST_HUMAN	qf23g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
870	13639	26310	8.23	8.0E-44	A1222985.1	EST_HUMAN	qf23g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
8437	21129	34266	2.87	8.0E-44	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10236	22884	36097	0.47	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
10236	22884	36098	0.47	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11117	23787	37064	3.78	8.0E-44	Y10408.2	NT	Homo sapiens myosin mRNA, partial cds
11688	24283	37606	1.36	8.0E-44	L29139.1	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12207	24673	31073	4.09	8.0E-44	11527389	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12248	25009	30976	1.38	8.0E-44	11418086	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12589	25186	30808	2.55	8.0E-44	11418099	NT	Y98901.1 Scores fetal liver spleen 1N1FS Homo sapiens cDNA clone IMAGE:124920 5'
844	13423		0.69	7.0E-44	R06035.1	EST_HUMAN	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2228	14856	27698	1.08	7.0E-44	5031888	NT	Homo sapiens minisatellite ms32 repeat region
2968	15732	28381	2.58	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2968	15732	28382	2.58	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3843	16594	29231	2.54	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4217	18958	29581	1.12	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4217	18958	29582	1.12	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5142	17860	30478	1.01	7.0E-44	4505648	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
8085	20779	33908	2.28	7.0E-44	AU159839.1	EST_HUMAN	Homo sapiens Y79AA1 Homo sapiens cDNA clone Y79AA1000498 3'
8012	18793	31756	0.94	6.0E-44	Z20948.1	EST_HUMAN	HSAAADEYLP, Human fetal Brain Whole tissue Homo sapiens cDNA
11781	24372	37702	1.76	6.0E-44	AW954050.1	EST_HUMAN	EST368120 MAGE resequencer, MAGE Homo sapiens cDNA
296	13102		3.3	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
323	13124		2.72	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
							t440402.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
							OFR OFR repetitive element
7788	20483	33607	4.96	5.0E-44	A1598523.1	EST_HUMAN	AF048729.1
9284	22038		2.34	5.0E-44	AU124571.1	EST_HUMAN	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
3409	16167	28816	3.75	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
7370	20050	33131	0.68	4.0E-44	BE883178.1	EST_HUMAN	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
8169	20863	33995	0.76	4.0E-44	L21948.1	NT	Human fibrillin (FBN1) locus polymorphism
8777	21469		0.51	4.0E-44	BE176818.1	EST_HUMAN	RC3-H10585-010400-023-d08 HT0585 Homo sapiens cDNA
11202	23868	37153	5.38	4.0E-44	U90878.1	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
3094	15859	28500	5.77	3.0E-44	AA189851.1	EST_HUMAN	zp18605.1 Stratagene fetal retina 037202 Homo sapiens cDNA clone IMAGE:609777 5'

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3870	18820	29280	1.37	3.0E-44	AA337234.1	EST_HUMAN	EST42298 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
9419	22097	35269	0.55	3.0E-44	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1027	13787	28446	2.64	2.0E-44	4826685	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1027	13787	28447	2.64	2.0E-44	4826685	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1185	13937	26602	3.36	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1185	13937	26603	3.36	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1185	13937	26603	3.36	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1289	14038	28711	4.06	2.0E-44	AF133588.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds
1347	14095	28770	1.3	2.0E-44	BE465325.1	EST_HUMAN	hw14g08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN
2147	14877	27612	2.22	2.0E-44	AF070851.1	NT	P220569 OXYSTEROL-BINDING PROTEIN ;
2618	15327	28873	1.31	2.0E-44	5801933	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
3463	16219	28873	1.13	2.0E-44	D87675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4531	17286	28899	1.54	2.0E-44	AW864379.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6004	18785	31747	1.87	2.0E-44	11449901	NT	PMA-SN0016-120500-003-a04 SN0016 Homo sapiens cDNA
6758	17927	30582	3.31	2.0E-44	AF038968.1	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
7313	19996	33074	4.57	2.0E-44	11419226	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, alternatively spliced product, complete cds
7313	19996	33075	4.57	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8327	21020	34155	0.87	2.0E-44	7706370	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8327	21020	34156	0.87	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8517	21209	34362	1.58	2.0E-44	BE389058.1	EST_HUMAN	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
11883	24456		1.82	2.0E-44	BE244602.1	EST_HUMAN	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
12780	25020		1.4	2.0E-44	11528283	NT	601286914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813588 5'
51	12880	25507	2.43	1.0E-44	7657334	NT	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens
51	12880	25508	2.43	1.0E-44	7657334	NT	cDNA clone TCBAP2795
566	13347	25976	2.44	1.0E-44	AW853132.1	EST_HUMAN	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
1175	13928		1.9	1.0E-44	AW694803.1	EST_HUMAN	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
1567	14314		5.78	1.0E-44	AL183303.2	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
2221	14949	27687	3.74	1.0E-44	AA434554.1	EST_HUMAN	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
2221	14949	27688	3.74	1.0E-44	AA434554.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C103
							zw53402.1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to
							contains THR.13 THR repetitive element;
							zw53402.1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to
							contains THR.13 THR repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2280	15560	27746	0.96	1.0E-44	AA398099.1	EST_HUMAN	z88g11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728476 5'
2763	15468	28211	1.44	1.0E-44	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3712	16465		3.73	1.0E-44	AA459869.1	EST_HUMAN	aa01c09.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5048	17767	30385	1.04	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5048	17767	30386	1.04	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8163	20857	33988	0.98	1.0E-44	AW987073.1	EST_HUMAN	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA
8163	20857	33989	0.98	1.0E-44	AW987073.1	EST_HUMAN	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA
8544	21236	34390	0.88	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8924	21615	34759	0.69	1.0E-44	AI337183.1	EST_HUMAN	q889g07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009628 3'
10936	20616		4.04	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
11516	24116	37427	3.92	1.0E-44	10092684	NT	Homo sapiens Sush1 domain (SCR repeat) containing (BK65A6.2), mRNA
11583	24182	37496	3.17	1.0E-44	AW848867.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
11583	24182	37497	3.17	1.0E-44	AW848867.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4539	17274	29906	1.38	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4539	17274	29907	1.38	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6552	19317	32323	1.31	9.0E-45	AB023212.1	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
2527	15243	27982	3.12	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5023	17744	30355	6.41	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
6414	19182	32181	0.66	8.0E-45	AW892763.1	EST_HUMAN	CMO-NN0005-130300-283-508 NN0005 Homo sapiens cDNA
8008	20701	33830	0.91	8.0E-45	AA377985.1	EST_HUMAN	EST190893 Synovial sarcoma Homo sapiens cDNA 5' end
1545	14291		1.01	6.0E-45	AI876425.1	EST_HUMAN	wb99c06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.11 L1 repetitive element;
3960	18709		4.09	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
12555	26378		1.65	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
872	13641		1.03	6.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1995	14731	27453	3.65	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-101 CN0044 Homo sapiens cDNA
3204	15967	28821	1.79	5.0E-45	AI523766.1	EST_HUMAN	ig04f07.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2118453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1;
5425	18224	30935	8.76	5.0E-45	AA397781.1	EST_HUMAN	272003.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element;
5928	18713	31669	1.31	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5929	18713	31670	1.31	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5974	18756	31717	0.79	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
5974	18756	31718	0.79	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6096	18874	31842	1.02	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6096	18874	31843	1.02	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8174	20868	34000	0.73	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8939	21630	34773	1.95	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11697	24292	37817	2.59	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1121	13877	26536	9.58	4.0E-45	X95826.1	NT	Homo sapiens ART4 gene
2289	15014	27750	2.42	4.0E-45	BE265822.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
8855	21546		0.82	4.0E-45	AA226220.1	EST_HUMAN	nc28a07.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element;
4086	16095		1.35	3.0E-45	T71480.1	EST_HUMAN	y33567.1 Scars fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:110245 5'
6142	18920	31890	1.36	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
6142	18920	31891	1.36	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
8350	21043	34526	1.4	3.0E-45	AV723978.1	EST_HUMAN	AV723978 HTB Homo sapiens cDNA clone HTBAAG01 5'
8690	21382	34526	3.74	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10206	22854	36068	13.43	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10206	22854	36069	13.43	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12870	25314		2.35	3.0E-45	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2506	15223		2.21	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3029	15795	28441	1.22	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6429	19197	32194	5.15	2.0E-45	LD1665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7510	20181	33274	1.22	2.0E-45	BE782184.1	EST_HUMAN	601467793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8314	21007	34145	0.78	2.0E-45	AW534834.1	EST_HUMAN	RCO-LT0001-150200-032-d11 LT0001 Homo sapiens cDNA
9485	22138	35318	0.48	2.0E-45	AI636786.1	EST_HUMAN	ts56a01.x1 NCL_CGAP_KidB Homo sapiens cDNA clone IMAGE:2232552 3'
10705	25130	36633	18.28	2.0E-45	BE934350.1	EST_HUMAN	MRO-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA
							aa8712.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
							TR:G1144569 G1144569 R-SLY1.
11129	23797	37073	4.18	2.0E-45	AA458770.1	EST_HUMAN	xp72a03.x1 NCL_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
11488	24089	37400	1.75	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
11488	24089	37401	1.75	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
12711	24987		3.93	2.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA11), mRNA
120	13185		-1.8	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
400	13185		2.17	1.0E-45	BE389855.1	EST_HUMAN	601284380F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
460	13245	25887	1.38	1.0E-45	4508412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1151	13906	26569	1.79	1.0E-45	7657290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3101	15866	28507	7.42	1.0E-45	U32169.1	NT	Human pro- $\alpha 2$ chain of collagen type XI (COL11A2) gene, complete cds
3483	16240	28897	1.38	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3560	16315	28962	1.19	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4442	17178	29804	5.01	1.0E-45	BE396633.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
4677	17411		1.04	1.0E-45	H57443.1	EST_HUMAN	y05b02.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:204363 5'
7930	20625	33752	0.77	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
7930	20625	33753	0.77	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8505	21197	34341	0.96	1.0E-45	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9019	21709	34881	5.08	1.0E-45	BE887843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9422	22100	35272	1.22	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
11734	24327	37651	1.33	1.0E-45	7019570	NT	Homo sapiens alpha-calactin-like protein (VR22), mRNA
12087	24592	31125	6.93	1.0E-45	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCAPB), mRNA
12263	24708		11.18	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12269	24711		5.28	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12680	24969	30981	2.6	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA1), mRNA
8127	20821	33958	1.7	9.0E-46	9910293	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
8532	21224		5.86	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10378	23024	36239	11.23	9.0E-46	AW246984.1	EST_HUMAN	2822449.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2443	15162	27899	13.53	8.0E-46	AI433261.1	EST_HUMAN	632708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2
2443	15162	27900	13.53	8.0E-46	AI433261.1	EST_HUMAN	632708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2
7953	20648		5.69	8.0E-46	BE187244.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
2232	14960	27700	1.03	7.0E-46	U46007.1	NT	RC5-HT0508-280200-012-C12 HT0508 Homo sapiens cDNA
4541	17276		3.38	7.0E-46	BE386185.1	EST_HUMAN	Rattus norvegicus espin mRNA, complete cds
4755	17487		1.33	7.0E-46	BE084386.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
5851	18733	31692	4.01	7.0E-46	BF105845.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
6402	19171	32170	1.14	7.0E-46	BF105845.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
2759	15464	28207	3.99	6.0E-46	AI894381.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
							W31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
							MER19 repetitive element;

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2759	15464	28208	3.98	6.0E-46	A1884381.1	EST_HUMAN	wm31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12 MER19 repetitive element;
6038	18818	31779	10.94	6.0E-46	A1635448.1	EST_HUMAN	hs58h10.x1 NCI_CGAP_K108 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:060363 O60363 SA GENE.;
7116	18804	32868	0.72	6.0E-46	AW513244.1	EST_HUMAN	xx42e04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gbl:08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
11364	23175		2.04	6.0E-46	BE784971.1	EST_HUMAN	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880995 5'
199	13012		8.9	5.0E-46	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3519	16275	28929	1.07	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3519	16275	28930	1.07	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6636	19398	32413	1.86	5.0E-46	BF590442.1	EST_HUMAN	naa38f07.x1 NCI_CGAP_K1011 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:075202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
6942	19542	32570	4.29	5.0E-46	BF347229.1	EST_HUMAN	075202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
6995	19687	32736	0.62	5.0E-46	AW582253.1	EST_HUMAN	602021164F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156670 5'
9515	22168	35350	0.47	5.0E-46	AA398381.1	EST_HUMAN	QV4-ST0212-120100-075-J09 ST0212 Homo sapiens cDNA z632c08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728928 3'
626	13405		1.4	4.0E-46	AA601143.1	EST_HUMAN	nc54e08.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1899	14442	27140	6.86	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
1899	14442	27141	6.86	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
2743	15449	28188	2.62	4.0E-46	MT8048.1	NT	Human endogenous retrovirus RTVL-H2
4384	17121	29753	1.04	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
4384	17121	29754	1.04	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
5350	18153	30834	2.43	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5350	18153	30835	2.43	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12513	24863	31014	2.71	4.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2155	14885	27618	0.9	3.0E-46	5453620	NT	Homo sapiens solute carrier family 35 (Clp-allelic acid transporter), member 1 (SLC35A1), mRNA
2429	15150	27884	0.95	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
4362	17100	29735	0.79	3.0E-46	4506378	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4724	17456	30081	1.2	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.1.1.2) germline; Ig-Lambda; VLambda

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4724	17456	30092	1.2	3.0E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
8647	21339	34483	7.59	3.0E-46	A1831462.1	EST_HUMAN	wf49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
11564	24163	37474	2.19	3.0E-46	D31765.1	NT	THR repetitive element
817	13588	28255	7.64	2.0E-46	AA468646.1	EST_HUMAN	Human mRNA for KIAA0061 gene, partial cds
1554	14301		1.55	2.0E-46	AA678246.1	EST_HUMAN	ne05a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
1637	14383	27070	3.43	2.0E-46	U78027.1	NT	repetitive element
4917	17645	30258	1.2	2.0E-46	AA399286.1	EST_HUMAN	2127a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'
7384	20064	33142	7.67	2.0E-46	9910569	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
7968	20663		1.46	2.0E-46	BE669151.1	EST_HUMAN	(L44L) and FTP3 (FTP3) genes, complete cds
12257	25179		1.5	2.0E-46	H48391.1	EST_HUMAN	Q1730 RSP-1 PROTEIN
12575	25170	30902	3.38	2.0E-46	AW277214.1	EST_HUMAN	Q1730 RSP-1 PROTEIN
1211	13961	26628	7.67	1.0E-46		NT	Q01730 RSP-1 PROTEIN
1566	14313	28969	1.23	1.0E-46	7662177	NT	Mus musculus sperm tail associated protein (Slap), mRNA
1568	14313	27000	1.23	1.0E-46		NT	601445137F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3848287 5'
2279	15005	27745	3.44	1.0E-46	AW978516.1	EST_HUMAN	y32d01.1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:2068977 5'
2399	15120	27857	3.06	1.0E-46	H97330.1	EST_HUMAN	q378h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
3243	16005	28654	4.55	1.0E-46	AA631912.1	EST_HUMAN	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
4818	17549		3.17	1.0E-46	AB023197.1	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
5613	18409	31322	6.88	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
5888	25080	31617	6.14	1.0E-46	8923762	NT	EST390625 MAGC resequences, MAGC Homo sapiens cDNA
5888	25080	31618	6.14	1.0E-46	8923762	NT	EST480095 WATM1 Homo sapiens cDNA clone 48b095
10770	18409	31322	5.27	1.0E-46	BF194707.1	EST_HUMAN	np78b02.e1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb.X76717 H.sapiens
11747	24338	37665	1.53	1.0E-46	AW023178.1	EST_HUMAN	MT-11 mRNA (HUMAN)
11747	24338	37666	1.53	1.0E-46	AW023178.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
12044	24564	31115	2.28	1.0E-46	BF531102.1	EST_HUMAN	7682b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
12044	24564	31116	2.28	1.0E-46	BF531102.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
12778	25032		2.37	1.0E-46	AV715377.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
750	13522		6.18	9.0E-47	AJ271735.1	NT	7682b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4879	17606	30229	3.02	9.0E-47	AW770928.1	EST_HUMAN	h83a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703
6284	19057	32037	0.6	9.0E-47	11425439	NT	HYPOTHETICAL 12.4 KD PROTEIN ;
12531	25270	30725	2	9.0E-47	11417966	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
1801	14541	27252	6.88	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1801	14541	27253	6.88	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
						NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2722	15429	28167	1.04	8.0E-47	5453956	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3024	15790	28438	1.89	8.0E-47	AJ229043.1	NT	Homo sapiens 959 kb contig between AVL1 and CBR1 on chromosome 21q22, segment 3/3
3613	16366	29009	0.68	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
3613	16366	29010	0.68	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
12604	25169		1.38	7.0E-47	AV683284.1	EST_HUMAN	AV683284 GCK Homo sapiens cDNA clone GKCASH11 5'
2550	15285	28000	1.66	6.0E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8592	21284	34423	0.49	6.0E-47	U77054.1	EST_HUMAN	HSU77054 Human Homo sapiens cDNA clone N7
9176	21846	35012	6.76	6.0E-47	AI695189.1	EST_HUMAN	tz88h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296659 3'
9612	22265	35450	0.68	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
9612	22265	35451	0.68	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6482	19249	32249	6.67	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
10698	23387		5.27	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stralagene (cat5936206) Homo sapiens cDNA clone HFBCF07
1379	14126	26801	3.29	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6733	19567	32599	1.9	4.0E-47	BE938896.1	EST_HUMAN	MR4-TN0108-280800-201-d04 TN0108 Homo sapiens cDNA
8379	21072	34210	2.42	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8379	21072	34211	2.42	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8516	21208	34351	0.61	4.0E-47	AW693777.1	EST_HUMAN	RC3-BN0034-220300-075-065 BN0034 Homo sapiens cDNA
						EST_HUMAN	xc68b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
11635	24232		2.83	4.0E-47	AW515509.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
531	13315	25950	2.05	3.0E-47	BE607634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896721 5'
531	13315	25951	2.05	3.0E-47	BE607634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896721 5'
799	13571	26232	6.45	3.0E-47	IN57483.1	EST_HUMAN	y64b04.s1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:277327 3'
924	13691	26355	10.25	3.0E-47	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3298	19058	28707	0.79	3.0E-47	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3948	16696		5.77	3.0E-47	U93181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
4328	17068	26696	1.32	3.0E-47	IM12959.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
5922	16707	31659	5.41	3.0E-47	AW408800.1	EST_HUMAN	UIHF-BM0-ack-4-07-0-UI.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5922	18707	31660	5.41	3.0E-47	AW408800.1	EST_HUMAN	U1-HF-BM0-adv-d-07-0-U1,r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6469	19236		1.76	3.0E-47	A1222413.1	EST_HUMAN	q04e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
8732	21424	34569	0.71	3.0E-47	AW963796.1	EST_HUMAN	EST375869 MAGC resequences, MAGH Homo sapiens cDNA
8732	21424	34570	0.71	3.0E-47	AW963796.1	EST_HUMAN	EST375869 MAGC resequences, MAGH Homo sapiens cDNA
143	12958	25600	1.61	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
947	13713	26377	2.69	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
947	13713	26378	2.69	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1580	14307		0.98	2.0E-47	A1969279.1	EST_HUMAN	wq96402.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2479851 3'
1588	14334	27022	1.75	2.0E-47	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1673	14418	27111	3.41	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:937607 3'
4313	17052	29677	2	2.0E-47	4504868	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4351	17090	29722	1.5	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4351	17090	29723	1.5	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4471	17206	29832	1.68	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4761	17493	30121	1.3	2.0E-47	AW965168.1	EST_HUMAN	EST377239 MAGC resequences, MAGI Homo sapiens cDNA
5696	18490	31411	1.12	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGSG6) mRNA, complete cds
5887	18673	31615	1.23	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
5887	18673	31616	1.23	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7598	25116		1.43	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
7864	20559	33685	1.92	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7864	20559	33686	1.92	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8618	21310	34452	1.87	2.0E-47	AF071771.1	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
9389	22051	36222	0.77	2.0E-47	11528136	NT	Human tyrosine kinase receptor (ad) mRNA, complete cds
11451	23218	36451	1.27	2.0E-47	M76125.1	NT	Human infant brain 1N1B Homo sapiens cDNA clone IMAGE:29968 3' similar to contains OFR repetitive element;
12077	25312	30709	1.75	2.0E-47	R42423.1	EST_HUMAN	y92e08.s1 Soares_infant brain 1N1B Homo sapiens cDNA clone IMAGE:1831189 3'
1384	14131	26804	7.35	1.0E-47	A1333426.1	EST_HUMAN	qp69h03.x1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1831189 3'
5017	17738	30347	1.98	1.0E-47	AW813908.1	EST_HUMAN	RC3-ST0197-130400-017-402 ST0197 Homo sapiens cDNA
8844	19426	32441	6.79	1.0E-47	A1880868.1	EST_HUMAN	at18e06.x1 Barslead acorta HP LR36 Homo sapiens cDNA clone IMAGE:2355588 3' similar to gb:M22895
8787	21459		0.56	1.0E-47	AW894648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10254	22902	36112	2.28	1.0E-47	L30115.1	NT	hi84a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M28326
							KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							Papilio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1607	14353	27041	3.03	9.0E-48	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3544	16299	28950	0.92	9.0E-48	BF559947.1	EST_HUMAN	CM2-MT0100-310700-290-705 MT0100 Homo sapiens cDNA
5594	18389	31299	0.86	9.0E-48	BE888196.1	EST_HUMAN	607511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
5594	18389	31300	0.86	9.0E-48	BE888196.1	EST_HUMAN	607511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
6010	18791	31754	0.86	9.0E-48	AI833188.1	EST_HUMAN	at75h09.x1 Barstead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:O60844
6131	18909	31877	0.64	9.0E-48	AU123240.1	EST_HUMAN	C60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN. ;
11060	23730	37002	3.09	9.0E-48	BE938313.1	EST_HUMAN	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
1228	13978		1.44	8.0E-48	4501900	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
1229	13978		1.7	8.0E-48	4501900	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
3132	15897	28541	4.38	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
3132	15897	28542	4.38	8.0E-48	AW768477.1	EST_HUMAN	hK61b03.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
3911	16661	29302	0.79	8.0E-48	4504116	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
478	13264		1.27	7.0E-48	AB033035.1	NT	hK61b03.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
479	13264		17.09	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1483	14230	26916	0.98	7.0E-48	6912719	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
1634	14380	27067	3.89	7.0E-48	5730038	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
6460	19227	32227	27.21	7.0E-48	11416631	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
6967	18749	31710	0.91	6.0E-48	AB006855.1	NT	Homo sapiens tousel-like kinase 1 (TLK1), mRNA
6888	19605	32645	1.08	6.0E-48	11420695	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7365	25111	33123	0.58	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for AIE-75, complete cds
7365	25111	33124	0.58	6.0E-48	AB046844.1	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
9022	21712	34866	2.07	6.0E-48	AF026816.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9441	22119	35296	1.74	6.0E-48	11427428	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9588	22241	35425	3.2	6.0E-48	AA189080.1	EST_HUMAN	Homo sapiens putative oncogene protein mRNA, partial cds
3304	17878	28713	1.94	5.0E-48	4826891	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
8474	21166	34310	1.25	5.0E-48	BE084410.1	EST_HUMAN	zq45b08.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains Alu repetitive element
11603	24202	37524	1.39	5.0E-48	AW890299.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
10878	23558	36805	3.86	4.0E-48	AI620420.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
1364	14112	28786	1.27	3.0E-48	AV690964.1	EST_HUMAN	MRO-NT0039-010500-002-08 NT0039 Homo sapiens cDNA
							tu47a02.x1 NCI CGAP P728 Homo sapiens cDNA clone IMAGE:2254164 3'
							AV690964 GKG Homo sapiens cDNA clone GKCDRE12 5'

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1969	14705	27422	15.26	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1969	14705	27423	15.26	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3622	16375	29017	0.75	3.0E-48	AW664531.1	EST_HUMAN	h14b12.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCORB_HUMAN
5804	18594	31519	2.47	3.0E-48	BE084571.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
5919	19655	32701	0.94	3.0E-48	AF087913.1	NT	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
8290	20984		3.41	3.0E-48	AA659630.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
10784	23467	36708	9.52	3.0E-48	BF514170.1	EST_HUMAN	nt030505.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1
44	12873	25495	1.71	2.0E-48	AA631940.1	EST_HUMAN	PTR5 repetitive element ;
1197	13949		5.15	2.0E-48	H24278.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082287 3'
4495	17231	29861	1.42	2.0E-48	BE246065.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
5724	18516	31436	0.61	2.0E-48	AA613171.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
5724	18516	31437	0.61	2.0E-48	AA613171.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
7419	20096	33182	4.77	2.0E-48	AB040934.1	NT	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
7419	20096	33183	4.77	2.0E-48	AB040934.1	NT	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
7432	20109	33197	3.35	2.0E-48	11496238	NT	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
8253	20947	34084	1.33	2.0E-48	AV743451.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
12041	17888	30486	4.27	2.0E-48	AA465007.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
12367	25232	30820	1.86	2.0E-48	BE737154.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
12716	13949		1.34	2.0E-48	H24278.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
54	12883	25511	2.3	1.0E-48	7706534	NT	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
853	13623	26293	17.13	1.0E-48	4502168	NT	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
1273	14023	26691	3.77	1.0E-48	5032032	NT	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
1911	14948	27359	30.36	1.0E-48	AL163302.2	NT	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
3481	16238	28894	0.96	1.0E-48	AL163246.2	NT	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
5081	17780	30398	1.6	1.0E-48	M10976.1	NT	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'
6195	18871	31946	1.17	1.0E-48	AB89077.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-LJ1 st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:3082287 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6195	18971	31947	1.17	1.0E-48	AB89077.1	EST_HUMAN	td17c01.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941:
6407	19176		0.94	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
6500	19265	32266	0.71	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6500	19265	32267	0.71	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
7157	19844	32913	2.52	1.0E-48	4755137	NT	Homo sapiens Huntington (Huntington disease) (HD) mRNA
8730	21422	34566	0.76	1.0E-48	4756695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8730	21422	34567	0.76	1.0E-48	4756695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9113	21801	34966	0.84	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9168	21838	35004	6.4	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9481	22134	35314	5.33	1.0E-48	BF304683.1	EST_HUMAN	60188096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10269	22917	36127	4.08	1.0E-48	11428908	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10269	22917	36128	4.08	1.0E-48	11428908	NT	Homo sapiens B cell linker protein (SLP65), mRNA
2002	14737	27461	1.13	8.0E-49	AB026497.1	NT	Mus musculus MyoPDZ mRNA for myosin containing PDZ domain, complete cds
5962	18744	31704	3.43	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
5962	18744	31705	3.43	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8194	20888	34026	3.17	8.0E-49	U23850.1	NT	Human Inositol 1,4,5 trisphosphate receptor type 1B, complete cds
9889	22539	35733	1.15	8.0E-49	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
135	13171	25814	1	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
135	13171	25815	1	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
384	13171	25814	1.73	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
384	13171	25815	1.73	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
385	13171	25814	2.94	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
385	13171	25815	2.94	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
1199	13951	26615	3.4	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6373	18173	30962	2.11	7.0E-49	AB07191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356683 3' similar to TR:O54923
5383	18183	30873	1.46	7.0E-49	AL120637.1	EST_HUMAN	O54923 RSEC15.1
5716	18173	30862	0.87	7.0E-49	AB07191.1	EST_HUMAN	DKFZp762C033_s1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762C033 3'
							wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356683 3' similar to TR:O54923
							O54923 RSEC15.1
							ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:U17206 40S
							RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element,
192	13005	25946	12.12	6.0E-49	AW731740.1	EST_HUMAN	complete (MOUSE);
4095	16837	29484	1.27	6.0E-49	AL182091.1	EST_HUMAN	DKFZp761A138_s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6349	19119	32109	0.94	6.0E-49	AU140742.1	EST_HUMAN	AU140742 PLACE4 Homo sapiens cDNA clone PLAGE400148 5'
7314	19997	33076	0.69	6.0E-49	AW511225.1	EST_HUMAN	h444e02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
9633	22285	35478	0.45	6.0E-49	9910293	NT	O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.
9633	22285	35479	0.45	6.0E-49	9910293	NT	Mus musculus keralin complex 2, gene 6g (Krl2-6g), mRNA
11248	23910	37202	2.5	6.0E-49	AW452218.1	EST_HUMAN	Mus musculus keralin complex 2, gene 6g (Krl2-6g), mRNA
11661	24257	37579	2.6	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
11661	24257	37580	2.6	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
12362	25151		2.03	6.0E-49	AA707567.1	EST_HUMAN	Z99c08.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
695	13470	26117	7	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
695	13470	26118	7	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1786	14927	27235	3.49	5.0E-49	AA172121.1	EST_HUMAN	zp29c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to
2754	15459	28201	4.25	5.0E-49	U17714.1	NT	TR:G233228 G233228 RTYL-H PROTEIN.; contains LTR7 LTR7 LTR7 repetitive element;
3267	16029	28678	2.64	5.0E-49		NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
512	13296	25927	47.84	4.0E-49	AW189533.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S27 (metalloproteinin 1) (H. sapiens) (LOC63362), mRNA
7172	19858	32530	0.95	4.0E-49	11525737	NT	X08601.x1 NCI_CGAP_U44 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:B0350.2B
7172	19858	32531	0.95	4.0E-49	11525737	NT	CE06703;
7172	19858	32531	0.95	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine; polypeptide N-acetyl-galactosaminyltransferase 8
7172	19858	32531	0.95	4.0E-49	11525737	NT	(GalNAc-T8) (GALNT8), mRNA
7710	20374	33488	0.9	4.0E-49	7662209	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine; polypeptide N-acetyl-galactosaminyltransferase 8
8763	21455	34604	0.47	4.0E-49	11425374	NT	(GalNAc-T8) (GALNT8), mRNA
8763	21455	34605	0.47	4.0E-49	11425374	NT	Homo sapiens K1AA0623 gene product (K1AA0623), mRNA
12221	25368		4.21	4.0E-49	AA210798.1	EST_HUMAN	Homo sapiens copine III (CPNE3), mRNA
12306	24730		4.1	4.0E-49	AF240786.1	NT	Homo sapiens copine III (CPNE3), mRNA
547	13330	25961	1.73	3.0E-49	X68968.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
2654	15364		1.9	3.0E-49	AA016131.1	EST_HUMAN	genes, complete cds
4923	17851	30264	2.33	3.0E-49	U46999.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
7319	20002	33081	11.87	3.0E-49	H39479.1	EST_HUMAN	ze31c05.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1
						EST_HUMAN	repetitive element;
						EST_HUMAN	Human type IV collagen (COL4A6) gene, exon 40
						EST_HUMAN	EST25612 WATM1 Homo sapiens cDNA clone 25612

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11272	23833	37226	1.98	3.0E-49	AA337561.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
646	13425		2.94	2.0E-49	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3216	15979	28630	1.64	2.0E-49	N28448.1	EST_HUMAN	Y23408.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262571 5'
							gb:M31470 RAS-RELATED PROTEIN TC10 (HUMAN); contains Alu repetitive element; contains element MER22 repetitive element;
4746	17478	30110	0.68	2.0E-49	AH167357.1	EST_HUMAN	U1H-B14-aps-4-02-Q-U1.s1 NC1 CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3088538 3'
4758	17490	30118	0.74	2.0E-49	BF511846.1	EST_HUMAN	AV171938 DCB Homo sapiens cDNA clone DCBALB01 5'
6637	19399	32414	1.17	2.0E-49	AV717938.1	EST_HUMAN	EST02558 Fetal brain, Stratiene (cat#36206) Homo sapiens cDNA clone HFBCY50
7998	20993		1.74	2.0E-49	M86033.1	EST_HUMAN	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
12316	25250		2.07	2.0E-49	AF163864.1	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882088 5'
879	13648		5	1.0E-49	BF035327.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
1546	14292	26978	1.11	1.0E-49	4557857	NT	601115769F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3356273 5'
1794	14534	27243	4.82	1.0E-49	BE255216.1	EST_HUMAN	601820033F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
5275	18080	30737	6.82	1.0E-49	BF131007.1	EST_HUMAN	yn4804.r1 Soares adult brain N2b5HB557 Homo sapiens cDNA clone IMAGE:171703 5' similar to SP_CBG1 HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT ;
5986	18767	31731	0.88	1.0E-49	H18291.1	EST_HUMAN	EST378713 IMAGE ressequences, MAGH Homo sapiens cDNA
5992	18773	31736	5.55	1.0E-49	AW964840.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCVDT11 5'
7117	19805	32869	0.62	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCVDT11 5'
7117	19805	32870	0.62	1.0E-49	AV703000.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7123	19811	32878	3.55	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7123	19811	32879	3.55	1.0E-49	BE398110.1	EST_HUMAN	Yw78g12.s1 Soares placenta, 8to6weeks 2NbHP8(c9W) Homo sapiens cDNA clone IMAGE:258406 3'
							similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7200	19886	32960	2.21	1.0E-49	N25884.1	EST_HUMAN	Yw78g12.s1 Soares placenta, 8to6weeks 2NbHP8(c9W) Homo sapiens cDNA clone IMAGE:258406 3'
							similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7200	19886	32961	2.21	1.0E-49	N25884.1	EST_HUMAN	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
7977	20672	33795	0.69	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
7977	20672	33796	0.69	1.0E-49	11321580	NT	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
8575	21267		0.66	1.0E-49	8994184	NT	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
8891	21562	34721	1.29	1.0E-49	BE408340.1	EST_HUMAN	601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10028	22674	35889	1.58	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: fites3) Homo sapiens cDNA clone DKFZp434D2423 5'
10979	23654	36907	1.43	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDAWE04 5'
11281	23942	37238	3.32	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12215	24677		2.46	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
4937	17865		1.4	9.0E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds

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6310	25421		0.95	9.0E-50	BE295758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
166	12990	25619	4.05	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
702	13477	26125	2.54	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
702	13477	26126	2.54	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1758	14500	27201	2.82	8.0E-50	4501890	NT	Homo sapiens mRNA for VIP receptor 2
2703	15410	28147	1.48	8.0E-50	4826658	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2833	14691		15.7	8.0E-50	D90334.1	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
11385	23992	37293	1.29	8.0E-50	AA633467.1	EST_HUMAN	Homo sapiens hepatocyte growth factor (HGF) gene, exon 18
605	13383	26015	0.76	7.0E-50	BE089591.1	EST_HUMAN	np62406.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1130891 3' similar to gb:J05459
6887	19604	32643	1.06	7.0E-50	BF091922.1	EST_HUMAN	GLUTATHIONE S-TRANSFERASE TESTIS/BRAIN (HUMAN);
6887	19604	32644	1.06	7.0E-50	BF091922.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
7205	19890	32966	0.6	7.0E-50	AA627822.1	EST_HUMAN	RC6-TN0073-150600-011-A12 TN0073 Homo sapiens cDNA
10556	23347	36584	7.65	7.0E-50	A1872137.1	EST_HUMAN	RC6-TN0073-150600-011-A12 TN0073 Homo sapiens cDNA
4309	17048		0.68	6.0E-50	BE794381.1	EST_HUMAN	RC6-TN0073-150600-011-A12 TN0073 Homo sapiens cDNA
8112	20806		5.67	6.0E-50	BE044076.1	EST_HUMAN	m59e12.s1 NCI_CGAP_Cx9 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X68391 60S
10717	23408	36646	12.6	6.0E-50	AA312079.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN);
10717	23406	36647	12.6	6.0E-50	AA312078.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA clone IMAGE:2439908 3'
1785	14526	27233	1.1	5.0E-50	BF332938.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1785	14526	27234	1.1	5.0E-50	BF332938.1	EST_HUMAN	GM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
8990	21680		5.26	5.0E-50	AA557683.1	EST_HUMAN	GM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
897	13665		1.71	4.0E-50	AA601143.1	EST_HUMAN	m45h10.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element
3441	18197	28847	0.99	4.0E-50	AL163248.2	NT	repetitive element
6268	19041	32018	0.98	4.0E-50	11440683	NT	repetitive element
7135	19822	32888	1.95	4.0E-50	BE087536.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1831	14667		4.13	3.0E-50	M18048.1	NT	Homo sapiens chromosome 21 segment HS21C048
3293	16054	28703	1.24	3.0E-50	AA746142.1	EST_HUMAN	Homo sapiens cysine-4RNA synthetase (CARS), mRNA
3734	16487	28124	1.14	3.0E-50	AW755254.1	EST_HUMAN	QV1-BT0681-260300-127-f12 BT0681 Homo sapiens cDNA
							Human endogenous retrovirus RTVL-H2
							db03006.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
							CMVA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMVA5
							Cardiomyopathy associated gene 5

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6687	19584	32618	1.52	3.0E-50	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
7544	20214	33314	4.85	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7544	20214	33315	4.85	3.0E-50	AF233438.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8481	21173	34318	0.71	3.0E-50	6601689	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9718	22369	35567	1.21	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
9727	22378	35580	0.99	3.0E-50	11418514	NT	Homo sapiens t-complex 10 (a murine top homolog) (TCP10), mRNA
10077	22725	35942	0.47	3.0E-50	Y18276.1	NT	Mus musculus mRNA for neurobeachin
10415	23061	36280	1.03	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
11045	23715	36984	1.61	3.0E-50	11436956	NT	Homo sapiens Grb2-associated binder 2 (KIA0571), mRNA
11441	23208	36439	5.35	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
760	13532		5.38	2.0E-50	AF050506.1	NT	Homo sapiens MHC class 1 region
1057	13815	26476	5.57	2.0E-50	4557762	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), mRNA
1424	14171	26857	2.25	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
6789	19513	32539	0.59	2.0E-50	AU124065.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001609 5'
8215	20909	34044	1.02	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8215	20909	34045	1.02	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8355	21048	34186	10.04	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8355	21048	34187	10.04	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
9784	22435	35641	1.51	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9784	22435	35642	1.51	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
11660	24256		1.8	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
449	13235	25874	1.92	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2365	15087		9.48	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
10083	22741	35956	1.57	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
5993	18678	31624	1.21	9.0E-51	AW511225.1	EST_HUMAN	h444602.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
6130	18908	31876	0.71	9.0E-51	AA744837.1	EST_HUMAN	O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
8572	21284	34403	0.65	9.0E-51	AI791154.1	EST_HUMAN	nt67603.s1 NCI CGAP GCBT1 Homo sapiens cDNA clone IMAGE:1283381 3'
9224	21803	35075	1.23	9.0E-51	AA043738.1	EST_HUMAN	nt623904.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN O04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9400	22082	35231	0.86	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW_PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;
9400	22082	35232	0.86	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW_PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;
11455	23222	36456	1.89	9.0E-51	H89078.1	EST_HUMAN	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
11455	23222	36457	1.88	9.0E-51	H89078.1	EST_HUMAN	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
11823	18908	31876	1.43	9.0E-51	AA744837.1	EST_HUMAN	ny67h03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283381 3'
4405	17142	29770	1.45	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4405	17142	29771	1.45	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4530	17265	29898	8.43	8.0E-51	AA610842.1	EST_HUMAN	np98e09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12871_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7552	20222	33325	2.24	8.0E-51	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
8364	21939		1.13	8.0E-51	AU138590.1	EST_HUMAN	AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008837 5'
11812	20222	33325	2.02	8.0E-51	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
3015	15781	28430	0.9	7.0E-51	AW274720.1	EST_HUMAN	x034a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695664 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
3276	16037	28687	1.45	7.0E-51	AW890219.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
4146	16888	29519	1.37	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4146	16888	29520	1.37	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4318	17057	29681	2.71	7.0E-51	AW286603.1	EST_HUMAN	U1-HBW0-aip-b-05-0.U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729817 3'
11686	24261	37603	1.34	7.0E-51	AF161449.1	NT	Homo sapiens HSPC331 mRNA, partial cds
1972	14708	27426	4.96	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3468	16222	28876	14.73	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
5001	16686	31634	1.56	6.0E-51	X01788.1	NT	Human haptoglobin related (Hpr) gene exon 3
5912	16896	31648	9.95	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
5912	16896	31649	9.95	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6083	19580	32615	1.02	6.0E-51	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6762	19536	32584	0.97	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC556990), mRNA
6888	17945	30540	2.2	6.0E-51	11426665	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
8035	21725	34878	0.68	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
8035	21725	34879	0.68	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
8582	22235	35419	2.18	6.0E-51	7681535	NT	Homo sapiens B9 protein (B9), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9602	22314	35511	0.67	6.0E-51	U50093.1	NT	Human ankyrin (ANK1) gene, exon 2
11221	23884	37169	1.51	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
11515	24115	37425	1.52	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
11515	24115	37426	1.52	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
774	13546	28207	11.81	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
785	13557	26219	1.96	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
970	15557	28400	0.95	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1803	14349	27038	0.96	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2801	15315	28052	8.67	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3925	16875	29316	1.52	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3825	16875	29317	1.52	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
11249	23911	37203	4.18	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
1163	13908	26571	3.65	3.0E-51	AI587348.1	EST_HUMAN	f81c08.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:224720 3' similar to gb:M26326
4292	17031	29659	1.87	3.0E-51	AL159142.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); Novel human gene mapping to chromosome 22
7479	20152	33246	3	3.0E-51	R15914.1	EST_HUMAN	ye47c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4 RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR5 repetitive element;
8738	21430		4.68	3.0E-51	M29063.1	NT	Human hnRNP G2 protein mRNA
8966	25430		0.47	3.0E-51	AW583777.1	EST_HUMAN	is04406.y1 Human Pancreatic Islets Homo sapiens cDNA 5'
357	13155	25796	2.01	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1683	14427	27124	6.16	2.0E-51	AA233352.1	EST_HUMAN	zr30a05.r1 Striatum NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233226 G233226 RTVL-H PROTEIN, contains LTR7.3 LTR7 repetitive element;
3716	16489	29107	1.57	2.0E-51	AI492415.1	EST_HUMAN	is27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4458	17194	29820	0.76	2.0E-51	AW137826.1	EST_HUMAN	U1-H-B1-adj-d-02-0-U1.1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
5352	18155	30837	0.7	2.0E-51	AI732851.1	EST_HUMAN	is34f08.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
5352	18155	30838	0.7	2.0E-51	AI732851.1	EST_HUMAN	is34f08.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
5925	18709	31663	3.66	2.0E-51	BE782015.1	EST_HUMAN	901470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7209	19894		0.81	2.0E-51	AF219627.1	NT	Homo sapiens diacylglycerol kinase lcta (DGKl) gene, exon 23

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7357	20038	33116	1.06	2.0E-51	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
8599	21291	34432	1.72	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
8599	21291	34433	1.72	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
8932	21623	34766	0.96	2.0E-51	11037064	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9412	22090	35261	1.45	2.0E-51	AI917078.1	EST_HUMAN	ts74a07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
9503	22156	35336	5.68	2.0E-51	BE165980.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
9519	22172	35355	0.8	2.0E-51	AB007926.1	NT	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10332	22979	36199	1.77	2.0E-51	AV682474.1	EST_HUMAN	Homo sapiens mRNA for KIAA0457 protein, partial cds
10370	23018	36232	2.67	2.0E-51	AA378559.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
11298	18155	30837	8.52	2.0E-51	AT732851.1	EST_HUMAN	EST81296 Synovial sarcoma Homo sapiens cDNA 5' end
11298	18155	30838	8.52	2.0E-51	AT732851.1	EST_HUMAN	ts34409.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
12523	24870	31017	2.1	2.0E-51	11419159	NT	P35436 GLUTAMATE [NM2A] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
112	12934	25571	5.74	1.0E-51	4503528	NT	P35436 GLUTAMATE [NM2A] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
1479	14226	30294	1.52	1.0E-51	BE779039.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4), mRNA
4659	17684	30294	4.1	1.0E-51	TI8862.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
5305	18110	30769	0.94	1.0E-51	AE72532.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCG12 5'
7549	20219	33322	0.81	1.0E-51	BF434359.1	EST_HUMAN	601464955F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868246 5'
7803	20498	33619	0.81	1.0E-51	BF434359.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b12056
11783	25434	36520	2	1.0E-51	AV760590.1	EST_HUMAN	ts39g02.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
10587	23282	36520	1.39	9.0E-52	R91638.1	EST_HUMAN	7c86b02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644091 3' similar to TR:P87882 P87882
10587	23282	36521	1.39	9.0E-52	R91638.1	EST_HUMAN	PROTEASE ;
12301	24726		5.36	9.0E-52	AA77621.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSB02 5'
148	12983	25605	9.99	8.0E-52	AA720574.1	EST_HUMAN	YQ10H04.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:196567 5' similar to
1482	14229	26915	1.65	8.0E-52	X94900.1	NT	SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
							YQ10H04.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:196567 5' similar to
							SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
							ts85a07.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to
							contains THR.B THR repetitive element ;
							rw21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
							THR repetitive element ;
							H.sapiens mRNA for laminin-5, alpha3b chain

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1650	14396	27085	3.13	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1650	14396	27086	3.13	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3978	14396	27085	6.6	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3978	14396	27086	6.6	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7417	20094	33178	0.67	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7417	20094	33179	0.67	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
8911	21602	34745	2.04	7.0E-52	W56471.1	EST_HUMAN	zc59a06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element
1164	13918		0.76	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271299-049-007 BT0537 Homo sapiens cDNA
1689	14433	27129	4.27	6.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PST and hypothetical protein genes, complete cds; and S171 gene, partial cds
5841	18436	31349	0.86	6.0E-52	AI208794.1	EST_HUMAN	gg44f04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
							tz4h04.y1 NCJ CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;
11170	23837	37119	1.84	6.0E-52	BE048172.1	EST_HUMAN	Homo sapiens FSHD region gene 1 (FRG1), mRNA
9292	21959	35132	0.6	5.0E-52	11437365	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCYAP1R1) mRNA
1723	14466	27165	1.32	4.0E-52	4501922	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
1780	14521	27225	1.02	4.0E-52	4758843	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3906	16856	29297	0.99	4.0E-52	4507500	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5204	18012	30633	1.33	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5204	18012	30634	1.33	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
7938	20633	33760	1.74	4.0E-52	BE622032.1	EST_HUMAN	801440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5'
8432	21125	34263	5.48	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17 beta) dehydrogenase 4 (HSD17B4), mRNA
12143	24631		5.11	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12627	24930		5.23	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P20M, complete cds
4071	16815		10.57	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
549	13332	25962	2.88	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
549	13332	25963	2.88	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment

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2503	15220	27963	2.04	2.0E-52	BE207575.1	EST_HUMAN	bb66b07.yt NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zpk-1 zinc finger protein (MOUSE);
2740	15446		6.03	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
4920	17648	30260	2.13	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
4952	17678	30287	1.29	2.0E-52	A1141802.1	EST_HUMAN	qa56e05.s1 Soares_Nih-HMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
4952	17678	30288	1.28	2.0E-52	A1141802.1	EST_HUMAN	qa56e05.s1 Soares_Nih-HMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5617	18413	31326	4.11	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214:231299-053-E12 GT0214 Homo sapiens cDNA
6274	19047	32024	1.96	2.0E-52	11141868	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
6613	19376	32390	0.99	2.0E-52	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6843	19543	32571	1.17	2.0E-52	A1792146.1	EST_HUMAN	os45d12.y5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'
8551	21243		9.03	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
8634	21526	34672	0.81	2.0E-52	AA778795.1	EST_HUMAN	2445g05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9379	21954		0.88	2.0E-52	4758789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10015	22663	35879	5.53	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10015	22663	35880	5.53	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11165	23632	37111	3.15	2.0E-52	A1831482.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11165	23632	37112	3.15	2.0E-52	A1831482.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11178	23845	37131	3.09	2.0E-52	A7715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCSAIE03 5'
11325	24016		1.72	2.0E-52	W70260.1	EST_HUMAN	zd48g12.11 Soares_fetal_heart_NH-H19W Homo sapiens cDNA clone IMAGE:344038 5'
11618	24215		2.76	2.0E-52	11417690	NT	Homo sapiens LIM domain kinase 2 (LMK2), mRNA
11961	25408	30601	24.36	2.0E-52	AW236297.1	EST_HUMAN	an72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Adu repetitive element; contains element LTR2 repetitive element;
12350	24756		4.49	2.0E-52	A1808985.1	EST_HUMAN	wf67d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859 Q16859 CARBOXYLESTERASE;
520	13304	25937	1.96	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1350	14098	26773	37.84	1.0E-52	4504026	NT	Homo sapiens glutamate-aminonia ligase (glutamine synthase) (GLUL) mRNA
2537	15252		0.9	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA polyreverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
3055	15821	28465	2.67	1.0E-52	S61070.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
5250	18056	30684	4.35	1.0E-52	M29426.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
6300	19073	32059	2.51	1.0E-52	U38864.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7330	20012	33090	5.31	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8364	21057		1.2	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8087	21776	34940	0.75	1.0E-52	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10476	23122		1.03	1.0E-52	AW020370.1	EST_HUMAN	df08g05.v1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10486	23132		1.39	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10665	23356	36596	1.81	1.0E-52	U48266.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
10740	23427		2.09	1.0E-52	11426321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
3771	16523	29161	1.05	9.0E-53	4506064	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4359	17097	29732	1.96	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12189	24650		3.18	7.0E-53	BF238465.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:4132793 5'
12800	25285		4.92	7.0E-53	AM21782.1	EST_HUMAN	ff44107.x1 NCL CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2099077 3' similar to contains THR.11
5086	17805	30422	1.02	6.0E-53	BE295719.1	EST_HUMAN	THR repetitive element
4078	16822	29448	2.28	5.0E-53	4758543	NT	60175776F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3530948 5'
12236	24688		1.58	5.0E-53	AW813563.1	EST_HUMAN	Homo sapiens heterogenous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
48	12877	25502	2.76	4.0E-53	AL163285.2	NT	RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
48	12877	25503	2.76	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4771	17503	30125	1.03	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
9316	21983		0.66	4.0E-53	AI613037.1	EST_HUMAN	Y08H04.x1 NCL CGAP_UK3 Homo sapiens cDNA clone IMAGE:2278327 3'
9656	22308		0.87	4.0E-53	F13080.1	EST_HUMAN	HSC3D041 normalized infant brain cDNA Homo sapiens cDNA clone c-3l004
11175	23842	37126	2.78	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
11175	23842	37127	2.78	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2665	15375	28114	1.77	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4549	17284	29914	0.74	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA
5339	18142	30803	0.7	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5538	18336	31243	0.82	3.0E-53	11526297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6101	18878	31846	0.85	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
6988	19690	32740	1.04	3.0E-53	Y10388.3	NT	H. sapiens graf gene
6998	19690	32741	1.04	3.0E-53	Y10388.3	NT	H. sapiens graf gene
8203	20897	34034	12.52	3.0E-53	S72043.1	NT	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
8758	21460	34597	0.85	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8955	21646		8.41	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
11826	24410	37748	2.79	3.0E-53	8923599	NT	Homo sapiens hypothetical protein FLJ20844 (FLJ20844), mRNA

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445	13231		5.82	2.0E-53	AA366558.1	EST_HUMAN	EST17525 P ancreas tumor III Homo sapiens cDNA 5' end
2327	18052	27788	2.79	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2538	15253		8.73	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
2728	15438	28172	1.48	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2728	15438	28173	1.46	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3239	16001	28651	3.72	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4036	16781	29411	2.53	2.0E-53	M61873.1	NT	Human Kruppel-related DNA-binding protein (TF34) gene, partial cds
5340	18143	30804	2.67	2.0E-53	BF334740.1	EST_HUMAN	PM1-C10396-170800-001-g03 CT0396 Homo sapiens cDNA
5340	18143	30805	2.67	2.0E-53	BF334740.1	EST_HUMAN	PM1-C10396-170800-001-g03 CT0396 Homo sapiens cDNA
7770	20466	33590	1	2.0E-53	AW975598.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sapiens cDNA
8908	21975		3.82	2.0E-53	AW245676.1	EST_HUMAN	2822665 Forime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5'
1428	14175	28860	1.51	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
3404	16162	28813	1.08	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6583	19356	32370	1.52	1.0E-53	BF364201.1	EST_HUMAN	GM4-NN1028-150800-543-e02 NN1029 Homo sapiens cDNA
7147	19834	32903	0.68	1.0E-53	BE012071.1	EST_HUMAN	RCS-BN1058-270400-031-D07 BN1058 Homo sapiens cDNA
7836	20531	33658	0.54	1.0E-53	AA248072.1	EST_HUMAN	19571.seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8957	21877	34828	5.91	1.0E-53	X79538.1	NT	H. sapiens mRNA for hnRNPcore protein A1
11833	24417	37757	1.41	1.0E-53	X98411.1	NT	H. sapiens mRNA for myosin-IE
11833	24417	37758	1.41	1.0E-53	X98411.1	NT	H. sapiens mRNA for myosin-IE
11955	24507	37255	2.28	1.0E-53	AW245422.1	EST_HUMAN	2822943 3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822943 3'
5219	25063	30651	6.16	9.0E-54	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
202	13015	25655	2.4	8.0E-54	BE398785.1	EST_HUMAN	601272833F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1827	14568	27278	1.77	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
5845	18633	31568	26.87	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
375	13200	25945	1.27	7.0E-54	AA812537.1	EST_HUMAN	at79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377048 3' similar to contains MER30.13 MER30 repetitive element;
1822	14561	27273	1.65	7.0E-54	Y16645.1	NT	Homo sapiens mRNA for monocyte chemoattractant protein-2
2202	14930	27687	6.38	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8to9weeks_2NbpHP869W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7_b3 LTR7 repetitive element;

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10028	22876	35892	2.08	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC83182), mRNA
11047	23717	36886	1.74	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11047	23717	36987	1.74	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11281	23923		4.35	7.0E-54	A180189.1	EST_HUMAN	q87g03.x1 Soares_fetal_heart_NH119W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 ORF repetitive element;
11811	24400	37736	1.49	7.0E-54	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11811	24400	37737	1.49	7.0E-54	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
122	12850	25465	1.41	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MCB, exon 4, 5 and partial cds
376	13201	25846	6.83	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
376	13201	25847	6.83	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3277	16038	28688	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3986	16734	29368	1.91	6.0E-54	4502872	NT	Homo sapiens chloride channel 8 (CLON8) mRNA
4429	17165	29794	0.86	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TFGAAC10 5'
4792	17523	30145	1.78	6.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4819	17550		1.15	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p66 isoform
11432	23199	38430	1.51	6.0E-54	AW813567.1	EST_HUMAN	RC3-ST0197-151099-011-f08 ST0197 Homo sapiens cDNA
2146	14876	27611	3.78	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
178	12990		13.34	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
936	13703	26368	57.5	4.0E-54	AA306784.1	EST_HUMAN	EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1798	14538	27248	3.22	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1798	14538	27249	3.22	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3199	15962		1	4.0E-54	A1935086.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329289 3' similar to TR:002711 O02711 PRO-POL-DUTPASE POLYPROTEIN;
92	12318	25555	4.47	3.0E-54	AA313487.1	EST_HUMAN	EST185371 Odon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
1565	14312		0.91	3.0E-54	AW515742.1	EST_HUMAN	h387g08.x1 NCI_CGAP_G068 Homo sapiens cDNA clone IMAGE:2316542 3'
2574	15288	28025	0.96	3.0E-54	AL110383.1	EST_HUMAN	DKFZp434E0731_t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731 5'
2630	15342		1.34	3.0E-54	A1908757.1	EST_HUMAN	IL-BT195-190399-007 BT189 Homo sapiens cDNA
5814	18803	31531	1.74	3.0E-54	4502434	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7288	19971	33048	2.1	3.0E-54	AA844061.1	EST_HUMAN	a192c08.s1 Soares_parathyroid_tumor_NH1PA Homo sapiens cDNA clone IMAGE:1388270 3'
7288	19971	33049	2.1	3.0E-54	AA844061.1	EST_HUMAN	a192c08.s1 Soares_parathyroid_tumor_NH1PA Homo sapiens cDNA clone IMAGE:1388270 3'

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10949	23827		1.83	3.0E-54	11434806	NT	Homo sapiens golgi autanigen, golgi subfamily a, 5 (GOLGA5), mRNA
11024	23696	36959	4.93	3.0E-54	BF345600.1	EST_HUMAN	80201940BF1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155121 5'
11341	24031	37335	3.26	3.0E-54	AA393362.1	EST_HUMAN	270112.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
12056	24573	31119	2.98	3.0E-54	AW954559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
12097	25373		2.51	3.0E-54	AW748965.1	EST_HUMAN	EST366829 MAGC resequences, MAGC Homo sapiens cDNA
627	13406	26040	8.86	2.0E-54	5031900	NT	RC1-BT0313-131199-011-509 BT0313 Homo sapiens cDNA
1344	14092	26767	0.96	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1539	14266	26972	1.37	2.0E-54	AA655008.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2541	15255	27995	1.22	2.0E-54	AW163175.1	EST_HUMAN	nt78a09.s1 NCI_CGAP_P13 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element ;
2608	15320	28062	1.85	2.0E-54	AL163210.2	NT	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW_CUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
2896	15663	28311	1.52	2.0E-54	AW057524.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3311	16071	28721	1.18	2.0E-54	AJ278314.1	NT	hy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
3536	16292		3.2	2.0E-54	AA632925.1	EST_HUMAN	Homo sapiens mRNA for phospholipase C-beta-1b (PLCB1 gene)
4181	16921		2.08	2.0E-54	4502642	NT	nt45g09.s1 NCI_CGAP_P13 Homo sapiens cDNA clone IMAGE:395488 similar to gb:X53777 60S
4825	17556	30178	1.02	2.0E-54	7706448	NT	RIBOSOMAL PROTEIN L23 (HUMAN).
5388	18188	30890	1.84	2.0E-54	4759069	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
5516	18314	31216	1.2	2.0E-54	BE047864.1	EST_HUMAN	Homo sapiens peptidylarginine deaminase type III (LOC51702), mRNA
5675	18469	31365	5.04	2.0E-54	11426657	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5771	18562	31489	13.99	2.0E-54	AB046811.1	NT	tz43c11.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
5771	18562	31490	13.99	2.0E-54	AB046811.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6559	19324	32331	0.88	2.0E-54	AF008915.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
6713	19628	32672	0.85	2.0E-54	AB023212.1	NT	Homo sapiens EV18 homolog mRNA, complete cds
6713	19628	32673	0.85	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
7023	19715	32772	8.8	2.0E-54	11426544	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
9529	22182	35368	4.11	2.0E-54	AB001025.1	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
9909	22558	35793	0.79	2.0E-54	11429127	NT	Homo sapiens mRNA for brain dynodine receptor, complete cds
10021	22669	35885	1.01	2.0E-54	11416782	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10021	22669	35888	1.01	2.0E-54	11416782	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10021	22669	35888	1.01	2.0E-54	11416782	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA

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10947	19324	32331	1.57	2.0E-54	AF009915.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
11727	24321		2.86	2.0E-54	7857454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
4432	17168		1.22	1.0E-54	BF315418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128835 5'
10153	22801	36018	0.52	1.0E-54	AA412409.1	EST_HUMAN	zu10e09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
10153	22801	36019	0.52	1.0E-54	AA412409.1	EST_HUMAN	zu10e09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
12710	24986		2.17	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugeno cDNA library Homo sapiens cDNA clone Zv6C380 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
10257	22905	36115	0.94	9.0E-55	BE081469.1	EST_HUMAN	QV2-BT0635-160400-143-H12 BT0635 Homo sapiens cDNA
1292	14041		1.09	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1295	14044		2.63	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11151	23818		1.67	8.0E-55	AW409714.1	EST_HUMAN	h02802.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980907 5'
1059	13817	26479	0.77	7.0E-55	R09346.1	EST_HUMAN	Y28e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to SP-C661_BOVIN P10897 CYTOCHROME
8703	21395		0.8	7.0E-55	AW103839.1	EST_HUMAN	xd76c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603522 3' similar to TR:060365
9080	21769	34932	1.26	7.0E-55	AA889581.1	EST_HUMAN	060365 FOS39554_1
9115	21803	34968	2.16	7.0E-55	AU139909.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407280 3'
11171	23838	37120	10.32	7.0E-55	A1561056.1	EST_HUMAN	AU139909 PLACET1 Homo sapiens cDNA clone PLAGE1011578 5'
11171	23838	37121	10.32	7.0E-55	A1561056.1	EST_HUMAN	h02909.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
12682	25303		2.5	7.0E-55	H23396.1	EST_HUMAN	h02909.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
11498	24099	37412	2.45	6.0E-55	AB040834.1	NT	ym57g07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32444 5'
1763	14505	27205	1.19	5.0E-55	AA704971.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
1763	14505	27206	1.19	5.0E-55	AA704971.1	EST_HUMAN	z95509.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
4720	17452	30086	1.81	5.0E-55	AW206021.1	EST_HUMAN	z95509.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
6448	18214	32211	1.65	5.0E-55	4502240	NT	UI-H-B11-afy-g-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'
6446	19214	32212	1.65	5.0E-55	4502240	NT	Homo sapiens arylsulfinase E (chondrodysplasia punctata 1) (ARSE), mRNA
6568	25094	32340	1.34	5.0E-55	4505952	NT	Homo sapiens arylsulfinase E (chondrodysplasia punctata 1) (ARSE), mRNA
6568	25094	32341	1.34	5.0E-55	4505952	NT	Homo sapiens arylsulfinase E (chondrodysplasia punctata 1) (ARSE), mRNA
6637	19672	32718	0.83	5.0E-55	7382477	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
7195	19881	32955	0.7	5.0E-55	11434422	NT	Homo sapiens Rho GTPase activating protein 6 (RHGAP6), transcript variant 5, mRNA
7693	20598	33718	0.72	5.0E-55	11526491	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
8842	21633	34777	3.53	5.0E-55	4506302	NT	Homo sapiens BCL2-associated athanogene (BAG1), mRNA
9219	21898		1.75	5.0E-55	BE064386.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
9937	22585	35786	1.77	5.0E-55	AB074511.1	NT	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
							Homo sapiens mRNA for KIAA0811 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9937	22585	35787	1.77	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10122	22770	35984	2.48	5.0E-55	5453765	NT	Homo sapiens nei (chicken)-like 2 (NELL2), mRNA
12137	24626		2.73	5.0E-55	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
657	13434	26075	65.4	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMV1A1) mRNA
1421	14189	28853	1.78	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3788), mRNA
1421	14189	26854	1.78	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3788), mRNA
1504	14250		1.7	4.0E-55	BF061411.1	EST_HUMAN	7152b10.x1 Soares NSF F8 9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L13 L1 repetitive element;
2019	14754	27482	0.97	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2019	14754	27483	0.97	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2079	14811	27542	6.47	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2079	14811	27543	6.47	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2308	15033	27771	2.29	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
2596	15310		1.21	4.0E-55	AJ271735.1	NT	Homo sapiens Xq pseudocautosomal region; segment 1/2
8242	20938		8.37	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11194	23859		2.3	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12057	24574		3.05	4.0E-55	BF303941.1	EST_HUMAN	601886575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
11998	24536		1.5	3.0E-55	BE176519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
12721	24993		1.85	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
368	13164	25907	1.98	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
538	13321		1.13	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
634	13413	26049	13.79	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products
4723	17455	30090	2.91	2.0E-55	BE719988.1	EST_HUMAN	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7403	25113	33162	0.76	2.0E-55	AW501988.1	EST_HUMAN	UI-HF-BNO-eks-f06-Q.U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
8963	21694	34804	0.52	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_KW11 Homo sapiens cDNA clone IMAGE:3134463 3'
8963	21694	34805	0.52	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_KW11 Homo sapiens cDNA clone IMAGE:3134463 3'
9058	21747		6.23	2.0E-55	AJ002836.1	EST_HUMAN	arr88h05.a1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR_b2 THR repetitive element;
9140	21828		0.72	2.0E-55	BE007659.1	EST_HUMAN	QV0-BN0147-280400-213-g06 BN0147 Homo sapiens cDNA
10870	23550	36798	1.95	2.0E-55	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
96	12921	25558	3.01	1.0E-55	4506080	NT	Homo sapiens marnose-6-phosphate receptor (cation dependent) (M6PR) mRNA
184	12997	25636	8.22	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabelia2) mRNA, complete cds
1127	13863	28543	3.53	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1943	14678	27391	1.58	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
1943	14678	27392	1.58	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2324	15049		2.48	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2338	15528	27799	1.17	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript 1 (TTY1) mRNA, partial cds
2521	15237	27976	9.05	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2559	15273	28009	4.19	1.0E-55	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2559	15273	28010	4.19	1.0E-55	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2617	15328	28071	1.72	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
3970	16719	29353	4.28	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4262	17003	29635	1.26	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4682	17416		1.02	1.0E-55	N77261.1	EST_HUMAN	y44g03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245620 5'
5410	18209	30917	0.97	1.0E-55	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6178	18955	31929	6.82	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6178	18955	31930	6.82	1.0E-55	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7888	20583	33712	1.64	1.0E-55	11432894	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
7888	20583	33713	1.84	1.0E-55	11432894	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
7980	20875	33789	0.89	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
7980	20875	33800	0.89	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
10829	23511	36751	1.75	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
10829	23511	36752	1.75	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11425	23192	36423	2.53	1.0E-55	U50850.1	NT	Homo sapiens chromosome 21 segment HS21C010
							Human infant brain unknown product mRNA, complete cds
11444	23211	36442	1.5	1.0E-55	T10045.1	EST_HUMAN	seq1575 b4HB3MA Co8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F161 5' similar to similar
11569	24188	37482	2.35	1.0E-55	10587821	NT	to Chinese Hamster DHFR-coamplified protein mRNA
7285	19949	33028	1.83	9.0E-56	BE378074.1	EST_HUMAN	Homo sapiens DNA-binding protein (LOC56242), mRNA
							601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
2737	15444	28182	5.32	7.0E-56	H19834.1	EST_HUMAN	y62g03.r1 Soares adult brain N265HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains
7540	20210	33309	1.67	7.0E-56	AW361213.1	EST_HUMAN	THR repetitive element;
7540	20210	33310	1.67	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1687	14431	27127	1.78	5.0E-56	AW997712.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
9059	21748	34908	0.86	5.0E-56	AW015507.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
10286	23534		1.81	5.0E-56	W28189.1	EST_HUMAN	UHL-B10p-aa-a-05-0-UI.s1 NCL CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
12220	25359	30610	2	5.0E-56	H55099.1	EST_HUMAN	49c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
26	12854	25488	8.58	4.0E-56	AF141349.1	NT	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
							Homo sapiens beta-tubulin mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
26	12854	25470	8.58	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2173	14902		2.69	4.0E-56	BF207586.1	EST_HUMAN	601862059F1 NIH MGC_53 Homo sapiens cDNA clone IMAGE:4081551 5'
2712	15419	28157	7.28	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2712	15419	28158	7.28	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2815	13297	25929	3.49	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2836	15331	28074	1.48	4.0E-56	AF32488.1	EST_HUMAN	w609708.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2305101 3' similar to SW:DCOR_MUSPA
2836	15331	28075	1.48	4.0E-56	AF32488.1	EST_HUMAN	P27119 ORNITHINE DECARBOXYLASE ;
6164	18941	31912	6.01	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6164	18941	31913	6.01	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10403	23049	36266	2.02	4.0E-56	AF043349.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
10841	23523	36764	8.88	4.0E-56	AF498066.1	EST_HUMAN	im65q12.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
10841	23523	36765	8.88	4.0E-56	AF498066.1	EST_HUMAN	im65q12.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
1319	14068	26742	4.17	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
3122	15887	28527	1.54	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3122	15887	28528	1.54	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3815	16567	29728	1.61	3.0E-56	AF055068.1	NT	Homo sapiens MHC class 1 region
4355	17093	29728	1.43	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4390	17127	29759	4.27	3.0E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4534	17269	29902	2.34	3.0E-56	5902085	NT	Homo sapiens superkiller viralkidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
5598	18393	31302	2.12	3.0E-56	4759163	NT	Homo sapiens sparc/osteoblast, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5598	18393	31303	2.12	3.0E-56	4759163	NT	Homo sapiens sparc/osteoblast, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6775	19519	32547	7.03	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7223	19508	32981	1.15	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
7223	19508	32982	1.15	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
8715	21407	34550	4.68	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8713	22364	35662	0.85	3.0E-56	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10379	23025	36240	1.38	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10842	23333	36571	1.71	3.0E-56	AB042556.1	NT	Homo sapiens mRNA, similar to rat myomesalin, complete cds
11284	23945	37239	6.37	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA

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11284	23945	37240	6.37	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11673	24268	37590	1.74	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
11673	24268	37591	1.74	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
12095	24597	31083	1.52	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12095	24597	31084	1.52	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
511	13295		1.7	2.0E-56	AA199818.1	EST_HUMAN	z652a08.s1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645206 3'
716	15550	26141	1.05	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
716	15550	26142	1.05	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2887	15753	28399	1.18	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3523	16279	28934	1.64	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
6990	19683	32731	1.47	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
959	13724		1.84	1.0E-56	AF190930.1	NT	Macaca fascicularis protein Mrosine phosphatase (PRL-1) mRNA, complete cds
3684	16417	29056	2.15	1.0E-56	AW599833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946452 3'
3684	16417	29057	2.15	1.0E-56	AW599833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946452 3'
4972	17696	30303	0.99	1.0E-56	AI905162.1	EST_HUMAN	QV-BT077-130199-079 BT077 Homo sapiens cDNA
5118	17838	30453	0.97	1.0E-56	6681002	NT	Mus musculus cytoplasmic polyadenylation element binding protein (Cpeb), mRNA
6724	19558	32589	0.57	1.0E-56	AW609520.1	EST_HUMAN	MR3-ST0203-180100-208-H02 ST0203 Homo sapiens cDNA
9855	22505		0.59	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9948	22596	35800	1.71	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220999-001-E02 CT0163 Homo sapiens cDNA
611	13389		2.52	9.0E-57	AW880885.1	EST_HUMAN	QV0-Q10033-070300-152-h03 OT0033 Homo sapiens cDNA
4180	16920	29548	1.14	9.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4180	16920	29549	1.14	9.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
11183	20848	37134	2.17	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11183	20848	37135	2.17	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11506	24107	37420	1.48	9.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
290	13096	25738	3.01	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-005 ST0234 Homo sapiens cDNA
884	13633	26303	6.36	8.0E-57	AW284599.1	EST_HUMAN	xc05d10.x1 NCI_CGAP_Brm63 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1809	14549	27284	1.51	8.0E-57	AA496109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
3376	16135	28791	0.98	8.0E-57	4758279	NT	z651b12.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:757151 5'
3376	16135	28792	0.98	8.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4852	17582	30205	1.3	8.0E-57	4557830	NT	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4) mRNA
5161	25276	30728	3.29	8.0E-57	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6306	19078	32063	1.85	8.0E-57	AB020705.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds

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Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6372	19141	32137	12.87	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
6372	19141	32138	12.87	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7349	20030	33107	0.64	8.0E-57	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7648	20312	33423	1.7	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
7648	20312	33424	1.7	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11460	17889	30487	3.29	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12459	24828	31028	2.74	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12473	24828	31028	1.69	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12820	25060		2.07	8.0E-57	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2639	15350	28063	1.71	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2639	15350	28094	1.71	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3244	16006	28655	0.9	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3244	16006	28656	0.9	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3265	16027	28677	1.08	7.0E-57	6005678	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3658	16608	29246	1.39	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3858	16608	29247	1.39	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
4388	17135		0.95	7.0E-57	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4730	17482	30089	0.95	7.0E-57	U11058.2	NT	Homo sapiens large conductance calcium- and voltage-dependent potassium channel alpha subunit (MaxK) mRNA, complete cds
12785	25310		2.63	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3736	16489	29125	1.67	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
786	13558	28220	0.78	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1308	14056		16.24	3.0E-57	AA230278.1	EST_HUMAN	nc1307.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2360	15111	27848	2.99	3.0E-57	AA348335.1	EST_HUMAN	P46783.40S RIBOSOMAL PROTEIN S10. ;
2707	15414	28151	0.95	3.0E-57	BE676822.1	EST_HUMAN	EST154770 Hippocampus II Homo sapiens cDNA 5' end
2707	15414	28152	0.95	3.0E-57	BE676822.1	EST_HUMAN	733b10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H9C.2
3550	16305	28955	1.74	3.0E-57	AF232708.1	NT	CE20263 ;
3685	16438		62.34	3.0E-57	AW853964.1	EST_HUMAN	733b10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H9C.2
							Homo sapiens cell-line tsA201a chloride ion current inducer protein [(Ch) gene, complete cds
							RC3-C10254-110300-027-d10 C10254 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5939	18721	31680	1.24	3.0E-57	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6033	18813	31773	3.23	3.0E-57	BE789537.1	EST_HUMAN	601598986F NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8044	20738	33871	3.77	3.0E-57	W28130.1	EST_HUMAN	4268 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8070	20764	33892	2.16	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11856 (FLJ11856), mRNA
8079	20764	33893	2.16	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11856 (FLJ11856), mRNA
8179	20873	34008	0.7	3.0E-57	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
8328	21021	34157	0.73	3.0E-57	J05262.1	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
8757	21449	34596	4.17	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9149	21880	35047	1.03	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
9149	21880	35048	1.03	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
10825	23508	36747	2.85	3.0E-57	AW248374.1	EST_HUMAN	2820473 Spime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
12101	25381	30618	8.38	3.0E-57	W23871.1	EST_HUMAN	zb45d11.1 Soares_Tetralung_NHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12460	25281	31010	2.32	3.0E-57	AW178575.1	EST_HUMAN	RC0-HT012-080999-001-C06 HT012 Homo sapiens cDNA
12623	24928	31010	1.48	3.0E-57	AJ003849.1	EST_HUMAN	AJ003849 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1p10-1L1
1487	14234	26919	1.39	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1487	14234	26920	1.39	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3432	16188	29301	1.24	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3910	16660	29301	0.79	2.0E-57	BE073284.1	EST_HUMAN	MRO-BT0551-060300-103-b03 BT0551 Homo sapiens cDNA
4474	17209	28834	6.73	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5582	18379		1.84	2.0E-57	AA016131.1	EST_HUMAN	ze31c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380584 5' similar to contains L1.13 L1 repetitive element;
5943	18725		33.81	2.0E-57	BF115266.1	EST_HUMAN	7n80f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570988 3' similar to contains TAR1.1
6067	18848	31810	0.86	2.0E-57	11431281	NT	MER22 repetitive element;
8526	21221	34363	1.08	2.0E-57	AF045452.1	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
8746	22397	35602	1.86	2.0E-57	AF057722.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
10525	23171	36398	0.49	2.0E-57	11434330	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
10525	23171	36399	0.49	2.0E-57	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
11238	23901	37189	2.42	2.0E-57	11424084	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
11238	23901	37190	2.42	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
8593	21286		3.82	1.0E-57	BE043031.1	EST_HUMAN	h032a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039082 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN;
12249	24696		5.08	1.0E-57	AW470791.1	EST_HUMAN	h033d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2876499 3' similar to contains THR.b3 THR repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5591	18387	31297	0.99	9.0E-58	AA297847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
12516	24865	31015	1.55	9.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3831000 5'
575	13355		1.76	8.0E-58	BE688715.1	EST_HUMAN	601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
639	13418	26055	4.18	8.0E-58	AI798376.1	EST_HUMAN	t34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
639	13418	26056	4.18	8.0E-58	AI798376.1	EST_HUMAN	t34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1849	14587	27301	2.37	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1849	14587	27302	2.37	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2974	15740		2.32	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
10762	23446		5.87	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
10847	23529	36773	3.6	7.0E-58	AW504108.1	EST_HUMAN	UI-HF-BND-ai-g-10-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
10847	23529	36774	3.6	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BND-ai-g-10-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2251	14979	27718	1.02	6.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3831000 5'
2375	15097	27837	3.78	8.0E-58	AU130689	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2902	15668	28316	1.2	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2902	15668	28317	1.2	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
6078	18857	31824	1.01	6.0E-58	AF106811.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10208	22856	36072	0.79	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12347	24754		1.58	6.0E-58	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
293	13099	25740	3.79	5.0E-58	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
694	13469	26116	5.41	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-018-b05 NT0057 Homo sapiens cDNA
1172	13926	26589	2.96	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1172	13926	26590	2.96	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1173	13926	26589	2.76	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1173	13926	26590	2.76	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3317	16077	28727	4.32	5.0E-58	AA888183.1	EST_HUMAN	cc58e07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4229	16970	29594	0.92	5.0E-58	AI636745.1	EST_HUMAN	ts89e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA
5541	18338		2.32	5.0E-58	11496282	NT	P19884 PROFILIN II ;
6085	18863	31829	6.86	5.0E-58	H23072.1	EST_HUMAN	Homo sapiens placenta-specific 1 (PLAC1), mRNA
							ym51107.r1 Soares Infant brain 1N18 Homo sapiens cDNA clone IMAGE:52071 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6301	19074	32060	0.95	5.0E-58	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6378	19148	32147	1.61	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
6680	19597	32635	0.88	5.0E-58	AF051334.1	NT	Homo sapiens ribirin (NBS) mRNA, complete cds
6680	19597	32636	0.88	5.0E-58	AF051334.1	NT	Homo sapiens ribirin (NBS) mRNA, complete cds
7006	19698	32752	0.73	5.0E-58	4885400	NT	Homo sapiens holochochrome c synthase (cytochrome c heme-lyase) (HCCS) mRNA
7969	20564	33691	7.69	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
8251	20945	34083	0.7	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
9239	21918	35089	0.68	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6PL) mRNA
9239	21918	35090	0.88	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6PL) mRNA
9757	22408	35614	0.83	5.0E-58	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10023	22671	35887	1.78	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10300	22947	36161	0.83	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10300	22947	36162	0.83	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
11819	24405	37740	2.69	5.0E-58	11431079	NT	Homo sapiens chimera (chimaerin) 1 (CHN1), mRNA
12071	25305		1.81	5.0E-58	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12512	25330		1.5	5.0E-58	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
12732	25001		2.87	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
364	13162	25804					Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
778	13551	26212	0.88	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1452	14199	26883	1.09	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2637	15349	28091	1.7	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3319	16079	28729	1.03	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3723	16478	29113	1.25	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
11315	23874	37275	7.06	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
328	13127	26781	2.57	3.0E-58	R17879.1	EST_HUMAN	y910a02.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
1368	14116	26781	2.36	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3174	15937	28585	2.78	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
3174	15937	28586	2.78	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
6167	18844	31915	0.83	3.0E-58	BE089509.1	EST_HUMAN	QV6-B10702-170400-194409 BT0702 Homo sapiens cDNA
6352	19122	32114	1.43	3.0E-58	F07056.1	EST_HUMAN	HSC1T0081 normalized infant brain cDNA Homo sapiens cDNA clone c-11g08
6544	19309	32314	1.4	3.0E-58	AV12977.1	EST_HUMAN	AV12977 DCA Homo sapiens cDNA clone DCAAZG04 5'
919	13686	28350	11.9	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1287	14016		10	2.0E-58	BE208532.1	EST_HUMAN	ba08607.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69381.60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987.M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5273	25065	30708	3.4	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5273	25065	30734	3.4	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5966	18748	31709	1.12	2.0E-58	BF513488.1	EST_HUMAN	U1H-BW1-ams-g-11-O-UJ.s1 NCL_CGAP_Sub57 Homo sapiens cDNA clone IMAGE:3071060 3'
							am57602.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP2K328.1 CE05065 UBIQUITIN CONJUGATING ENZYME/ RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6031	18811	31771	1.88	2.0E-58	A1124874.1	EST_HUMAN	yq08h06.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:196378 5'
6062	18841	31803	0.8	2.0E-58	R92567.1	EST_HUMAN	qm84c01.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1805424 3'
8828	19489	32511	1.12	2.0E-58	A1291407.1	EST_HUMAN	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7056	19747	32809	2.83	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7056	19747	32810	2.83	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
10641	23332	36570	21.77	2.0E-58	BF307745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
10885	23565	36813	2.43	2.0E-58	AW872641.1	EST_HUMAN	hm25f08.x1 NCL_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
705	13480	26128	0.86	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
1046	13805	26484	2.41	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1304	14053	26726	1.61	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1304	14053	26727	1.61	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1376	14124	26798	1.13	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alt repeat elements
2805	15510	28251	2.37	1.0E-58	4759169	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
2834	14738	27462	1.6	1.0E-58	5174444	NT	Homo sapiens G protein-coupled receptor 69A (GPR69A) mRNA
3526	16282	28938	0.86	1.0E-58	4759081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3526	16282	28939	0.86	1.0E-58	4759081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
4913	17641	30256	4.75	1.0E-58	A1141063.1	EST_HUMAN	hm24h01.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678128 3'
5751	18543	31465	1.31	1.0E-58	BE061860.1	EST_HUMAN	RC1-BT0254-290100-015-e01 BT0254 Homo sapiens cDNA
6764	19508	32533	0.8	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
8013	20708		0.5	1.0E-58	AW975307.1	EST_HUMAN	EST365637 MAGE resequences, MAGM Homo sapiens cDNA
8768	21460	34609	0.66	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (16kD) (MYOM2), mRNA
8880	21571	34714	0.91	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH09 5'
8979	21680	34818	0.66	1.0E-58	AA412397.1	EST_HUMAN	z69505.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
8979	21689	34819	0.66	1.0E-58	AA412397.1	EST_HUMAN	z69505.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
10086	22734	35949	1.21	1.0E-58	11432894	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11780	24371		2.11	1.0E-58	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
11816	24404	37739	1.57	1.0E-58	D81405.1	NT	Human MSH3 gene, exon 10
2225	14953	27691	29.49	8.0E-59	4507378	NT	Human TATA box binding protein (TBP) mRNA
8080	20774	33904	2.49	8.0E-59	A1761963.1	EST_HUMAN	wf50408.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
173	15536		1.74	6.0E-59	BF035327.1	EST_HUMAN	601458531F1 NH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
8144	20838	33970	0.61	6.0E-59	A1750970.1	EST_HUMAN	cn06h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06h02 random
1748	14490	27189	1.32	5.0E-59	AW157281.1	EST_HUMAN	au93h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.1
1748	14490	27190	1.32	5.0E-59	AW157281.1	EST_HUMAN	au93h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to
3124	15889	28530	6.98	5.0E-59	A1807484.1	EST_HUMAN	TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.1
4610	17345	29978	6.55	5.0E-59	X83497.1	NT	wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
6892	17968	30526	7.5	5.0E-59	AW162304.1	EST_HUMAN	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
8705	21397	34544	1.04	5.0E-59	11421778	NT	au68c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element
8604	22257	35443	1.62	5.0E-59	AV762869.1	EST_HUMAN	Homo sapiens polymerase (RNA) III (DNA directed) (39KD) (RPC39), mRNA
10823	23506	36745	3.78	5.0E-59	11434908	NT	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
776	13548	26210	1.56	4.0E-59	D80006.1	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
5450	18249	31138	1.03	4.0E-59	11034810	NT	Human mRNA for KIAA0184 gene, partial cds
12203	25238		1.91	4.0E-59	AF057720.1	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
9	12836		6.13	3.0E-59	AW865524.1	EST_HUMAN	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
219	13030	25666	4.58	3.0E-59	7662247	NT	EST377562 MAGE resequences, MAGI Homo sapiens cDNA
1705	14448	27147	8.2	3.0E-59	4505860	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1705	14448	27148	8.2	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2125	14856	27585	5.59	3.0E-59	AB028035.1	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2125	14856	27586	5.59	3.0E-59	AB028035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3128	15891	28534	3.77	3.0E-59	4502014	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3128	15891	28535	3.77	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3905	16557	29189	1.45	3.0E-59	4508044	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
4638	17372	30007	0.98	3.0E-59	AL163284.2	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4738	17470	30107	0.92	3.0E-59	4759329	NT	Homo sapiens chromosome 21 segment HS21C084
							Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4789	17520	30143	1.57	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
4890	17713		0.97	3.0E-59	M95961.1	NT	Human prolactin converting enzyme (NEC2) gene, exon 2
6126	18904	31872	2.12	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7259	19943	33020	1.94	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
7832	20527	33653	1.16	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
7832	20527	33654	1.16	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
9844	22592	35794	0.87	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
9844	22592	35795	0.87	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12327	24746		6.04	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
7893	20357		0.71	2.0E-59	BF373329.1	EST_HUMAN	MRO-FT0144-250700-002-a10 FT0144 Homo sapiens cDNA
9537	22190		6.32	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
10425	23071		1.19	2.0E-59	BF365554.1	EST_HUMAN	RCO-NT0036-100700-032-a07 NT0036 Homo sapiens cDNA
10734	23421	36563	2.6	2.0E-59	AW410698.1	EST_HUMAN	fl07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
10734	23421	36564	2.6	2.0E-59	AW410698.1	EST_HUMAN	fl07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
11311	23970	37274	1.31	2.0E-59	H61604.1	EST_HUMAN	y49h09.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208873 5' similar to SP:POL_FENV1 P31792 POL POLYPROTEIN ;
12091	24595	31126	2.93	2.0E-59	A1631809.1	EST_HUMAN	wa36c12.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
12605	25263	30719	4.85	2.0E-59	L11845.1	NT	Q86542 RTVL-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
159	12974		3.03	1.0E-59	BE26641.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
1529	14276	26964	0.93	1.0E-59	T92522.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
2412	15133	27870	1.19	1.0E-59	D11456.2	NT	ye25609.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118768 5' similar to SP:S21348
2412	15133	27871	1.19	1.0E-59	D11456.2	NT	S21348 HYPOTHETICAL PROTEIN 4 - ;
2623	18335		2.47	1.0E-59	AA748468.1	EST_HUMAN	Homo sapiens Xdha mRNA for xanthine dehydrogenase, complete cds
7462	20135	33227	1.08	1.0E-59	AJ130894.1	NT	Homo sapiens Xdha mRNA for xanthine dehydrogenase, complete cds
7617	20283	33392	0.97	1.0E-59	BE256814.1	EST_HUMAN	Q13537 MER37 TRANSCRIPTION ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7617	20283	33393	0.97	1.0E-59	BE256814.1	EST_HUMAN	Q13537 MER37 TRANSCRIPTION ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9285	22039	35210	0.86	1.0E-59	11419630	NT	Q13537 MER37 TRANSCRIPTION ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9504	22157	35337	0.54	1.0E-59	11428949	NT	Homo sapiens mRNA for transcription factor
9504	22157	35338	0.54	1.0E-59	11428949	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
10760	20135	33227	12.88	1.0E-59	AJ130894.1	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
747	13520	26176	0.85	8.0E-60	AW977845.1	EST_HUMAN	Homo sapiens mRNA for transcription factor

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1455	14202	26886	2.65	8.0E-60	4759159	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2169	14898	27632	3.8	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2169	14898	27633	3.6	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
5892	18677	31623	1.12	8.0E-60	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6411	19179	32178	1.07	8.0E-60	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
7596	20264	33372	1.07	8.0E-60	11420841	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA
7865	20560	33687	2.28	8.0E-60	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8837	21529	34875	2.6	8.0E-60	11428949	NT	Homo sapiens S-antigen, retina and pineal gland (arrestin) (SAG), mRNA
9371	21946	35119	0.96	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9371	21946	35119	0.96	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10473	23119	36348	0.59	8.0E-60	5453987	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10736	23423	36666	6.36	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10736	23423	36667	6.36	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
737	13511	26169	3.61	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
738	13511	26169	17.82	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
796	13568	28228	0.98	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2124	14855	27584	1.08	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2788	15493	28233	1.53	7.0E-60	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4158	16898	29627	2.58	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
9307	21974	35149	4.02	7.0E-60	H58041.1	EST_HUMAN	Y12104.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
11337	24027	37331	2.11	7.0E-60	H58041.1	EST_HUMAN	Y12104.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
2177	14908	27639	1.06	6.0E-60	BE984974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
8336	21029		10.5	6.0E-60	H52456.1	EST_HUMAN	Y178109.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains OFR repetitive element;
82	12908	25545	2.29	5.0E-60	AI807817.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
82	12908	25548	2.29	5.0E-60	AI807817.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2972	15738		1.27	4.0E-60	AA299037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
							tr81R05.x1 NCL_CQAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
7253	19937	33012	0.89	4.0E-60	BF196068.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1;
9024	21714		0.68	4.0E-60	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11267	23929	37219	1.28	4.0E-60	11433597	NT	Homo sapiens v-far-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11267	23929	37220	1.29	4.0E-60	11433597	NT	Homo sapiens v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
1852	14590	27305	4.44	3.0E-60	BE562611.1	EST_HUMAN	601338446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1852	14590	27306	4.44	3.0E-60	BE562611.1	EST_HUMAN	601338446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1862	14600		1.92	3.0E-60	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
4424	17160	29790	1.94	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
5294	18099	30758	0.57	3.0E-60	BF365143.1	EST_HUMAN	QV4-NN1149-250900-423-01 NN1149 Homo sapiens cDNA
5554	18351	31260	2.12	3.0E-60	AW836196.1	EST_HUMAN	RC3-L10023-200100-012-a01 L10023 Homo sapiens cDNA
6856	17933	30569	1	3.0E-60	AJ792814.1	EST_HUMAN	o60h11.y5 NCL CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE
8301	20995	34132	4.97	3.0E-60	5174644	NT	P52624 URIDINE PHOSPHORYLASE;
8301	20995	34133	4.97	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8482	21174	34319	0.51	3.0E-60	AJ040235.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8641	21333	34477	4.32	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
9559	22212	35398	0.47	3.0E-60	BF102812.1	EST_HUMAN	601646227F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3830990 5'
11162	23829	37107	1.26	3.0E-60	11427120	NT	Homo sapiens CGI-152 protein (LOC57130), mRNA
11162	23829	37108	1.26	3.0E-60	11427120	NT	Homo sapiens CGI-152 protein (LOC57130), mRNA
12686	25297		2.06	3.0E-60	AA485286.1	EST_HUMAN	ab07h04.r1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.H1 LTR10 repetitive element;
29	12857	25474	3.63	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1404	14151	26831	7.35	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to raf ERK2
1715	14458	27155	1.28	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
1724	14467	27166	1.59	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2714	15421	28160	1.96	2.0E-60	AW978005.1	EST_HUMAN	EST390T14 MAGE resequences, MAGE Homo sapiens cDNA
3568	18321	28989	0.89	2.0E-60	4757887	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3895	16845	29285	0.73	2.0E-60	AF231818.1	NT	Homo sapiens chromosome 21 unknown mRNA
6208	18983	31962	0.86	2.0E-60	AJ791952.1	EST_HUMAN	nm01112.y5 NCL CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.H1 THR repetitive element;
6400	19169	32168	1.87	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6615	18378	32393	0.96	2.0E-60	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
6750	17918	30583	2.43	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6750	17919	30584	2.43	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7010	19702	32757	2.73	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7010	19702	32758	2.73	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7124	19812	32880	0.59	2.0E-60	AI308124.1	EST_HUMAN	b23d09.x1 NCL CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2055185 3' similar to SW:GALR_RAT
7532	20202		0.79	2.0E-60	BF512608.1	EST_HUMAN	Q62805 GALANIN RECEPTOR
7904	20596	33729	0.84	2.0E-60	X85597.1	EST_HUMAN	UIH-BW1-amy-c-02-U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
8768	21458	34808	3.01	2.0E-60	L36033.1	NT	HS15BEST human adult testis Homo sapiens cDNA clone CAM_IEST15
							Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
9878	22528	35724	2.29	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TIM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
9878	22528	35725	2.29	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TIM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
11449	23216	36448	1.53	2.0E-60	11434729	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5), mRNA
11809	24398	37732	1.8	2.0E-60	BF530674.1	EST_HUMAN	602071973F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214683 5'
11809	24398	37733	1.8	2.0E-60	BF530674.1	EST_HUMAN	602071973F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214683 5'
12364	24767		3.02	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12494	25228		1.93	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12496	24851		2.34	2.0E-60	11418068	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC63504), mRNA
12510	24862		1.77	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
509	13293	25925	1.13	1.0E-60	BE178568.1	EST_HUMAN	PM3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA
3882	16632	29271	1.16	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
4901	17628	30245	1.2	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7848	20543	33671	0.91	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-N06 BT0311 Homo sapiens cDNA
							nc04612.r1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 repetitive element:
8853	21345		3.46	1.0E-60	AA244041.1	EST_HUMAN	
8681	21373	34517	1.41	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1077	13835	28493	2.21	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2876	15385	28126	1.16	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2876	15385	28127	1.16	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2951	15717		1.53	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
7796	20491	33614	1.05	8.0E-61	AA583968.1	EST_HUMAN	nn59g06.s1 NCL CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
124	12941	25583	1.97	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
124	12941	25584	1.97	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
125	12941	25583	2.38	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
125	12941	25584	2.38	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5034	12941	25583	1.04	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
5034	12941	25584	1.04	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
259	13067	25705	2.95	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
793	13565	26226	1.62	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1298	14047	26719	15	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1626	14372	27061	0.97	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1643	14389	27078	2.63	6.0E-61	AA596033.1	EST_HUMAN	nt68h09.s1 NCI_CGAP_Lart Homo sapiens cDNA clone IMAGE:1088897 3'
2123	14854	27583	1.58	6.0E-61	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3301	16063	28711	9.37	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
5941	18723	31682	3.37	6.0E-61	S79249.1	NT	Ig-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7242	19927	33003	1.82	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
7518	20189	33282	1.67	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, complete cds
11474	24075	37384	1.35	6.0E-61	AF090386.1	NT	Homo sapiens napsin A mRNA, complete cds
12265	13565	26226	1.62	6.0E-61	BE409310.1	EST_HUMAN	Homo sapiens napsin A mRNA, complete cds
350	13149	25789	1.73	5.0E-61	4507500	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1674	14419	27112	2.22	5.0E-61	4506008	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3032	15798	28444	2.56	5.0E-61	AL163279.2	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3193	15956	28608	3.27	5.0E-61	4502166	NT	Homo sapiens chromosome 21 segment HS21C079
3963	16712		1.78	5.0E-61	AJ229041.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4941	13149	25789	1.07	5.0E-61	4507500	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5090	17799	30416	3.38	5.0E-61	4502286	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5725	18517	31438	0.87	4.0E-61	7661637	NT	Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1) mRNA
12088	24582		3.51	4.0E-61	AV731140.1	EST_HUMAN	Homo sapiens DKFZP566B023 protein (DKFZP566B023), mRNA
8320	21013	34151	0.89	3.0E-61	AF150190.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFAR801 5'
8596	21288	34427	0.84	3.0E-61	AA301233.1	EST_HUMAN	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04
8596	21288	34428	0.64	3.0E-61	AA301233.1	EST_HUMAN	EST14323 Testis tumor Homo sapiens cDNA 5' and
486	13271	25906	1.52	2.0E-61	8922829	NT	EST14323 Testis tumor Homo sapiens cDNA 5' and
1190	13942	26607	0.82	2.0E-61	BE168410.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
1190	13942	26608	0.82	2.0E-61	BE168410.1	EST_HUMAN	OV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1660	14406	27097	1	2.0E-61	N53039.1	EST_HUMAN	OV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
							Y53d11.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:246453 3' similar to
							gb:L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2647	15357		1.04	2.0E-61	N39397.1	EST_HUMAN	yy03f11.r1 Soeres melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270189 5'
6332	19102	32090	0.98	2.0E-61		NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116KD) (ATP6N1A), mRNA
8913	21604	34748	0.98	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKC Homo sapiens cDNA clone GKCE1G06 5'
9462	22012		0.99	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
9822	22473	35676	1.67	2.0E-61	AW500256.1	EST_HUMAN	U1HF-BNO-akd4-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
10150	22798	36014	2.3	2.0E-61		NT	Homo sapiens polymerase (RNA) III (DNA directed) (39KD) (RPC39), mRNA
10799	23482		1.81	2.0E-61	11421778	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
756	13528	26188	1.11	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1851	14589	27304	3.71	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2193	14922	27656	1.42	1.0E-61	AW827281.1	EST_HUMAN	xx11b09.y1 NCJ_CGAP_L15 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element MSRI repetitive element ;
2839	15607	28257	1.47	1.0E-61	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
3369	16128	28786	0.86	1.0E-61	7662319	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3715	16468	29106	1.2	1.0E-61	BE174455.1	EST_HUMAN	QV2-HT0577-140300-077-g06 HT0577 Homo sapiens cDNA
4407	17144	29773	0.81	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4407	17144	29774	0.81	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4804	17535	30157	8.11	1.0E-61	AW298181.1	EST_HUMAN	U1H-BW0-ajl-b-08-0-U1.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
4804	17535	30158	8.11	1.0E-61	AW298181.1	EST_HUMAN	U1H-BW0-ajl-b-08-0-U1.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
4905	17632	30247	0.75	1.0E-61	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5309	18114	30772	1.82	1.0E-61	M78423.1	NT	H.sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5603	18398	31310	0.79	1.0E-61	7662303	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
5793	18584	31511	1.29	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
6800	19461	32482	7.11	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
6891	19684	32732	0.67	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
7091	19780	32845	1.42	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7091	19780	32846	1.42	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8033	20728	33861	3	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8212	20906	34041	3.06	1.0E-61	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
9182	21852		2.7	1.0E-61	AW999726.1	EST_HUMAN	MRO-BN0070-040400-010-h01 BN0070 Homo sapiens cDNA
9257	21836	35110	7.73	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
9628	22576	35775	5.24	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10531	23228	39492	2.84	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10855	23535	36780	1.49	1.0E-61	AB044550.1	NT	Homo sapiens P/OKcl.19 mRNA for ubiquitin-conjugating enzyme E2, complete cds
11006	23678	36935	1.53	1.0E-61	AB007830.1	NT	Homo sapiens mRNA for GSR2, complete cds
12007	25273	30726	3.02	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12007	25273	30727	3.02	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12659	24959	30988	11.56	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10255	22903	36113	1.45	9.0E-62	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
4514	17249	28885	1.1	8.0E-62	AA830420.1	EST_HUMAN	cc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVK
1085	13843	26501	1.62	7.0E-62	AV714334.1	EST_HUMAN	P31795 POL. POLYPYRROLINE ;
3497	16263	28907	0.74	7.0E-62	P17480	SWISSPROT	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5'
5826	18615	31547	0.64	7.0E-62	11427965	NT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
11323	24014	37317	7.1	7.0E-62	AI208681.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20261), mRNA
2998	15764		1.42	6.0E-62	U09410.1	NT	gg56a04.x1 Scores, testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15:103
3379	16138		4.1	6.0E-62	11418255	NT	O15103 HYPOTHETICAL 27.3 KD PROTEIN. ;
7525	20196	33289	3.03	6.0E-62	AI762801.1	EST_HUMAN	Human zinc finger protein ZNF131 mRNA, partial cds
7525	20196	33290	3.03	6.0E-62	AI762801.1	EST_HUMAN	Homo sapiens CGI-56 protein (CGI-56), mRNA
7984	20679	33981	0.72	6.0E-62	AW501124.1	EST_HUMAN	wf04d02.x1 NCI_CGAP_GCL1 Homo sapiens cDNA clone IMAGE:2389251 3'
8155	20849	33981	1.45	6.0E-62	11431139	NT	wf04d02.x1 NCI_CGAP_GCL1 Homo sapiens cDNA clone IMAGE:2389251 3'
8254	21933	35106	3.27	6.0E-62	AW814393.1	EST_HUMAN	UI-HF-BP0p-ak-d-09-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
407	13192	25840	2.8	5.0E-62	AI950528.1	EST_HUMAN	Homo sapiens CGI-18 protein (LOC51008), mRNA
2408	15127	27863	4.25	5.0E-62	AJ271735.1	NT	MR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA
2408	15127	27864	4.25	5.0E-62	AJ271735.1	NT	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
2598	15312	28048	1.35	5.0E-62	U39487.1	NT	Q08379 GOLGIN-95, contains element MER22 repetitive element ;
2598	15312	28049	1.35	5.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3413	16171	28820	2.92	5.0E-62	4506758	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4293	17032	29660	2.6	5.0E-62	AA431093.1	EST_HUMAN	Human xanthine dehydrogenase/oxidase mRNA, complete cds
8447	21139	34278	0.55	5.0E-62	4506758	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
9417	22095	35267	6.45	5.0E-62	AW410687.1	EST_HUMAN	Human vaniline dehydrogenase/oxidase mRNA, complete cds
11231	23894	37180	2.85	5.0E-62	11425674	NT	Homo sapiens ryandine receptor 3 (RYR3) mRNA
11231	23894	37181	2.85	5.0E-62	11425674	NT	Homo sapiens ryandine receptor 3 (RYR3) mRNA
							zaw78a08.x1 Scores, testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
							P47245 NARDILYSIN ;
							Homo sapiens ryandine receptor 3 (RYR3) mRNA
							fn07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961616 5'
							Homo sapiens muscle specific gene (M6), mRNA
							Homo sapiens muscle specific gene (M6), mRNA

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820	13591	26258	1.95	4.0E-62	AW161479.1	EST_HUMAN	au71d03.v1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
820	13591	26259	1.95	4.0E-62	AW161479.1	EST_HUMAN	au71d03.v1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
821	13591	26258	2.98	4.0E-62	AW161479.1	EST_HUMAN	au71d03.v1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
821	13591	26259	2.96	4.0E-62	AW161479.1	EST_HUMAN	au71d03.v1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2459	15177	27916	1.78	4.0E-62	A1827900.1	EST_HUMAN	wf12b08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_mna1 HISTONE H2B.2 (HUMAN);
2459	15177	27917	1.78	4.0E-62	A1827900.1	EST_HUMAN	wf12b08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_mna1 HISTONE H2B.2 (HUMAN);
3394	18153		6.34	4.0E-62	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5833	18622	31555	1.84	4.0E-62	4506978	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
6204	18979	31958	1.9	4.0E-62	11420854	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7071	19782	32826	1.84	4.0E-62	11421041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
7534	20204	33299	2.48	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39KD) (EIF2B2), mRNA
7534	20204	33300	2.48	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39KD) (EIF2B2), mRNA
8071	20765	33894	1.06	4.0E-62	11428973	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
8745	21437	34584	4.97	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
10834	23614	36864	4.45	4.0E-62	Z78768.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
10934	23614	36865	4.45	4.0E-62	Z78768.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
11995	24533	37270	2.81	4.0E-62	11418086	NT	Homo sapiens putative nuclear protein (HRHFB2122), mRNA
12590	24947	30984	1.34	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (KIAA0330), mRNA
12845	24942	30981	16.72	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12845	24942	30982	16.72	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12892	24976	30993	2.72	4.0E-62	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
72	12699	25535	0.89	3.0E-62	4557784	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
3041	15807	28452	1.11	3.0E-62	AB040908.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3041	15807	28453	1.11	3.0E-62	AB040908.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3888	16439	29081	5.41	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene

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8438	21130	34267	5.82	3.0E-62	AI632733.1	EST_HUMAN	w33f04.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:229903 3' similar to contains THR.12
1209	13960	26827	2.36	2.0E-62	AL163284.2	NT	THR repetitive element
8673	21365	34511	4.89	2.0E-62	BF329911.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
8673	21365	34512	4.89	2.0E-62	BF329911.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10072	22720		3.8	2.0E-62	AF224689.1	NT	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
11689	24284		4.81	2.0E-62	BF330676.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
1021	13781	26443	1.87	1.0E-62	AF248540.1	NT	(UBE2D3) genes, complete cds
1536	14283	26970	11.01	1.0E-62	L78810.1	NT	QVA-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
1791	14531	27239	1.04	1.0E-62	AA625207.1	EST_HUMAN	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
2915	15681	28328	0.99	1.0E-62	AL039044.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4317	17056		0.71	1.0E-62	BE166413.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4490	17226	29855	1.57	1.0E-62	8923201	NT	af70e11.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
5071	17790	30405	0.9	1.0E-62	L23503.1	NT	CE03453
6196	18972	31948	0.86	1.0E-62	U52111.2	NT	DKFZp568F104_r1 568 (synonym: hlkd2) Homo sapiens cDNA clone DKFZp568F104 5'
7034	19726	32782	0.91	1.0E-62	AA490060.1	EST_HUMAN	QV0-HT0493-280200-135-h12 HT0493 Homo sapiens cDNA
7045	19736	32796	2.94	1.0E-62	AA722878.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
7045	19736	32797	2.94	1.0E-62	AA722878.1	EST_HUMAN	Homo sapiens glucagon-like peptide-1 receptor (GLP-1) mRNA, complete cds
8655	21347	34491	0.5	1.0E-62	AA260050.1	EST_HUMAN	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8956	21647	34797	2.13	1.0E-62	7662289	NT	ab05c02.s1 Stralagene fetal retina 637202 Homo sapiens cDNA clone IMAGE:839506 3'
8956	21647	34798	2.13	1.0E-62	7662289	NT	zq89f10.s1 Soares_feal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
8999	21689	34838	2.02	1.0E-62	X15533.1	NT	zq89f10.s1 Soares_feal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
8999	21689	34839	2.02	1.0E-62	X15533.1	NT	zq89f10.s1 Soares_feal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
9457	22007	35177	3.54	1.0E-62	AA465170.1	EST_HUMAN	zq89f10.s1 NCI_OGAP_GCB1 Homo sapiens cDNA clone IMAGE:705060 5'
11339	24029	37333	2.01	1.0E-62	Z78698.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11866	24450	37792	1.52	1.0E-62	11424055	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12474	24836		2.25	1.0E-62	11418322	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
12673	24886	30990	2.99	1.0E-62	11430460	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
329	13130	25765	2.59	9.0E-63	AW816405.1	EST_HUMAN	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
2345	15068		1.53	9.0E-63	C18159.1	EST_HUMAN	ea33d08.s1 NCI_OGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
							H. sapiens flow-sorted chromosome 6 HindIII fragment, SC8pa1.408
							Homo sapiens exosome component 1 Rrp46 (LOC56815), mRNA
							Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
							QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
							C18159 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-556C10 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4020	16766	29395	7.42	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4020	16766	29396	7.42	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5164	17895	37798	3.05	9.0E-63	11418185	NT	Homo sapiens acinlase 2, mitochondrial (ACO2), mRNA
5379	18179	30869	1.63	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for Pk8 kinase
7082	18772	32837	3.86	9.0E-63	11426985	NT	Homo sapiens nucleoporin 88KD (NUP88), mRNA
7724	20387	33501	0.91	9.0E-63	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3), mRNA
8224	20918	34055	1.38	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
10816	23499	36736	2.03	9.0E-63	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
10816	23499	36737	2.03	9.0E-63	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
2343	15066	27803	1.32	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2373	15095	27834	2.06	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3454	16210	28861	3.02	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3454	16210	28862	3.02	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4234	16975	29600	3.31	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
908	13675		2.09	7.0E-63	AB872137.1	EST_HUMAN	wm55g11.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908.3'
						EST_HUMAN	nc63102.r1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00381.60S
5255	18061		48.05	6.0E-63	AA420803.1	EST_HUMAN	RIBOSOMAL PROTEIN (HUMAN);
8773	21465	34612	1.97	5.0E-63	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3315	16075	28726	0.84	4.0E-63	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3788	16540	29174	1.16	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
3788	16540	29175	1.16	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6353	19123	32115	3.64	4.0E-63	AW750372.1	EST_HUMAN	GM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
6353	19123	32116	3.64	4.0E-63	AW750372.1	EST_HUMAN	GM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
11077	23747	37021	2.3	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-a-02-Q-U1.st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482.3'
11077	23747	37022	2.3	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-a-02-Q-U1.st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482.3'
11846	24430	37771	4.32	4.0E-63	AA36284.1	EST_HUMAN	EST72607 Ovary II Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
1928	14664	27377	2.82	3.0E-63	AB018290.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2782	15487	28225	2.26	3.0E-63	J00310.1	NT	Human Mel-fRNA-i gene 1
2824	13967	26636	11.81	3.0E-63	6005963	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
6382	19151	32150	32.78	3.0E-63	11545810	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA
9605	22258	35444	1.15	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253.5'
9605	22258	35445	1.15	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253.5'
186	12899	25639	1.08	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
183	13006	25647	1.68	2.0E-63	4885228	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
485	13270		2.34	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
807	13579	26244	5.57	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
1559	14306	26994	1.43	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood OE group antigen polypeptide, complete cds
1559	14306	26995	1.43	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood OE group antigen polypeptide, complete cds
1760	14502	27203	1.1	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE3636103 5'
3154	15917	28563	3.44	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3279	18040	28690	2.02	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3885	16835	29274	3.74	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4813	17544	30169	1	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5099	17818	30435	0.96	2.0E-63	6892617	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5181	25062	30505	1.25	2.0E-63	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
5794	18585	31512	2.96	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
5794	18585	31513	2.96	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6093	18871	31837	0.84	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6093	18871	31838	0.84	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human germ-line T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2NT, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6602	19365	32379	1.67	2.0E-63	U65059.1	NT	Homo sapiens MIST mRNA, partial cds
6649	19411	32425	0.88	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6649	19411	32426	0.88	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6975	19456	32477	1.45	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6975	19456	32478	1.45	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7878	20342	33454	0.87	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
							Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
7713	20377	33490	0.56	2.0E-63	11421514	NT	(semaphorin) 3A (H. sapiens) (LOC63232), mRNA
8431	21124	34262	3.96	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8952	21643	34791	1.35	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
8952	21643	34792	1.35	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9839	22490	35691	1.12	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10647	23338	36577	8.43	2.0E-63	N78945.1	EST_HUMAN	Zb18b05.s1 Soares_fetal_lung_NH1L19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN);
10672	23363	36604	2.96	2.0E-63	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
10672	23363	36805	2.96	2.0E-63	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
12098	25177	30807	5.97	2.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
1502	14248	26934	1.28	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
1502	14248	26935	1.28	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4308	17047	29672	2.92	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4308	17047	29673	2.92	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5288	18074	30703	0.8	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5683	18476	31394	1.4	1.0E-63	AW592268.1	EST_HUMAN	QV0-ST0215-060100-083-509 ST0215 Homo sapiens cDNA
6298	19071	32055	0.68	1.0E-63	AW451950.1	EST_HUMAN	UI-H-B13-alk-H-02-0-UI.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:3088763 3'
6298	19071	32056	0.68	1.0E-63	AW451950.1	EST_HUMAN	UI-H-B13-alk-H-02-0-UI.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:3088763 3'
8371	21064		2.68	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12737	25286		4.04	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
7766	20462	33596	4.36	9.0E-64	AL478186.1	EST_HUMAN	Im50b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1024	13784		6.16	8.0E-64	BE280798.1	EST_HUMAN	801155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6049	18829	31792	3.88	8.0E-64	BE885755.1	EST_HUMAN	801508968F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
11916	24479		7.34	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
11970	24516		1.6	8.0E-64	T80651.1	EST_HUMAN	y98b02.r1 Stragogene lung (8937210) Homo sapiens cDNA clone IMAGE:78179 5'
3520	16276		1.13	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4883	17417	30052	2.73	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4883	17417	30053	2.73	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
9833	22581	35779	3.43	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar22, mp22 and bam22 genes
1716	14459	27156	1.63	6.0E-64	AB51992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1716	14459	27157	1.63	6.0E-64	AB51992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3120	15885	28524	4.39	6.0E-64	AW028445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
3120	15885	28525	4.39	6.0E-64	AW028445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
5534	18332	31237	2.48	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5534	18332	31238	2.48	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5555	18352	31281	4.08	6.0E-64	MI3975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds

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5584	18361	31269	1.26	6.0E-64	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; actin receptor interacting protein 1 (KIAA0705), mRNA
5739	18531	31453	0.82	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALGR), mRNA
5739	18531	31454	0.82	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALGR), mRNA
7136	19823	32889	2.34	6.0E-64	11528879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7136	19823	32890	2.34	6.0E-64	11528879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9226	21905	35077	6.76	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
9406	22068	35240	2.09	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
9618	22271	35458	2.78	6.0E-64	S76475.1	NT	tKc [human, brain, mRNA, 2715 nt]
10689	23360	36600	6.01	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
10689	23360	36601	6.01	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
10941	15885	28524	1.84	6.0E-64	AW026445.1	EST_HUMAN	wf13e03.x1 NCI CGAP Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
10941	15885	28525	1.84	6.0E-64	AW026445.1	EST_HUMAN	wf13e03.x1 NCI CGAP Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
12115	24608	31089	4.97	6.0E-64	11526198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
801	13573	26235	2.85	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
801	13573	26236	2.85	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1315	14064	26738	1.84	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1401	14148	26827	1.3	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1401	14148	26828	1.3	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1706	14449	27149	1.37	5.0E-64	U89358.1	NT	Human (3)mb1 protein homolog mRNA, complete cds
2829	14210	26897	4.85	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2829	14210	26898	4.85	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3840	16690	29328	6.71	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
4085	16828	29455	1.05	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
7716	20380	33493	0.58	4.0E-64	BE794607.1	EST_HUMAN	601590382F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3944397 5'
10715	23404	36644	2.23	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-e03 ST0197 Homo sapiens cDNA
10715	23404	36645	2.23	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-e03 ST0197 Homo sapiens cDNA
2195	14824	27658	5.41	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-569E02 5'
3249	16011	28662	0.89	3.0E-64	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC 7 Homo sapiens cDNA clone DCAAMC01 5'
3436	16192	28841	2.22	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3436	16192	28842	2.22	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
5990	18771	31734	1.21	3.0E-64	Z28273.1	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 28
6401	19170	32169	3.34	3.0E-64	BF370000.1	EST_HUMAN	RC8-FN0019-290800-011-G11 FN0019 Homo sapiens cDNA
8365	21058	34198	1.93	3.0E-64	AF248953.1	NT	Homo sapiens gelsin matrix protein GM130 (GOLGA2) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8366	21058	34199	1.93	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8393	21086	34220	3.69	3.0E-64	BE206521.1	EST_HUMAN	b57h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
8393	21086	34221	3.69	3.0E-64	BE206521.1	EST_HUMAN	b57h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
9327	21994	35165	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9327	21994	35166	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9414	22092	35263	0.6	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGe resequences, MAGO Homo sapiens cDNA
9414	22092	35264	0.6	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGe resequences, MAGO Homo sapiens cDNA
11891	24286	37608	1.8	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1066	13824	26484	1.84	2.0E-64	AA609940.1	EST_HUMAN	af09408.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1377	14125	26799	1.54	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2528	15244		1.82	2.0E-64	AI927030.1	EST_HUMAN	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2533	15248	27987	2.05	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2533	15248	27988	2.05	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3137	15901	28546	1.42	2.0E-64	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GO T2), nuclear gene encoding mitochondrial protein, mRNA
3787	16519	29157	0.78	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGe resequences, MAGO Homo sapiens cDNA
3787	16519	29158	0.78	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGe resequences, MAGO Homo sapiens cDNA
5916	18701	31655	2.78	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6148	18925	31895	1.47	2.0E-64	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6394	19163	32164	5.21	2.0E-64	BF668537.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
6497	19263	32264	1.16	2.0E-64	AI078387.1	EST_HUMAN	aa29b03.x1 Soares, total, fetus, NB2HF8_9w Homo sapiens cDNA clone IMAGE:1678717 3'
6601	19364	32378	4.54	2.0E-64	M77165.1	NT	H.sapiens dopamine receptor D5 pseudogene 1, partial cds
7707	20371	33484	0.7	2.0E-64	11431054	NT	Homo sapiens ataxin 2-binding protein 1 (AZBP1), mRNA
7732	20395	33510	0.65	2.0E-64	AW606785.1	EST_HUMAN	GV1-HT0413-010200-059-h12 HT0413 Homo sapiens cDNA
8567	21259	34395	0.73	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
8567	21259	34396	0.73	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9038	21728	34882	0.56	2.0E-64	11423508	NT	Homo sapiens hypothetical protein SBB167 (LOC57115), mRNA
9130	21818	34984	0.97	2.0E-64	AU132570.1	EST_HUMAN	AU132570 NT2RP4 Homo sapiens cDNA clone NT2RP4000109 5'
9879	22529	35726	0.59	2.0E-64	T06397.1	EST_HUMAN	EST04286 Fetal brain, Stratagene (cat#938206) Homo sapiens cDNA clone HFBDS88
9879	22529	35727	0.59	2.0E-64	T06397.1	EST_HUMAN	EST04286 Fetal brain, Stratagene (cat#938206) Homo sapiens cDNA clone HFBDS88
10662	23353	36592	3.72	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4180556 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10981	23656	36909	5.97	2.0E-64	A1922811.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
10981	23656	36910	5.97	2.0E-64	A1922811.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
11198	23863	37149	1.76	2.0E-64	AW864773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
12039	24562	31114	1.55	2.0E-64	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12468	24834		4.85	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
251	13060	25698	2.94	1.0E-64	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
1772	14514	27214	10.45	1.0E-64	A1929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519138 3' similar to gb:L21698_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element;
3010	15776	28426	0.79	1.0E-64	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
3501	16257	28912	5.74	1.0E-64	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α -
3572	16327	28974	1.27	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3572	16327	28975	1.27	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3881	16631	29270	0.79	1.0E-64	8822829	NT	Homo sapiens TRIAD3 mRNA, partial cds
8964	22612	35816	1.07	1.0E-64	AA042975.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
12012	23545		1.81	1.0E-64	AL163248.2	NT	zK5308.s1 Soares_pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:486567 3'
2274	15000	27738	1.53	9.0E-65	X89211.1	NT	Homo sapiens chromosome 21 segment HS21C046
2274	15000	27739	1.53	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
11523	24123		10.43	9.0E-65	BF330976.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
11493	24094	37405	10.87	8.0E-65	A1929244.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
10055	22703	35921	2.01	7.0E-65	BE061653.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW_RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21.;
11807	24397	37731	1.27	7.0E-65	Z21378.1	EST_HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA
1034	13794	28454	3.59	6.0E-65	AV721898.1	EST_HUMAN	HSAAEAOWO TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test346 (b)
1915	14652		4.73	6.0E-65	AA506929.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTB87C06 5'
6475	19242	32242	0.62	6.0E-65	AA503892.1	EST_HUMAN	ribosomal protein L32 (HUMAN);
						EST_HUMAN	ribosomal protein L32 (HUMAN);
						EST_HUMAN	ribosomal protein L32 (HUMAN);
						EST_HUMAN	ribosomal protein L32 (HUMAN);
8945	21337	34481	2.3	6.0E-65	AW083252.1	EST_HUMAN	nc07b09.x1 NCI_CGAP_P15 Homo sapiens cDNA clone IMAGE:954517
8909	21600	34742	3.46	6.0E-65	AA427878.1	EST_HUMAN	xc07b09.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63308 Q63308
8909	21600	34743	3.46	6.0E-65	AA427878.1	EST_HUMAN	LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFs; contains L1 b2 L1 repetitive element;
8973	21653	34814	0.81	6.0E-65	AI085314.1	EST_HUMAN	zw53b06.s1 Soares_fetal_fetus NB2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8973	21663	34815	0.81	6.0E-65	AI085314.1	EST_HUMAN	qf18n05.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750425 3'
10783	23466	36707	3.82	6.0E-65	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
10968	23644	36897	1.52	6.0E-65	BF340825.1	EST_HUMAN	602037721F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185677 5'
11480	24081	37392	1.86	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1331	14080	26754	1.6	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1331	14080	26755	1.6	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2151	14881	27615	1.6	5.0E-65	AB033768.1	NT	Homo sapiens HPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3250	16012	28663	1.6	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
3250	16012	28664	1.6	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
10364	23011	36226	1.01	5.0E-65	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
188	13001	25642	2.02	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
728	13502	26156	1.37	4.0E-65	AI266468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2Nbl-HP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
728	13502	26157	1.37	4.0E-65	AI266468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2Nbl-HP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
1056	13814	26475	1.38	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1469	14216	26903	11.06	4.0E-65	4506636	NT	Homo sapiens ribosomal protein L34 (RPL34), mRNA
2336	15060	27796	0.81	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2336	15060	27797	0.91	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
3630	16680	26321	1.08	4.0E-65	AW593185.1	EST_HUMAN	RC2-BN0033-160200-013-a03 BN0033 Homo sapiens cDNA
5124	17842	30459	1.03	4.0E-65	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI7), mRNA
5124	17842	30460	1.03	4.0E-65	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI7), mRNA
6063	18842	31804	4.6	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6063	18842	31805	4.6	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6983	19076	32723	0.55	4.0E-65	A7008372.1	NT	Homo sapiens oxysterol binding protein-related protein 3 (ORP3), complete cds
7017	19709	32765	0.97	4.0E-65	M19878.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7119	19807	32873	2.52	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7448	20124	33215	0.97	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7448	20124	33216	0.97	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7741	20437	33558	1.86	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
7741	20437	33559	1.86	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
9044	21734	34888	0.63	4.0E-65	11429127	NT	Homo sapiens Janus Kinase 2 (e protein tyrosine kinase) (JAK2), mRNA
10480	23126		2.04	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor

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10874	23554	36801	1.97	4.0E-65	AV738764.1	EST_HUMAN	AV738764 CB Homo sapiens cDNA clone CBC0BE05 5'
11041	23712	36982	3.68	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12319	13814	28475	1.46	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1210	15522		3.8	3.0E-65	X78932.1	NT	H.sapiens HZF9 mRNA for zinc finger protein
1551	14297	26984	0.91	3.0E-65	4504826	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1816	14558	27271	0.93	3.0E-65	A1000692.1	EST_HUMAN	ov2303.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
3271	16032	26683	0.75	3.0E-65	4504950	NT	MSR1 repetitive element;
3709	16462	29101	0.99	3.0E-65	A1000692.1	EST_HUMAN	Homo sapiens lamrinin, beta 1 (LAMB1), mRNA
4602	17337	29966	1.91	3.0E-65	6912385	NT	ov2303.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
9969	22617	35920	1.44	3.0E-65	BE787366.1	EST_HUMAN	MSR1 repetitive element;
11363	23174	38402	11.12	3.0E-65	AA430006.1	EST_HUMAN	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
3399	16157	28809	5.75	2.0E-65	BF680294.1	EST_HUMAN	601479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'
8442	19210		2.46	2.0E-65	BE263373.1	EST_HUMAN	zw65a06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
7032	19724	32780	32.07	2.0E-65	BF576922.1	EST_HUMAN	602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295966 5'
8744	21436	34582	1.06	2.0E-65	AK024463.1	NT	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
8744	21436	34583	1.06	2.0E-65	AK024463.1	NT	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
10552	23248	36485	2	2.0E-65	11419247	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
11969	24515		3.95	2.0E-65	AA307604.1	EST_HUMAN	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
12431	25156		2.2	2.0E-65	BF246096.1	EST_HUMAN	EST1178765 Odon cardthoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous
89	12915		1.59	1.0E-65	BF125644.1	EST_HUMAN	retrovirus
528	13310	25943	1.44	1.0E-65	7657495	NT	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
2033	14768	27498	1.29	1.0E-65	AB040946.1	NT	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4076501 5'
3365	16124	28781	0.81	1.0E-65	BE466681.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX6), mRNA
3980	16728	28362	2.47	1.0E-65	4504032	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3980	16728	29363	2.47	1.0E-65	4504032	NT	h224a09.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:3208888 3'
4183	16923	29551	2.01	1.0E-65	AW026340.1	EST_HUMAN	Homo sapiens glypican 4 (GPC4) mRNA
4183	16923	29551	2.01	1.0E-65	AW026340.1	EST_HUMAN	Homo sapiens glypican 4 (GPC4) mRNA
4183	16923	29551	2.01	1.0E-65	AW026340.1	EST_HUMAN	wd08a09.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
8152	20846	33977	2.04	1.0E-65	AW820481.1	EST_HUMAN	wd08a09.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
8152	20846	33978	2.04	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
8152	20846	33978	2.04	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA

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4332	17071	29700	1.15	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
8333	21026		0.48	6.0E-66	BE178563.1	EST_HUMAN	CE18595 ;
11108	23778	37062	3.14	6.0E-66	X69181.1	NT	H.sapiens mRNA for ribosomal protein L31
1346	14094	26769	1.45	5.0E-66	BE064410.1	EST_HUMAN	RC4.BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
5046	17765	30382	0.74	5.0E-66	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3951791 5'
5046	17765	30383	0.74	5.0E-66	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3951791 5'
9194	21864	35028	16.11	5.0E-66	11420357	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
773	13545	26206	0.88	4.0E-66	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1729	14471	27170	1.14	4.0E-66	AW897788.1	EST_HUMAN	RC1.NN0063-100500-022-a02 NN0063 Homo sapiens cDNA
2278	15004	27144	1.83	4.0E-66	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2477	15195		3.02	4.0E-66	A1223364.1	NT	Homo sapiens germ-line DNA upstream of Ikappa locus
4733	17465		10.89	4.0E-66	9635487	NT	Human endogenous retrovirus, complete genome
5463	18262	31153	3.73	4.0E-66	11428843	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5657	18452	31366	1.15	4.0E-66	AW639119.1	EST_HUMAN	QV1-DT0069-110200-087-g10 DT0069 Homo sapiens cDNA
6757	17826	30561	4.83	4.0E-66	AW965473.1	EST_HUMAN	EST377546 IMAGE resequences, MAGI Homo sapiens cDNA
7031	19723	32779	7.93	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
7528	18262	31153	0.72	4.0E-66	11428843	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
7876	20671	33794	5.63	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
8034	20729	33862	0.73	4.0E-66	X57147.1	NT	Human endogenous retrovirus pHE 1 (ERV9)
10556	23252	36489	1.97	4.0E-66	BF507483.1	EST_HUMAN	U1-H-BW1-amr-a-10-0-U1a1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
11351	24041	37344	1.28	4.0E-66	AB023215.1	NT	Homo sapiens mRNA for KIAA0888 protein, partial cds
1407	14154	26835	10.96	3.0E-66	4502088	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1407	14154	26836	10.96	3.0E-66	4502088	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1975	14711	27429	1.16	3.0E-66	N55323.1	EST_HUMAN	yc27g12.1 Soares multiple sclerosis 2/NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to
1976	14711	27430	1.16	3.0E-66	N55323.1	EST_HUMAN	yc27g12.1 Soares multiple sclerosis 2/NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1975	14711	27431	1.16	3.0E-66	N55323.1	EST_HUMAN	Y27G12.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2. [2] PIR:B56612;
2711	15418	28156	3.54	3.0E-66	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3115	15880	28520	6.3	3.0E-66	7682223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5380	18180	30870	1.14	3.0E-66	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5490	18289	31186	0.73	3.0E-66	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5686	18479	31397	1.92	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5686	18479	31398	1.92	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
9425	22103	35275	0.62	3.0E-66	AK024453.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
9619	22272	35459	0.52	3.0E-66	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9973	22821	35826	0.8	3.0E-66	7019480	NT	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
10420	23066	36287	0.97	3.0E-66	AF155559.1	NT	Homo sapiens myoblast fusion cofactor blosynthesis protein E (MCBPE) mRNA, complete cds
11494	24095	37406	6.18	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
11808	24396	37730	1.57	3.0E-66	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
50	12879	25505	2.15	2.0E-66	7857334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
50	12879	25506	2.15	2.0E-66	7857334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
413	12824	25437	1.76	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
413	12824	25438	1.76	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1819	14558	27272	2.05	2.0E-66	AL183301.2	NT	Homo sapiens chromosome 21 segment HS21G101
3510	16266	28920	0.77	2.0E-66	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3747	16500	29134	0.68	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4044	16789	29417	0.8	2.0E-66	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4807	17342	29973	9.48	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4807	17342	29974	9.48	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
5726	18518	31439	1.3	2.0E-66	AW968854.1	EST_HUMAN	EST380930 IMAGE: ressequences, MAGJ Homo sapiens cDNA
5726	18518	31440	1.3	2.0E-66	AW968854.1	EST_HUMAN	EST380930 IMAGE: ressequences, MAGJ Homo sapiens cDNA
8748	21438	34585	2.26	2.0E-66	N45480.1	EST_HUMAN	Y56942.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:277828 5'
12329	25370		2.37	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
1678	14422		1.15	1.0E-66	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909931 5'
2885	15682	28309	1.36	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBAD007 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2895	15662	28310	1.36	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4352	15662	28309	3.81	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4352	15662	28310	3.81	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5297	18102	30781	5.96	1.0E-66	BF673088.1	EST_HUMAN	60215296F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
5992	18486	31406	0.77	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
5992	18486	31407	0.77	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
6839	19501	32526	1.57	1.0E-66	BF328623.1	EST_HUMAN	RC5-BN0193-010900-034-G06 BN0193 Homo sapiens cDNA
8357	21050	34189	1.19	1.0E-66	AA668858.1	EST_HUMAN	aa680e04.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:827262 3'
9326	21993	35164	0.84	1.0E-66	AA018828.1	EST_HUMAN	ze57e12.r1 Soares retina N2B4HR Homo sapiens cDNA clone IMAGE:363118 5'
10270	22918	36129	0.92	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10270	22918	36130	0.92	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10862	23542	36789	2.48	1.0E-66	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11509	24109	37422	1.8	1.0E-66	AW968744.1	EST_HUMAN	EST380820 MAGE resequences, MAGJ Homo sapiens cDNA
12113	24606		2.61	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
371	13196	25841	1.52	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
1361	14109	26784	2.89	7.0E-67	AA383416.1	EST_HUMAN	EST96812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1547	14293	26979	1.38	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1547	14293	26980	1.38	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2026	14761	27489	2.06	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2026	14761	27490	2.06	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2813	13196	25841	3.4	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
5989	18770	31733	0.78	7.0E-67	10190693	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6177	18954	31927	2.02	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6177	18954	31928	2.02	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6623	19385	32399	1.29	7.0E-67	4885084	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6A1A), mRNA
7531	20201	33296	1	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC558972), mRNA
7531	20201	33297	1	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC558972), mRNA
8222	20916	34052	0.59	7.0E-67	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8830	21522	34669	0.58	7.0E-67	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11256	23918		1.56	7.0E-67	11434579	NT	Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA
11677	24272	37594	6.37	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
11898	24465	37803	2.24	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11898	24465	37804	2.24	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12355	24759	31061	1.58	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
546	13329	25960	2.12	6.0E-67	X68968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
778	13550	26211	0.92	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1250	13999	26666	1.29	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3, 4, 5, 6 & 7
3166	15929	28578	1.17	6.0E-67	4509434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3431	16187	28835	1.64	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3431	16187	28836	1.64	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4106	16849	29474	0.7	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4106	16849	29475	0.7	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4657	17391	30025	5.01	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4657	17391	30026	5.01	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5101	17635		1.23	6.0E-67	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3215	15978	28629	1.91	5.0E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
10905	23585		1.68	5.0E-67	BE010038.1	EST_HUMAN	PK43-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1305	14054	26728	0.93	4.0E-67	R90819.1	EST_HUMAN	Y102d11.1 Soares adult brain N264HB55Y Homo sapiens cDNA IMAGE:187253 5'
7920	20815	33743	0.82	4.0E-67	AI733032.1	EST_HUMAN	Q06730 ZINC FINGER PROTEIN 33A ;
8281	20975		1.24	4.0E-67	BF357321.1	EST_HUMAN	RC0-HT0634-150900-026-g03 HT0934 Homo sapiens cDNA
10996	23669		1.39	4.0E-67	AA714294.1	EST_HUMAN	hw06a01.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1236472 3' similar to TR:O10385 O10385
2816	13396	26031	1.55	3.0E-67	AA333768.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN ;
3446	16202	28652	0.98	3.0E-67	BE084410.1	EST_HUMAN	EST37903 Embryo 8 week Homo sapiens cDNA 5' end
4646	17380	30012	2.87	3.0E-67	AW868159.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
9081	20775	33905	1.53	3.0E-67	BF196068.1	EST_HUMAN	MF3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
11224	23887		14.39	3.0E-67	AA927874.1	EST_HUMAN	hw1105.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
183	12996	25635	0.81	2.0E-67	BE348354.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1 ;
825	13595	26265	7.3	2.0E-67	AW816405.1	EST_HUMAN	am18b07.s1 Soares NFL_T_GBC ST Homo sapiens cDNA clone IMAGE:1541365 3'
1083	13841		1.75	2.0E-67	AF167480.1	NT	hw16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3163136 3' similar to WP:F23H11.9
							CE09617 ;
							QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
							Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4

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1877	14614	27325	1.36	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 O94892 KIAA0798 PROTEIN. ;
1877	14614	27326	1.36	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 O94892 KIAA0798 PROTEIN. ;
2235	14963	27702	1.3	2.0E-67	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (D462023.2), mRNA
2235	14963	27703	1.3	2.0E-67	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (D462023.2), mRNA
2384	15105	27845	1.09	2.0E-67	AF308561.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
2432	15153	27837	1.28	2.0E-67	4758785	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3460	16216	28870	3.8	2.0E-67	AA625755.1	EST_HUMAN	zu91g07.s1 Soares_testis NIH Homo sapiens cDNA clone IMAGE:745392 3'
3984	16732	29366	3.03	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5981	18762	31726	0.6	2.0E-67	AL049784.1	NT	Novel human gene mapping to chromosome 13
6034	18814	31774	5.54	2.0E-67	BF240758.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
6203	18978	31966	2.46	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6203	18978	31957	2.46	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6545	19310	32315	0.76	2.0E-67	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
8456	21148	34290	0.82	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
8456	21148	34291	0.82	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
8895	21586	34724	1.21	2.0E-67	AW602835.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
8895	21586	34725	1.21	2.0E-67	AW602835.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9466	22076	35246	0.83	2.0E-67	AV731333.1	EST_HUMAN	AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
9608	22261	35447	0.97	2.0E-67	AW293624.1	EST_HUMAN	U1-H-B12-ahn-9-10-0-JLs1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
10970	23646	36899	3.72	2.0E-67	BF034485.1	EST_HUMAN	601455282F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858975 5'
10988	25433		4.67	2.0E-67	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11193	23858	37145	2.11	2.0E-67	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11434	23201	36433	1.86	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
12235	25231	30819	1.38	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70KD (Ku antigen) (G22P1), mRNA
12527	24874	31018	2.05	2.0E-67	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
246	13055	25895	9.34	1.0E-67	4502196	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neurin-II, Alzheimer disease) (APP), mRNA
882	13467	26114	1.01	1.0E-67	AA702794.1	EST_HUMAN	290004.s1 Soares_fetal_liver_spleen_1NFSL S1 Homo sapiens cDNA clone IMAGE:448015 3'
11845	24429	37770	8.58	1.0E-67	AI654867.1	EST_HUMAN	wb3c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2310550 3'
2174	14903	27636	2.13	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3851	16801	29238	4.96	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.r1 Strabigene INT neuron (#637233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3851	16601	29239	4.96	8.0E-68	AA209456.1	EST_HUMAN	z82h10.r1 Stragene hNT neuron (8937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN. ;
8000	20695	33822	0.55	7.0E-68	A1810505.1	EST_HUMAN	w89e03.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2312860 3'
7737	20402	33518	0.56	6.0E-68	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
10347	22994	36213	2.47	8.0E-68	11422088	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
11097	23767	37042	1.61	6.0E-68	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
12529	24875		1.78	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3855761 5'
12772	25026	30963	1.4	6.0E-68	BF310675.1	EST_HUMAN	601894635F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5'
800	13572	26233	5.05	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
800	13572	26234	5.05	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2783	15488	28226	1.36	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3144	15908	28553	3.23	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4457	17193	29819	0.73	5.0E-68	AL157645.1	EST_HUMAN	DKFZp547D207_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D207 5'
6627	19389	32402	0.61	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3)-like 1 (RAB3IL1), mRNA
6627	19389	32403	0.61	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3)-like 1 (RAB3IL1), mRNA
4918	17646		9.55	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
5098	17817	30434	0.87	4.0E-68	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
5874	18661	31602	0.7	4.0E-68	AF157063.1	NT	Homo sapiens sedlin (SEDL) gene, exon 4
6675	19592	32629	6.51	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCPT1), mRNA
6675	19592	32630	6.51	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCPT1), mRNA
7582	20250	33356	0.66	4.0E-68	7661683	NT	Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA
8938	21629	34771	5.05	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8938	21629	34772	5.05	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9077	21766	34929	3.08	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
10925	23605	36854	1.68	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
10925	23605	36855	1.68	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11115	23785	37081	1.26	4.0E-68	AB040948.1	NT	Homo sapiens mRNA for KIAA1515 protein, partial cds
11828	24412	37749	1.39	4.0E-68	AJ251760.1	NT	Homo sapiens NESP55, GNAS1 antisense (partial) and XLalphas (partial) genes
11864	24448	37789	12.15	4.0E-68	4758267	NT	Homo sapiens echinoderm microtubule-associated protein-like (EMAPL), mRNA
11864	24448	37790	12.15	4.0E-68	4758267	NT	Homo sapiens echinoderm microtubule-associated protein-like (EMAPL), mRNA
3653	16406	29045	5.37	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9357	20428		5.82	3.0E-68	A1342232.1	EST_HUMAN	q58h02.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR12 THR repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10399	23045	36281	1.23	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
2865	17883		15.31	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4633	17368	30004	1.38	2.0E-68	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
6776	19520		9.54	2.0E-68	R45088.1	EST_HUMAN	y938g04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34896 3'
6983	19445	32462	5.38	2.0E-68	BF035316.1	EST_HUMAN	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
7270	19954	33030	0.73	2.0E-68	BF336745.1	EST_HUMAN	IL3-CT0534-180900-273-A01 CT0534 Homo sapiens cDNA
8848	21539	34685	0.63	2.0E-68	O05859	SWISSPROT	FORMIN 4 (LIMB DEFORMITY PROTEIN)
10505	23151	36376	0.75	2.0E-68	N78483.1	EST_HUMAN	y278d07.1 Soares multiple sclerosis 2N1bMSP Homo sapiens cDNA clone IMAGE:289165 5'
11210	23873	37160	1.66	2.0E-68	BF330594.1	EST_HUMAN	QV0-BT0074-130999-014-g04 BT0074 Homo sapiens cDNA
77	12903	25541	1	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
289	13095	25737	1.03	1.0E-68	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
2249	14977	27715	1.03	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2249	14977	27716	1.03	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
3991	16739	29373	0.95	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
4969	17694	30302	0.92	1.0E-68	AA887343.1	EST_HUMAN	al47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5239	18045	30674	1.37	1.0E-68	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
7576	20245	33350	1	1.0E-68	11436716	NT	Homo sapiens sentrin/SUMO-specific protease (SENP1), mRNA
10373	23019	36235	0.6	1.0E-68	AA429538.1	EST_HUMAN	zw74d02.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781923 5'
10756	23441	36685	1.85	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10756	23441	36686	1.85	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10819	23502	36741	3.5	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSMIT3) mRNA, complete cds
11148	23815	37088	1.71	1.0E-68	11433277	NT	Homo sapiens myosin IC (MYO1C), mRNA
11226	23889	37176	1.62	1.0E-68	AF043129.1	NT	Homo sapiens Interleukin-7 receptor precursor (IL7R) gene, exons 7 and 8 and complete cds
11270	23931	37223	1.26	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11270	23931	37224	1.26	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11666	24261	37584	1.48	1.0E-68	11418431	NT	Homo sapiens CGI-78 protein (LOC51632), mRNA
11666	24261	37585	1.48	1.0E-68	11418431	NT	Homo sapiens CGI-78 protein (LOC51632), mRNA
12511	12903	25541	2.68	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12719	25322	30712	2.11	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
19	12847	25480	1.18	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
19	12847	25481	1.16	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1006	13766	26428	1.41	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1006	13766	26427	1.41	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2275	18001	27740	1.15	9.0E-69	4758279	NT	Homo sapiens Epha4 (EPHA4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2275	15001	27741	1.15	9.0E-69	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4109	16852	29479	0.71	9.0E-69	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
10805	23488		6.5	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3381	16140		1.09	8.0E-69	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
6259	19033	32008	6.49	7.0E-69	9968912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
7762	20458	33581	9.09	6.0E-69	AI192764.1	EST_HUMAN	q62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb.L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
7762	20458	33582	9.09	6.0E-69	AI192764.1	EST_HUMAN	q62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb.L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8873	21564	34709	1.01	5.0E-69	AA826039.1	EST_HUMAN	cd60a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1372300 3'
507	13291		1.76	4.0E-69	AI873830.1	EST_HUMAN	wm28h1.1.x1 NCI_CGAP_UH4 Homo sapiens cDNA clone IMAGE:2437125 3'
5674	25073	31384	1.42	4.0E-69	BE561063.1	EST_HUMAN	601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677641 5'
5753	18545	31467	5.28	4.0E-69	AI764973.1	EST_HUMAN	wh57b08.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137
6531	19297	32301	2.71	4.0E-69	4557732	NT	O55137 ACYL-COA THIOESTERASE.;
6531	19297	32302	2.71	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8812	21504	34651	0.52	4.0E-69	AU119634.1	EST_HUMAN	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5'
377	13202	25848	3.69	3.0E-69	BE258012.1	EST_HUMAN	601110371F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3351352 5'
598	13376	26008	2.32	3.0E-69	AF221712.1	NT	Homo sapiens Smead- and Olf-interacting zinc finger protein mRNA, partial cds
1548	14294		3.19	3.0E-69	T80514.1	EST_HUMAN	yd08a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP:A48836
5163	17894	37797	3.64	3.0E-69	11418185	NT	A48836 SPEGF III-EGF REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN - SEA URCHIN ;
6705	19620		0.67	3.0E-69	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
6759	17928	30563	0.74	3.0E-69	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
7272	19556	33032	0.68	3.0E-69	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene
7320	20003	33082	1.83	3.0E-69	U52351.1	NT	encoding mitochondrial protein, complete cds
7451	20127	33219	8.32	3.0E-69	AF268075.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds
8270	20964	34706	0.88	3.0E-69	AW139646.1	EST_HUMAN	Homo sapiens TRAF8-binding protein TBP mRNA, complete cds
8666	21358		0.65	3.0E-69	AA376399.1	EST_HUMAN	UHH-B11-aeow-g-01-QJL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715940 3'
9313	21980	35152	1.01	3.0E-69	X13223.1	NT	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to ribosomal protein S18
							H. sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9433	22111	35286	2.03	3.0E-69	X06233.1	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
9729	22380	35582	0.75	3.0E-69	5730036	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10538	23235	36468	1.44	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
10745	23432		7.81	3.0E-69	AA376399.1	EST_HUMAN	EST18807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
12024	24552		5.17	3.0E-69	11419157	NT	Homo sapiens HGC8.2 protein (HGC8.2), mRNA
126	13180	25827	1.64	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
128	13180	25828	1.84	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
395	13180	25827	10.33	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
395	13180	25828	10.33	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1878	14815	27327	2.08	2.0E-69	BE257857.1	EST_HUMAN	6011029444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2848	15616		3.16	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
8452	21144	34284	1.08	2.0E-69	AA114270.1	EST_HUMAN	zn29g01.1 Stralegene pancreas (#937208) Homo sapiens cDNA clone IMAGE:527088 5'
1698	14441	27139	1.98	1.0E-69	AF053788.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP80 mRNA, partial cds
4962	17687		0.74	1.0E-69	BE409094.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
5959	18741	31700	0.87	1.0E-69	BE902501.1	EST_HUMAN	601875788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
5959	18741	31701	0.87	1.0E-69	BE902501.1	EST_HUMAN	601875788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
6508	19273	32274	4.37	1.0E-69	AW383988.1	EST_HUMAN	QV0-TT0010-031199-046-co7 TT0010 Homo sapiens cDNA
6721	19636	32879	1.26	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6721	19636	32880	1.26	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6737	19571	32603	3.01	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6737	19571	32604	3.01	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6782	19526	32554	1.14	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
6782	19526	32555	1.14	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
10073	22721	35937	4.91	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10073	22721	35938	4.91	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10168	22816	36034	1.38	1.0E-69	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10314	22981	36177	0.57	1.0E-69	BF528429.1	EST_HUMAN	602043782F1 NCI CGAP Bim87 Homo sapiens cDNA clone IMAGE:4181325 5'
10782	23465		10.52	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
11894	24512	37261	1.74	1.0E-69	BF125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12368	24769		4.45	1.0E-69	AI809994.1	EST_HUMAN	wf84e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element/contains element MIR repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2331	15591	27791	2.08	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4340	17079	29708	1.93	8.0E-70	L77566.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1806	14546	27280	1.01	7.0E-70	A1497807.1	EST_HUMAN	Im89101.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1806	14546	27281	1.01	7.0E-70	A1497807.1	EST_HUMAN	Im89101.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1923	14680	27371	1.66	7.0E-70	AA282955.1	EST_HUMAN	z15904.1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:713239 5'
2056	14788		2.92	7.0E-70	5031668	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4199	16940	29566	3.67	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5395	18195	30888	4.88	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5395	18195	30889	4.88	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6826	19487	32509	2.16	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
8330	21023	34159	2.2	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8330	21023	34160	2.2	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8622	21314	34457	3.58	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
8622	21314	34458	3.58	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9055	21744	34902	3.8	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9055	21744	34903	3.8	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9335	20406	33522	3.43	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9361	20431	33551	2.69	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9361	20431	33552	2.69	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9556	22209	35394	0.57	7.0E-70	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLO) mRNA
10196	22844	36058	0.62	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
10196	22844	36059	0.62	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
11010	23682	36941	1.54	7.0E-70	11429685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
11010	23682	36942	1.54	7.0E-70	11429685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
11597	24198	37515	1.65	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11597	24198	37516	1.65	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
851	13621	26291	1.77	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2133	14863	27593	1.21	6.0E-70	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2513	15230	27970	1.22	6.0E-70	8923899	NT	Homo sapiens GMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
2555	15598	28003	2.18	5.0E-70	7682307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2555	15598	28004	2.18	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
11974	24519		2.75	5.0E-70	BE166034.1	EST_HUMAN	MR3-HIT0487-150200-115-a08 HT0487 Homo sapiens cDNA
6656	19417	32431	1.03	4.0E-70	T06037.1	EST_HUMAN	EST03928 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBDN25
6656	19813	32653	1.78	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
6656	19813	32854	1.78	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
1584	14330	27016	1.23	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1584	14330	27017	1.23	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
5532	18330	31234	0.65	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5532	18330	31235	0.65	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5655	18642	31581	1.6	3.0E-70	A1831975.1	EST_HUMAN	wh90d03.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2388005 3'
6280	19053	32031	1.65	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
6280	19053	32032	1.65	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
10008	22656	35669	0.58	3.0E-70	BE502873.1	EST_HUMAN	hz81h02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214419 3'
37	12865	25484	1.2	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
673	13449	26089	14.09	2.0E-70	N42161.1	EST_HUMAN	Y07a10.r1 Soares melanocyte 2NbfHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
673	13449	26090	14.09	2.0E-70	N42161.1	EST_HUMAN	Y07a10.r1 Soares melanocyte 2NbfHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
689	13484	26113	1.7	2.0E-70	A1246899.1	EST_HUMAN	qx51h01.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004813 3'
1000	13760	26421	1.56	2.0E-70	8923668	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1161	13915	26578	3.05	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1161	13915	26579	3.05	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1736	14478	27177	1.68	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2318	15043		5.32	2.0E-70	AA054010.1	EST_HUMAN	Zf48g04.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A P03345 GAG POLYPEPTIDE ;
3615	16368	29011	0.78	2.0E-70	H37988.1	EST_HUMAN	yp58b04.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:191599 5'
4027	16772	29404	5.06	2.0E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5428	18227	30839	8.7	2.0E-70	XZ2662.1	NT	H. sapiens gene for schwannomin (CS8)
5428	18227	30940	8.7	2.0E-70	XZ2662.1	NT	H. sapiens gene for schwannomin (CS8)
6111	18888	31857	1.27	2.0E-70	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6538	19303	32307	1.75	2.0E-70	D12825.1	NT	Human mRNA for NIF1 protein isoform (neurofibromin isoform), complete cds
6568	19333	32342	12.14	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6568	19333	32343	12.14	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6897	17973	30530	1.68	2.0E-70	11422842	NT	Homo sapiens slyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
7303	19986	33062	0.76	2.0E-70	AF288207.1	NT	Homo sapiens cysteinyl-tRNA synthetase mRNA, complete cds, alternatively spliced
7819	20514	33639	9.02	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
8121	20815	33951	0.5	2.0E-70	11423599	NT	Homo sapiens amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type II) (AGL), mRNA
8558	21250	34918	0.8	2.0E-70	H47959.1	EST_HUMAN	yp79g02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193682 5'
9067	21756	35904	0.95	2.0E-70	11526355	NT	Homo sapiens dynactin p62 subunit (LOC51164), mRNA
10038	22686	36373	1.46	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10500	23146	36373	0.47	2.0E-70	AB033042.1	NT	Homo sapiens mRNA for KIAA1216 protein, partial cds
11005	23677	36933	3.75	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11005	23677	36934	3.75	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11639	24236	37559	7.32	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (EIF3S6) mRNA
12353	24757	31058	3.06	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12353	24757	31059	3.06	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3388	16147		2.63	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
9180	21850		0.89	1.0E-70	W85795.1	EST_HUMAN	zh55g05.r1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:416024 5'
9698	22349		0.65	1.0E-70	AA442292.1	EST_HUMAN	z54c03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
10852	23532	36777	7.13	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLGB10 5'
5854	18641	31579	7.05	9.0E-71	AI143870.1	EST_HUMAN	qo4f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
5854	18641	31580	7.05	9.0E-71	AI143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE ;
6932	19668	32714	2.23	9.0E-71	AI654903.1	EST_HUMAN	qo4f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
11508	19668	32714	4.79	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCLCGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
8968	21658		5.03	8.0E-71	AA171451.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
7275	19959	33036	8.9	7.0E-71	AA442230.1	EST_HUMAN	wb52c05.x1 NCLCGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
8578	21270	34408	1.02	7.0E-71	AA705457.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
11302	23981	37262	2.07	7.0E-71	AL163210.2	NT	zp21d11.r1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610101 5' similar to
2207	14835	27673	5.97	5.0E-71	AF056322.1	NT	TR:G1143081 G1143061 STRAIN XA34 POL ;
							z60h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
							z61a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
							Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4101	16844	29472	1.36	5.0E-71	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
5790	18581	31508	2.23	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6584	19329	32336	1.42	5.0E-71	11641408	NT	Homo sapiens keratin, hair, acidic, 7 (KRT47), mRNA
6821	19482	32504	1.43	5.0E-71	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6878	17954	30550	0.82	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
6878	17954	30551	0.82	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7046	19737	32798	0.76	5.0E-71	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7410	20087	33171	1.47	5.0E-71	M38106.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
7607	20273	33381	0.75	5.0E-71	11526445	NT	Homo sapiens MAGUK protein p551; Protein Associated with Lims 2 (LOC51678), mRNA
7634	20299	33408	22.56	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8421	21114	34251	0.81	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
8421	21114	34252	0.81	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
9811	22462		2.67	5.0E-71	X13487.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
10530	23227	36461	1.45	5.0E-71	5729900	NT	Homo sapiens IGF-II mRNA-binding protein 3 (KOC1), mRNA
10901	23581	36831					Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective
11147	23814	37097	2.93	5.0E-71	11436514	NT	Issue-activating peptide III, neutrophil-activating peptide-2 (PPBP), mRNA
340	13141	25778	2.57	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC633325), mRNA
340	13141	25779	102.7	4.0E-71	AF157826.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2889	15656	28299	102.7	4.0E-71	AF157826.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
4394	17431	29762	1.97	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4926	17654	30266	3.37	4.0E-71	AF058322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
			5.57	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
5069	17788	30404					Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 3 (130KD) (CRSP3), mRNA
7833	20828		1.1	4.0E-71	7019352	NT	AU135734 PLACE1 Homo sapiens cDNA clone PLACE1002775 5'
			1.41	3.0E-71	AU135734.1	EST_HUMAN	nl45h10.s1 NCI CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5
10591	23285	36523					repetitive element;
1208	13959	26826	3.38	3.0E-71	AA557683.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
5237	18043	30672	2.02	2.0E-71	AL163206.2	NT	Homo sapiens mRNA for KIAA0272 gene, partial cds
5237	18043	30673	8.24	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5237	18043	30673	8.24	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
6871	17948	30543	0.55	2.0E-71	AL042439.1	EST_HUMAN	DKFZp434D1721_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1721 5'
							7h85c11.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571221 3' similar to TR:092165
8903	21594	34735	0.64	2.0E-71	BF195585.1	EST_HUMAN	Q82165 PUTATIVE FOUR REPEAT ION CHANNEL ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10485	23131	36357	3.88	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10485	23131	36358	3.88	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10593	23287	36524	3.21	2.0E-71	BE018477.1	EST_HUMAN	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B:
11552	24151	37463	1.36	2.0E-71	BF149173.1	EST_HUMAN	Tm01022 Human Epidermal Keratinocyte Subtraction Library. Upregulated Transcripts Homo sapiens cDNA similar to gl 6598881
11552	24151	37464	1.36	2.0E-71	BF149173.1	EST_HUMAN	Tm01022 Human Epidermal Keratinocyte Subtraction Library. Upregulated Transcripts Homo sapiens cDNA similar to gl 6598881
11576	24175	37490	2.35	2.0E-71	R55626.1	EST_HUMAN	M77c1.1.1 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:154772 5'
12038	24561		8.43	2.0E-71	T85489.1	EST_HUMAN	ye43e09.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120520 5'
623	13402	26037	1.83	1.0E-71	A1077927.1	EST_HUMAN	oy15e03.s1 Soares senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element:
920	13687	26351	2.37	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1078	13836	26494	6.15	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1317	14066	28740	11.71	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2074	14806	27936	1.38	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2074	14806	27537	1.38	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2698	15407	28142	3.91	1.0E-71	7657153	NT	Homo sapiens hairyenhancer-of-split related with YRPW motif-like (HEYL), mRNA
3493	16249	28903	2.53	1.0E-71	AF119665.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3583	16338	28982	5.88	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3583	16338	28983	5.88	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3639	16392	29031	0.98	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library. Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3639	16392	29032	0.98	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library. Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3724	16477	29114	2	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4437	17173	29801	1.92	1.0E-71	D28478.1	NT	Human mRNA for KIAA0045 gene, complete cds
4552	17287	29916	0.88	1.0E-71	H23176.1	EST_HUMAN	ym56h10.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:62528 5'
6643	19405	32420	1.07	1.0E-71	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
6886	19879	32726	1.39	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
7211	19896	32871	13.35	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds

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8046	20740	33872	0.69	1.0E-71	AF105287.1	NT	Homo sapiens glycican-6 (GPC6) mRNA, complete cds
8069	20763	33891	2.26	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8345	21038	34174	4.09	1.0E-71	8922811	NT	Homo sapiens hypofibronectin protein FLJ10998 (FLJ10998), mRNA
8345	21038	34175	4.09	1.0E-71	8922811	NT	Homo sapiens hypofibronectin protein FLJ10998 (FLJ10998), mRNA
9128	21816	34982	0.78	1.0E-71	S72393.1	NT	CSNK2A1 =casein kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
9908	22557	35752	7.89	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
9968	22616		2.05	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10436	23082	36309	1.45	1.0E-71	11433142	NT	Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA
10884	23375		2.58	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10796	23479	36720	2.19	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11093	23763	37037	1.73	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11093	23763	37038	1.73	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
12401	24786		4.96	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
398	13183	25830	1.72	9.0E-72	AI857635.1	EST_HUMAN	wk95g03.x1 NCJ CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
398	13183	25831	1.72	9.0E-72	AI857635.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
6020	18801	31762	0.97	8.0E-72	BF035752.1	EST_HUMAN	wk95g03.x1 NCJ CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
4092	16834	29458	2.63	7.0E-72	4501866	NT	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
4092	16834	29459	2.63	7.0E-72	4501866	NT	601458747F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3982451 5'
4092	16834	29460	2.63	7.0E-72	4501866	NT	Homo sapiens acornitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7024	19716	32773	2.99	7.0E-72	S41694.1	NT	Homo sapiens acornitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
12520	24868		1.9	7.0E-72	F26259.1	EST_HUMAN	Homo sapiens acornitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
8283	20977		4.14	8.0E-72	AL163248.2	NT	(pseudogene) PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
60	12889	25521	1.06	5.0E-72	BF333707.1	EST_HUMAN	HSPD13870 HM3 Homo sapiens cDNA clone s4000031G02
61	12889	25522	1.06	5.0E-72	BF333707.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
61	12889	25521	3.47	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
61	12889	25522	3.47	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1117	13674		3.62	5.0E-72	L11645.1	NT	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
6851	19551	32581	1.59	5.0E-72	AU128584.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
							Homo sapiens alpha-tubulin mRNA, complete cds
							AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003761 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7731	20394	33509	0.73	5.0E-72	AA316632.1	EST_HUMAN	EST188312 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to FAC1
8675	21367	34514	3.71	5.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to
9861	22511	35708	0.89	5.0E-72	AV724632.1	EST_HUMAN	TR:Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ;contains element MSR1 repetitive element :
11208	23871	37157	3.45	5.0E-72	BF331571.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAK801 5'
11208	23871	37158	3.45	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11643	24240	37563	1.61	5.0E-72	BE208545.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11643	24240	37564	1.61	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
12107	25386	37564	2.82	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
5378	18178	30868	0.62	4.0E-72	AF170025.1	NT	QV1-BT0632-280800-342-af10 BT0632 Homo sapiens cDNA
6462	19229	32230	0.68	4.0E-72	T87947.1	EST_HUMAN	Homo sapiens zinc finger protein ZFP-65 (ZFP95) mRNA, alternatively spliced, complete cds
7309	19992	33069	2.03	4.0E-72	5729867	NT	SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
9884	22336	35531	1.3	4.0E-72	8923669	NT	Homo sapiens hest domain and RLD 2 (HERC2), mRNA
10292	22939	36152	0.48	4.0E-72	AW836230.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10292	22939	36153	0.48	4.0E-72	AW836230.1	EST_HUMAN	RC3-LT0023-200100-012-411 LT0023 Homo sapiens cDNA
10320	22967	36186	0.92	4.0E-72	A1248796.1	EST_HUMAN	RC3-LT0023-200100-012-411 LT0023 Homo sapiens cDNA
11255	23917	37210	1.57	4.0E-72	AA465388.1	EST_HUMAN	q167c02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to
11255	23917	37211	1.57	4.0E-72	AA465388.1	EST_HUMAN	TR:Q14498 Q14498 SPLICING FACTOR, [1] ;contains Alu repetitive element ;contains element L1 repetitive element ;
11514	24114	37424	7.78	4.0E-72	H79421.1	EST_HUMAN	aa2309.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:GPTR_FLAPR
11637	24234	37555	1.75	4.0E-72	7657057	NT	P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
11637	24234	37556	1.75	4.0E-72	7657057	NT	aa2309.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:GPTR_FLAPR
11680	24275	37597	2.16	4.0E-72	T81910.1	EST_HUMAN	P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
12453	24822	31025	8.92	4.0E-72	AJ277546.2	NT	ya28a03.t1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:235084 5'
18	12846	25459	0.69	3.0E-72	5031976	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
883	13652		1.52	3.0E-72	AA723823.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							ya28a03.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:109649 3'
							Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
							Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
							af63a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310280 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1132	13898	26546	6.64	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1132	13898	26547	6.64	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1171	13925	26587	0.72	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1171	13925	26588	0.72	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1510	14256	26942	1.24	3.0E-72	BE242161.1	EST_HUMAN	TCAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1252
3072	15838	28481	11.45	3.0E-72	AJ22043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3273	16034	28684	2.17	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3803	16555	29186	2.69	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction) [human, precursor B-cell line REH, mRNA Partial, 211 nt]
4508	17243	29876	3.12	3.0E-72	11416196	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4715	17447	30079	1.07	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4715	17447	30080	1.07	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4862	17591	30215	0.95	3.0E-72	A1654337.1	EST_HUMAN	wb31608.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307254 3'
5433	18292		1.27	3.0E-72	4759093	NT	Homo sapiens semaphorin W (SEMAW) mRNA
5891	18676	31621	2.1	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5891	18676	31622	2.1	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6074	18853	31819	4.82	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6074	18853	31820	4.82	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
8516	19281	32284	3.63	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
7485	20157	33249	2.15	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8075	20769	33898	0.96	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
10331	22978	36198	1.2	3.0E-72	X98289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
5889	18658	31597	1.91	2.0E-72	11426671	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
8993	21683	34832	0.71	2.0E-72	BF308560.1	EST_HUMAN	601800419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
8993	21683	34833	0.71	2.0E-72	BF308560.1	EST_HUMAN	601800419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
10840	23331	36569	2.47	2.0E-72	AA789277.1	EST_HUMAN	aj28069.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb.X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
12448	24819	31022	5.75	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphatidylethanolpyruvate translocator mRNA, complete cds
2068	14800	27527	1.19	1.0E-72	AA846225.1	EST_HUMAN	af83d02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3'

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5680	18473	31390	3.63	1.0E-72	7657676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6464	19231	32231	1.31	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6464	19231	32232	1.31	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6536	25093	32305	1.2	1.0E-72	AV751818.1	EST_HUMAN	AV751818 NP2 Homo sapiens cDNA clone NP2AIE11 5'
7537	20207	33304	3.7	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
7537	20207	33305	3.7	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9491	22144	35324	10.25	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
9491	22144	35325	10.25	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1444	14191	26875	1.35	9.0E-73	AW374988.1	EST_HUMAN	MRO-C10063-071099-002-111 G10063 Homo sapiens cDNA
10871	23551		15.11	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1015	13774	26434	2.29	8.0E-73	AW071755.1	EST_HUMAN	ws5506.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q59050
5493	18292	31190	1	8.0E-73	4505708	NT	Q59050 HYPOTHETICAL PROTEIN MJ1656 ;
6478	19245	32245	5.16	8.0E-73	11426469	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7994	20689	33817	2.87	8.0E-73	AF113129.1	NT	Homo sapiens lysosome homolog (LOC57151), mRNA
							Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9253	21932	35105	6.25	8.0E-73	BE019900.1	EST_HUMAN	bb62a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:U04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
9640	22292	35484	1.92	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9640	22292	35485	1.92	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10507	23153	36379	0.45	8.0E-73	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
11573	24172	37488	1.28	8.0E-73	11418786	NT	Homo sapiens DEAD-box protein (HAGE), mRNA
12506	24859	31012	3.31	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70KD (Ku antigen) (G22P1), mRNA
1112	13869	26528	0.89	7.0E-73	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3295	16056	28705	1.18	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
4891	17618		1.35	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
154	12869		3.07	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7072	19763	32827	3.48	6.0E-73	BE166574.1	EST_HUMAN	QV6-HT0494-020300-137-403 HT0494 Homo sapiens cDNA
5173	17982	30497	2.2	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM4A1), mRNA
1318	14087	26741	2.77	3.0E-73	AW843789.1	EST_HUMAN	CMQ-CN0044-260100-164-108 CN0044 Homo sapiens cDNA
8598	19361	32374	0.71	3.0E-73	AA136403.1	EST_HUMAN	zn95604.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:565950 3' similar to
8656	21348	34492	0.85	3.0E-73	AV729428.1	EST_HUMAN	gb:Z23084_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8656	21348	34493	0.85	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAA4F071 5'
							AV729428 HTC Homo sapiens cDNA clone HTCAA4F071 5'

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11611	24209		1.51	3.0E-73	AI004040.1	EST_HUMAN	ou11d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1625955 3'
12734	25003		1.5	3.0E-73	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12738	25005		1.54	3.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
831	13601	26271	1.43	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1939	14874		1.78	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2296	15021		1.3	2.0E-73	U013117.1	NT	Human beta globin region on chromosome 11
3177	15940	28580	3.99	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3538	16294	28943	0.91	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3538	16294	28944	0.91	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4401	17138		1.03	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6344	19114	32102	0.89	2.0E-73	AF086824.1	NT	Mus musculus rhoLac-interacting citron kinase (Crik) mRNA, complete cds
6344	19114	32103	0.89	2.0E-73	AF086824.1	NT	Mus musculus rhoLac-interacting citron kinase (Crik) mRNA, complete cds
6389	19158	32159	0.27	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6600	19363	32376	1.27	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6600	19363	32377	1.27	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7699	20382	33476	0.69	2.0E-73	M94048.1	NT	Human peripheral myelin protein 22 mRNA, complete cds
7701	20384	33478	0.73	2.0E-73	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
9432	22110	35284	0.52	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
9432	22110	35285	0.52	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10322	22969	36189	1.21	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10394	23040	36257	1.31	2.0E-73	11496980	NT	Homo sapiens supravillin (SVIL), transcript variant 1, mRNA
10394	23040	36258	1.31	2.0E-73	11496980	NT	Homo sapiens supravillin (SVIL), transcript variant 1, mRNA
10987	23662	36917	3.37	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
10987	23662	36918	3.37	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11020	23692	36955	1.82	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12293	14674		1.83	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1776	14518	27221	1.71	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2488	15205	27946	1.12	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
6268	19039	32015	1.07	1.0E-73	BE151283.1	EST_HUMAN	GM1-HT0282-11199-042-h10 HT0282 Homo sapiens cDNA
9399	22061	35230	1.37	1.0E-73	AH147427.1	EST_HUMAN	qq61b07.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1839837 5' similar to contains element
11428	23195	36426	2.95	1.0E-73	BE395477.1	EST_HUMAN	MER22 repetitive element

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723	13497	26150	1.06	8.0E-74	4557426	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
5824	18613	31544	2.2	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
5824	18613	31545	2.2	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
10791	23474		1.36	8.0E-74	N52239.1	EST_HUMAN	y46g10.s1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:245828 3'
1942	14677	27390	2.59	7.0E-74	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
3322	16082	28732	1.08	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9142	21873	35038	2.83	7.0E-74	BE967432.1	EST_HUMAN	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932997 5'
12505	24858	31011	5.51	7.0E-74	BE266305.1	EST_HUMAN	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'
1100	13858	26518	2.4	6.0E-74	AF109907.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
2314	15039	27776	11.78	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2314	15039	27777	11.78	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2867	15634	28278	1.32	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-0-U1.s1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2867	15634	28280	1.32	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-0-U1.s1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3700	16453	29092	1.34	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3700	16453	29093	1.34	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5281	18086	30744	3.02	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
885	13654	26322	7.33	5.0E-74	AW020986.1	EST_HUMAN	af17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2708	15413		2.62	5.0E-74	AW362756.1	EST_HUMAN	PM0-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
5322	18125	30784	1.86	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5703	18497	31419	12.98	5.0E-74	X89670.1	NT	H. sapiens mRNA for TPCR18 protein
5748	18540	31462					Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5819	18608	31536	7.41	5.0E-74	4507868	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
5819	18608	31537	1.84	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6795	19539	32587	5.98	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7569	19539	32587	0.6	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7836	20631	33758	2.78	5.0E-74	11345483	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
10638	23328	36565	2.56	5.0E-74	Y09420.1	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10638	23328	36566	2.56	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
10636	23328	36566	2.56	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
10757	23442	36887	2.68	5.0E-74	5729788	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
273	13080	25723	1.79	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
832	13602	26272	5.15	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1955	14690	27403	2.02	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1955	14690	27404	2.02	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2055	14797	27523	2.75	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2055	14797	27524	2.75	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2128	14859	27589	1.99	4.0E-74	AB032994.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2427	15148	27882	27.23	4.0E-74	AB032994.1	NT	Homo sapiens PLP gene
3088	15853	28495	5.2	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3518	16274	28828	0.82	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21O010
4041	16786	29414	1.03	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21O047
4520	17255	29889	2.23	4.0E-74	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4573	17308	29937	0.88	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5015	17736	30343	0.96	4.0E-74	4504326	NT	Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
5015	17736	30344	0.96	4.0E-74	4504326	NT	Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
8448	21140		8.45	3.0E-74	AA300376.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
8473	21165	34309	0.79	3.0E-74	9966912	NT	Homo sapiens actin-related protein 3-beta (ARPC3BETA), mRNA
9272	22026	35196	2.99	3.0E-74	M78884.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Striatum (cat. #938205) Homo sapiens cDNA clone HHCP91
10237	22885	36099	2.88	3.0E-74	AA001493.1	EST_HUMAN	nc17g05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
938	13705	26370	175.01	2.0E-74	7668491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
938	13705	26371	175.01	2.0E-74	7668491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1152	13907	26570	1.11	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1222	13972	26644	1.36	2.0E-74	A1950528.1	EST_HUMAN	w51e07.x1 NCI_CGAP Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95, contains element MER22 repetitive element
1590	14336	27024	3.79	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1590	14336	27025	3.79	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2609	15321	28063	0.94	2.0E-74	A1557280.1	EST_HUMAN	PT21.1_15_G11.1 tumor2 Homo sapiens cDNA 3'
4945	17872	30281	2.44	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
4945	17872	30282	2.44	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4949	17676	30286	1.11	2.0E-74	J02963.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5709	25074	31424	2.5	2.0E-74	BE711134.1	EST_HUMAN	RC6-HT0678-220500-011-C03 HT0678 Homo sapiens cDNA
5806	25077	31521	1.89	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/INY-CO-38), mRNA
5806	25077	31522	1.89	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/INY-CO-38), mRNA
5876	25077	31521	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/INY-CO-38), mRNA
5876	25077	31522	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/INY-CO-38), mRNA
7003	19695	32748	0.92	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
7841	20536	33663	1.29	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
9282	22036	35208	6.06	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12234	24687		3.95	2.0E-74	AA196181.1	EST_HUMAN	zp98a06.s1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
52	12881	25509	1.89	1.0E-74	7657334	NT	Homo sapiens Missipat/NIK-related kinase (MINK), mRNA
328	13129	25764	5.02	1.0E-74	AW816405.1	EST_HUMAN	QVA-ST0234-181199-037-R05 ST0234 Homo sapiens cDNA
487	13272	25907	1.05	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
493	13277	25912	13.6	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
587	13367	25995	1.47	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
765	13538	26197	1.81	1.0E-74	AB020540.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
979	13744	26406	2.27	1.0E-74	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
2223	14951	27690	4.39	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3136	15900	28545	3.55	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3366	16125	28782	0.9	1.0E-74	AA258549.1	EST_HUMAN	zp80c01.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:687776 5'
3366	16125	28783	0.86	1.0E-74	AA258549.1	EST_HUMAN	zp80c01.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:687776 5'
3901	16651	29292	0.86	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3901	16651	29293	0.86	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3950	16700	29338	4.81	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4042	16787	29415	1.15	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-008 BT0642 Homo sapiens cDNA
6805	19388	32380	1.86	1.0E-74	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
7526	20197	33291	1.15	1.0E-74	11417977	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
7955	20650	33773	1.13	1.0E-74	BE549105.1	EST_HUMAN	601070089F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
7955	20650	33774	1.13	1.0E-74	BE549105.1	EST_HUMAN	601070089F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8704	21396	34543	4.92	1.0E-74	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8733	21425	34571	0.86	1.0E-74	BF351951.1	EST_HUMAN	MRO-HT0559-230500-021-003 HT0559 Homo sapiens cDNA
10140	22788	36001	0.55	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10140	22788	36002	0.55	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10380	23026	36241	1.38	1.0E-74	11420549	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11885	24458	37800	2.92	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
11885	24513		5.01	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12103	14951	27690	1.58	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12567	24897		1.53	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2650	15360		3.68	8.0E-75	AF176228.1	NT	Homo sapiens DNA, cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12254	24700		1.86	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21O002
2319	15044	27781	1.47	6.0E-75	A1817415.1	EST_HUMAN	wk38a08.x1 NCI_CGAP_Py22 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4
7688	20352	33486	0.61	5.0E-75	AA573446.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN);
7688	20352	33467	0.61	5.0E-75	AA573446.1	EST_HUMAN	nk59d03.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:1028933 3'
8806	21498	34643	0.94	5.0E-75	BE272325.1	EST_HUMAN	nk59d03.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:1028933 3'
9015	21705	34655	0.6	5.0E-75	AA132611.1	EST_HUMAN	601126086F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989965 5'
9083	21782	34946	0.78	5.0E-75	BE561655.1	EST_HUMAN	2017e08.l1 Strategene cdon (#337204) Homo sapiens cDNA clone IMAGE:587174 5'
9083	21782	34947	0.78	5.0E-75	BE561655.1	EST_HUMAN	60134609F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9273	22027	35197	1.53	5.0E-75	BF680254.1	EST_HUMAN	602186618T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
10134	22782	35983	2.39	5.0E-75	A1638623.1	EST_HUMAN	k31c12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361
110	12931	25568	2.16	4.0E-75	BE081335.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN ;
446	13232		1.02	4.0E-75	N36757.1	EST_HUMAN	QV1-BT0632-210200-079-c02 BT0632 Homo sapiens cDNA
1759	14501	27202	1.5	4.0E-75	AW897230.1	EST_HUMAN	yx90h08.l1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:269055 5'
2853	15621	28266	4.89	4.0E-75	BE409464.1	EST_HUMAN	CH0-NN0057-150400-335-at1 NN0057 Homo sapiens cDNA
3492	16248	28902	0.94	4.0E-75	8922837	NT	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
5442	18241	31128	0.56	4.0E-75	11417946	NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA
5442	18241	31129	0.56	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6176	18953	31926	5.78	4.0E-75	5579457	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6861	19421	32436	2.26	4.0E-75	11417946	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (EIF3S8), mRNA
6861	19421	32437	2.26	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10584	23279	36517	18.12	4.0E-75	7669505	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
982	13747	26409	3.72	3.0E-75	AF157623.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
983	13747	26409	2.41	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1828	14567	27279	2.76	3.0E-75	AB011153.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2105	14838	27570	1.11	3.0E-75	4507334	NT	Homo sapiens mRNA for KIA0581 protein, partial cds
2422	15143	27876	5.86	3.0E-75	4759153	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
							Homo sapiens synapjanin-associated protein, 20kD (SNAP29) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3021	15787	28434	0.97	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3184	15947	28597	1.32	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3345	16104	28757	0.75	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3345	16104	28758	0.75	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4147	16889	29521	3.27	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4404	17141	29769	0.73	3.0E-75	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5171	17980	30493	0.83	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
5171	17980	30494	0.83	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6871	19588	32623	1.68	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6871	19588	32624	1.68	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7035	19727	32783	4.56	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7035	19727	32784	4.56	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7522	20193	33284	2.52	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7522	20193	33285	2.52	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
8883	21574	34717	1.21	3.0E-75	11420804	NT	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNAI1), mRNA
8577	22230	35414	0.77	3.0E-75	11420222	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
10440	23086	36314	2.28	3.0E-75	11436430	NT	Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), mRNA
5587	18384		1.41	2.0E-75	AV734690.1	EST_HUMAN	AV734690 cDNA Homo sapiens cDNA clone cdABED02 5'
8848	21340	34484	2.45	2.0E-75	A1311783.1	EST_HUMAN	qc61a02.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916898 3' similar to TR-Q68386 Q68386 POL/ENV GENE ;
2076	14808	27539	1.12	1.0E-75	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2078	14908	27540	1.12	1.0E-75	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2301	15028	27762	6.68	1.0E-75	AW168135.1	EST_HUMAN	hg60402.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.H.
2947	15713	28366	3.27	1.0E-75	X52221.1	NT	PTR7 repetitive element ;
8313	21006		4.27	1.0E-75	AA399270.1	EST_HUMAN	H. sapiens ERCC2 gene, exons 1 & 2 (partial)
9328	21995	35167	3.75	1.0E-75	BF313645.1	EST_HUMAN	z157h03.a1 Soares testis NHT Homo sapiens cDNA clone IMAGE:726486 3' similar to gb:M13932 40S RIBOSOMAL PROTEIN S17 (HUMAN);
9328	21995	35168	3.75	1.0E-75	BF313645.1	EST_HUMAN	601900284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
10797	23480		10.83	1.0E-75	AA684377.1	EST_HUMAN	601900284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
11033	23704	36872	2.56	1.0E-75	AF223391.1	NT	ec77008.61 Stragene lung (H37210) Homo sapiens cDNA clone IMAGE:868599 3' Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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11860	24444	37785	1.38	1.0E-75	AA417112.1	EST_HUMAN	z04b03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730829 5'
12152	17912	30598	1.64	1.0E-75	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
43	12872	25493	1.24	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
43	12872	25494	1.24	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
8801	22452	35654	43.62	9.0E-76	M12937.1	NT	Human ferritin Heavy subunit mRNA, complete cds
917	13684	26347	1.06	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
917	13684	26348	1.06	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2910	18676	28325	1	8.0E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
6079	18858	31825	6.36	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7388	20067	33145	1.26	8.0E-76	11435213	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
7465	20139	33231	0.86	8.0E-76	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8195	20889	34027	0.67	8.0E-76	11416961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8995	21685	34835	0.55	8.0E-76	AB046764.1	NT	Homo sapiens mRNA for KIAA1544 protein, partial cds
10277	22925	36137	1.35	8.0E-76	M13792.1	NT	Human adenoshine deaminase (ADA) gene, complete cds
10564	23260	36497	4.81	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
12491	24849		2	8.0E-76	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
759	13531	26191	1.41	7.0E-76	5016092	NT	Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3288	16049	28697	2.97	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3294	16055	28704	7.55	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3330	16090	28743	0.93	7.0E-76	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
4338	17077	29705	4.73	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydropterin:NADP+ oxidoreductase) (SPR) mRNA
4338	17077	29706	4.73	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydropterin:NADP+ oxidoreductase) (SPR) mRNA
1212	13962	38440	31.63	6.0E-76	BE396253.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
11442	23209	38440	3.76	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'
1936	14671	27385	4.83	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1936	14671	27386	4.83	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1936	14671	27387	4.83	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5188	14871	30512	1.26	4.0E-76	BE783412.1	EST_HUMAN	601471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
9923	22571	35768	6.42	4.0E-76	D81625.1	EST_HUMAN	HUM178501B Human fetal brain (Fujiwara) Homo sapiens cDNA clone GEN-178G01 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9923	22571	35769	6.42	4.0E-76	D81825.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujivara) Homo sapiens cDNA clone GEN-178G01 5'
615	13393	26026	3.2	3.0E-76	BF516282.1	EST_HUMAN	UI-H-BW1-enz-b-04-0-UI.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
615	13393	26027	3.2	3.0E-76	BF516282.1	EST_HUMAN	UI-H-BW1-enz-b-04-0-UI.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1594	14340	27029	3.26	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1594	14340	27030	3.26	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3422	16179	28828	4.96	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3422	16179	28829	4.96	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
4058	16803	29434	1.07	3.0E-76	BE348893.1	EST_HUMAN	h187112.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3151823 3' similar to TR-084886 094886
5158	17891	37796	2.07	3.0E-76	Z41314.1	EST_HUMAN	KIAA0792 PROTEIN ;
5846	18441	31354	1.09	3.0E-76	AA160811.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
6275	19048	32025	9.57	3.0E-76	AF286598.1	NT	gb:L32876 MIXED LINEAGE KINASE 1 (HUMAN);
8050	20744	33877	0.88	3.0E-76	N42671.1	EST_HUMAN	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
9616	22269	35456	3.34	3.0E-76	AW299353.1	EST_HUMAN	Y202g10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:271842 5'
9641	22293	35486	0.99	3.0E-76	AA442309.1	EST_HUMAN	xs49h01.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
9641	22293	35487	0.99	3.0E-76	AA442309.1	EST_HUMAN	xs49h01.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
11876	25181	30812	1.93	3.0E-76	AW967894.1	EST_HUMAN	z64d11.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757481 5'
11979	25398	30802	4.88	3.0E-76	AW966455.1	EST_HUMAN	z64d11.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757481 5'
275	13082	25725	1.59	2.0E-76	D84295.1	NT	EST380059 MAGE resequences, MAGJ Homo sapiens cDNA
333	13134	25768	4.39	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
333	13134	25769	4.39	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
448	13234	25984	1.19	2.0E-76	4557682	NT	Human mRNA for possible protein TPRDII, complete cds
576	13356	25984	1.08	2.0E-76	4503944	NT	Human sapiens immunoglobulin (GD79A) binding protein 1 (IGBP1) mRNA
1008	13768	26430	1	2.0E-76	4758053	NT	Homo sapiens glucagon (GCG) mRNA
1526	14273	26960	1.91	2.0E-76	4504028	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1526	14273	26961	1.91	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1921	14658	27369	0.91	2.0E-76	AA253954.1	EST_HUMAN	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
2846	15614	28261	3.34	2.0E-76	P23268	SWISSPROT	zs60h11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
3291	16052	28701	2.08	2.0E-76	AA445992.1	EST_HUMAN	OLFATORY RECEPTOR-LIKE PROTEIN F5
3291	16052	28702	2.08	2.0E-76	AA445992.1	EST_HUMAN	z64e02.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:780988 3' similar to SW:ITB5_HUMAN
3291	16052	28702	2.08	2.0E-76	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3291	16052	28702	2.08	2.0E-76	AA445992.1	EST_HUMAN	z64e02.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:780988 3' similar to SW:ITB5_HUMAN
3291	16052	28702	2.08	2.0E-76	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;

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3469	16225	28879	0.97	2.0E-76	A1821149.1	EST_HUMAN	ec33b02.y6 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:O14591
4114	13082	25725	1.23	2.0E-76	D84295.1	NT	O14591 SIMILARITY TO P22059:
4895	17622	30240	6.21	2.0E-76	AW879618.1	EST_HUMAN	Human mRNA for possible protein TPRDII, complete cds
5055	17774	30390	1.49	2.0E-76	5031680	NT	QV3-O10028-220300-132-b11 OT0028 Homo sapiens cDNA
5226	18033		1.6	2.0E-76	AF127845.1	NT	Homo sapiens EGF-like repeats and discardin like domains 3 (EDIL3), mRNA
5531	18329	31233	6.47	2.0E-76	AB028004.1	NT	Gorilla gorilla olfactory receptor (GGO18) gene, partial cds
7334	20016	33094	0.75	2.0E-76	11426908	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7560	20230	33333	1.91	2.0E-76	11427410	NT	Homo sapiens A kinase (PKA) anchor protein 10 (AKAP10), mRNA
10182	22830	36045	3.53	2.0E-76	11437211	NT	Homo sapiens TPOCR86 protein (HSTPCR86P), mRNA
10839	23521	36763	3.98	2.0E-76	7549807	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC83150), mRNA
4265	17006	29638	2.38	1.0E-76	D63874.1	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRP4), mRNA
4265	17006	29639	2.38	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5362	18164	30849	6.12	1.0E-76	BE796537.1	EST_HUMAN	Human mRNA for HMG-1, complete cds
6150	18927		0.72	1.0E-76	AA333207.1	EST_HUMAN	601589596F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6825	19486	32508	4.53	9.0E-77	BE89525.1	EST_HUMAN	EST37301 Embryo, 8 week / Homo sapiens cDNA 5' and
12644	24941		1.4	9.0E-77	BE410354.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
182	12894	25633	0.92	8.0E-77	R83144.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638753 5'
4486	17221	29849	1.09	8.0E-77	BF205181.1	EST_HUMAN	yp11h02.r1 Soares breast 3NbhBst Homo sapiens cDNA clone IMAGE:187155 5' similar to
5368	18168	30854	1.74	8.0E-77	4506230	NT	SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1;
11360	24048	37351	1.91	8.0E-77	AA019770.1	EST_HUMAN	601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
11360	24048	37352	1.91	8.0E-77	AA019770.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mv34 homolog) (PSMD7)
12620	24925	31008	4.02	8.0E-77	R00245.1	EST_HUMAN	mRNA
1922	14659	27370	2.4	7.0E-77	AA625755.1	EST_HUMAN	z62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
2411	15132	27868	2.52	7.0E-77	4505944	NT	z62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
2411	15132	27869	2.52	7.0E-77	4505944	NT	y63904.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains
256	13064	25703	8.53	6.0E-77	4504600	NT	MER10 repetitive element:
1534	14281	26986	3.22	6.0E-77	AI204066.1	EST_HUMAN	zu67g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
1214	13984	26631	2.11	5.0E-77	AF041015.1	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
1339	14087	26763	1.77	5.0E-77	4557250	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2091	15400	28139	0.98	5.0E-77	AF162668.1	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
							qe77h12.x1 Soares fetal lung_NthL19W Homo sapiens cDNA clone IMAGE:1745063 3'
							7 Homo sapiens glucokinase (GCK) gene, exon 2
							Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
							Homo sapiens tousel-like kinase 1 (TLK1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2767	15472	28214	0.99	5.0E-77	4503180	NT	Homo sapiens cullin 1 (CUL1) mRNA
3512	16288	28923	0.89	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18) mRNA
4655	17389	30022	2.47	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3) mRNA
4655	17389	30023	2.47	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3) mRNA
4884	17811	30231	2.96	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728.5
6886	19603	32842	0.57	5.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7730	20393	33508	0.59	5.0E-77	8923319	NT	Homo sapiens hypothetical protein FLJ20343 (FLJ20343) mRNA
8286	20980	34099	1.28	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH) mRNA
8286	20980	34100	1.28	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH) mRNA
9469	22078	35249	2.48	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5) mRNA
9469	22078	35250	2.48	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5) mRNA
10388	23034	36249	1.22	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
10388	23034	36250	1.22	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
11794	24384	37716	3.12	5.0E-77	U37194.1	NT	Human UNC-104- and KIF1A-related protein mRNA, partial cds
11794	24384	37717	3.12	5.0E-77	U37194.1	NT	Human UNC-104- and KIF1A-related protein mRNA, partial cds
1965	14701	27417	1.09	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1965	14701	27418	1.09	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10188	22836	36050	0.79	3.0E-77	H65187.1	EST_HUMAN	y64g01.1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -;
10188	22836	36051	0.79	3.0E-77	H65187.1	EST_HUMAN	y64g01.1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -;
10785	23488	36709	3.58	3.0E-77	BF359817.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1330	14079	26763	1.4	2.0E-77	AV764817.1	EST_HUMAN	AV764817 MDS Homo sapiens cDNA clone MDSBT10 5'
1412	14180	26844	1.91	2.0E-77	AW99712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2084	14816	27548	1.13	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2096	14827	27560	5.23	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634) mRNA
2602	15599	28053	1.92	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2602	15599	28054	1.92	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4012	16758	29396	1.96	2.0E-77	BE044316.1	EST_HUMAN	ho43b05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4379	17116	29749	0.74	2.0E-77	A613519.1	EST_HUMAN	hw22g02.x1 NC1 CGAP Bm52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR:O65245
4379	17116	29750	0.74	2.0E-77	A613519.1	EST_HUMAN	hw22g02.x1 NC1 CGAP Bm52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR:O65245

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4557	17282		0.86	2.0E-77	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4717	17449	30082	1.59	2.0E-77	AA653025.1	EST_HUMAN	ns88g12.s1 NCL_CGAP_P-2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN
5885	18652	31583	1.9	2.0E-77	BE286940.1	EST_HUMAN	P47914 60S RIBOSOMAL PROTEIN L29. [1]; contains element MSR1 repetitive element ;
6080	18859	31826	1.73	2.0E-77	BE787143.1	EST_HUMAN	601118852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
7074	19765	32829	15.45	2.0E-77	AI833003.1	EST_HUMAN	601476902F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
8427	21120	34259	0.82	2.0E-77	AI362707.1	EST_HUMAN	at74a09.x1 Barstead cdon HPLR87 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311
9428	22106	35280	5.05	2.0E-77	U50321.1	NT	Q13311 TAX1-BINDING PROTEIN TXBP151. [1];
9428	22106	35281	5.05	2.0E-77	U50321.1	NT	qy70c09.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2017360 3' similar to WP:F29D11.1
9895	22545	35738	0.47	2.0E-77	BF310349.1	EST_HUMAN	CE05765 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN ;
9895	22545	35739	0.47	2.0E-77	BF310349.1	EST_HUMAN	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
42	12870	25489	1.03	1.0E-77	AB033102.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
42	12870	25490	1.03	1.0E-77	AB033102.1	NT	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
266	13074	25714	7.19	1.0E-77	4502166	NT	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
266	13074	25715	7.19	1.0E-77	4502166	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
855	15554	28296	17.31	1.0E-77	4502166	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
855	15554	28297	17.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1912	14649	27360	0.9	1.0E-77	AW058118.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2445	15184	27802	1.32	1.0E-77	AB029024.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3040	15806	28451	1.72	1.0E-77	45033001	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4320	17059	29684	3.37	1.0E-77	7706299	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4488	17223	29851	18.41	1.0E-77	AJ229041.1	NT	Homo sapiens CGI-60 protein (LOC51628), mRNA
4803	17338	29987	2.29	1.0E-77	6552322	NT	Homo sapiens 958 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5010	17732	30337	1	1.0E-77	7681849	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
5010	17732	30338	1	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5839	18627	31561	2.45	1.0E-77	AJ086944.1	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5839	18627	31562	2.45	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5956	18738	31697	1.4	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6358	19126	32120	0.82	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
6953	19435	32450	21.7	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7564	20234	33338	1.05	1.0E-77	11420159	NT	Homo sapiens cullin 1 (CUL1), mRNA
7683	20327	33437	0.89	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9165	21835	35000	0.82	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
9185	21835	35001	0.82	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10421	23087	36288	3.1	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10449	23095	36326	2.55	9.0E-78	AW753302.1	EST_HUMAN	RC3-C10254-280959-011-b05 C10254 Homo sapiens cDNA
6354	19124	32117	3.11	8.0E-78	AW947061.1	EST_HUMAN	RC2-E10023-080500-012-e05 E10023 Homo sapiens cDNA
84	12810	26548	1.87	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
84	12910	25549	1.87	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
6465	19232	25663	2.54	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
212	13024	25663	0.72	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11318 (FLJ11318), mRNA
2567	15281	28019	5.53	5.0E-78	AW673424.1	EST_HUMAN	ba54H03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP.Y48B8A.8
3380	16139	28797	3.81	5.0E-78	M65586.1	NT	CE22121:
5327	18130	30789	2.33	5.0E-78	AF036536.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5488	18287	31183	11.12	5.0E-78	11416589	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
7054	18745	32808	2.23	5.0E-78	AW953120.1	EST_HUMAN	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
8981	21671	34821	6.76	5.0E-78	U60889.1	NT	EST1385190 MAGE resequences, MAGB Homo sapiens cDNA
8982	21672	34822	3.31	5.0E-78	BE960836.1	EST_HUMAN	Human lysosomal alpha-mannosidase (manB) gene, exon 7
1115	13872	26531	1.07	4.0E-78	AL043314.2	EST_HUMAN	60184801F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
1508	14254	28940	1.78	4.0E-78	AL355841.1	NT	DKFZp434N0323 t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
1644	14390	27079	1.09	4.0E-78	A1985094.1	EST_HUMAN	Novel human gene mapping to chromosome 22
2316	15041	27779	2.08	4.0E-78	AF107405.1	NT	wf87b12.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2495616 3' similar to SW.WAP_PIG
4288	17027	28652	1.73	4.0E-78	7858876	NT	O46655 WHEY ACIDIC PROTEIN PRECURSOR:
4722	17454	30088	2.81	4.0E-78	4505906	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4722	17454	30089	2.81	4.0E-78	4505806	NT	Homo sapiens synoxin (LOC30816), mRNA
5681	18474	31391	1.41	4.0E-78	11420732	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
							Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
							Homo sapiens SFRS3 protein kinase 2 (SRPK2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7390	20069	33148	0.58	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
8752	21444	34591	2.86	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
8752	21444	34592	2.86	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
9268	22022	35192	0.6	4.0E-78	11417251	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10342	22989	36206	1.96	4.0E-78	11580151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10342	22989	36207	1.96	4.0E-78	11580151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11396	24002	37305	5.18	4.0E-78	AF169149.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds
11547	24146	37456	2.15	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12517	24866	31016	3.57	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
157	12972	25610	1.39	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
157	12972	25611	1.39	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
3746	16489	29181	0.98	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLAGE3 Homo sapiens cDNA clone PLAGE3000373 5'
3796	16548	29181	0.72	3.0E-78	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
4084	16548	29181	0.96	3.0E-78	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
5094	17813	30430	0.93	3.0E-78	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
10186	22834	36832	5.14	3.0E-78	BE144758.1	EST_HUMAN	GM0-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA
10902	23582	36832	1.97	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g08 HT0367 Homo sapiens cDNA
3119	15884		2.17	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
3995	16743		1.87	2.0E-78	AA311872.1	EST_HUMAN	EST182563 Jurkat T-cells VI Homo sapiens cDNA 5' end
7367	20047	33126	1.54	2.0E-78	AW402306.1	EST_HUMAN	UHF-BKO-eaf-g-10-0-UJ1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5'
7367	20047	33127	1.54	2.0E-78	AW402306.1	EST_HUMAN	UHF-BKO-eaf-g-10-0-UJ1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5'
7631	20297	33405	3.99	2.0E-78	BF689800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4286599 5'
7940	20635	33762	2.33	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAW/F09 5'
8351	21044	34180	1.4	2.0E-78	AI557509.1	EST_HUMAN	P2.1_18 B07.r tumor2 Homo sapiens cDNA 3'
8351	21044	34181	1.4	2.0E-78	AI557509.1	EST_HUMAN	P2.1_16 B07.r tumor2 Homo sapiens cDNA 3'
11017	23689	36952	3.27	2.0E-78	AI197837.1	EST_HUMAN	q150405.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1859961 3' similar to WP:R90.1
11068	23738	37012	3.89	2.0E-78	N68951.1	EST_HUMAN	CE06325 PROTEIN KINASE
4123	16865	29491	3.07	1.0E-78	4507098	NT	z48f12.31 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:285823 3'
4123	16865	29492	3.07	1.0E-78	4507098	NT	Homo sapiens synapjanin-associated protein, 25kD (SNAP25) mRNA
5222	18028	30655	2.93	1.0E-78	11417304	NT	Homo sapiens synapjanin-associated protein, 25kD (SNAP25) mRNA
6857	17934	30570	0.76	1.0E-78	AV648699.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
7736	20401	33517	0.55	1.0E-78	AU122163.1	EST_HUMAN	AV648699 GLC Homo sapiens cDNA clone GLOBMCO1 3'
							AU122163 MAMMA1 Homo sapiens cDNA clone MAMMA1001785 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8059	20753		3.28	1.0E-78	U52373.1	NT	Human serine/threonine kinase MNB (mtb) mRNA, complete cds
12045	24565	31117	1.39	1.0E-78	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12477	25244	30718	1.55	1.0E-78	AI650919.1	EST_HUMAN	w20b08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:228615 3'
4650	17394	30016	4.05	9.0E-79	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
4811	17542	30166	8.05	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
5346	18149	30829	16.87	9.0E-79	AB028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6248	19022	31984	2.38	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
7251	25108		0.99	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7473	20146	33239	0.79	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7473	20146	33240	0.79	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
8244	20938	34074	0.49	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8244	20938	34075	0.49	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8961	21652	34802	5.1	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
8961	21652	34803	5.1	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9280	22034	35206	0.58	9.0E-79	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10263	22911	36121	0.82	9.0E-79	11438643	NT	Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA
10318	22965	36182	1.73	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10318	22965	36183	1.73	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
11001	23674	36930	3.13	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11497	24098	37410	3.55	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
11497	24098	37411	3.55	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
3725	16478	28115	0.91	8.0E-78	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11866	17910	30596	1.82	8.0E-79	8567387	NT	Homo sapiens perid (Drosophila) homolog 3 (PER3), mRNA
3247	16009	28660	26.39	7.0E-78	BE619648.1	EST_HUMAN	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
11899	24466		4.32	6.0E-79	AA698829.1	EST_HUMAN	294404.s1 Soares_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
11478	24079	37390	2.52	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3173	15936		1.49	4.0E-79	8922325	NT	Homo sapiens chromosome 21 segment HS21C083, mRNA
305	13109	25749	1.28	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
957	13722	26388	3.85	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Gn) gene, complete cds
3095	15860	28501	1.51	3.0E-79	U08410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5277	18082	30738	5.24	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5637	18432	31345	1.24	3.0E-79	AB020899.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5682	18457	31371	0.93	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5682	18457	31372	0.93	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5682	18475	31392	3.56	3.0E-79	11426770	NT	Homo sapiens nefin 1 (NTN1), mRNA
5682	18475	31393	3.56	3.0E-79	11426770	NT	Homo sapiens nefin 1 (NTN1), mRNA
6646	19408	32422	0.67	3.0E-79	BE256893.1	EST_HUMAN	60112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
6960	19442	32457	3.35	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
6960	19442	32458	3.35	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
7726	20389	33503	0.76	3.0E-79	6912455	NT	Homo sapiens Bcl-2-associated transcription factor for Rap1 (KIAA0277), mRNA
8064	20758	33987	1.61	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
9303	21970	35144	1.33	3.0E-79	10835036	NT	Homo sapiens tetrahydropteridine repeat domain 3 (TTCS), mRNA
10245	22893		1.24	3.0E-79	AV698115.1	EST_HUMAN	AV698115 GK Homo sapiens cDNA clone GKCAHE11 5'
10768	23452	36694	1.52	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
10768	23452	36695	1.52	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
281	13088		0.99	2.0E-79	H63128.1	EST_HUMAN	y48f03 s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208541 3'
619	13398	26033	1.6	2.0E-79	BE379926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
907	13674	26339	2.28	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2), mRNA
1012	13772		2.09	2.0E-79	AI523747.1	EST_HUMAN	h18r07 x1 NCJ_CGAP_P28 Homo sapiens cDNA clone IMAGE:2118685 3'
1781	14522	27226	1.12	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1781	14522	27227	1.12	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
2144	14874	27607	5.93	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2144	14874	27608	5.93	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2189	14918	27652	1.07	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2721	15428	28168	1.09	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0937 protein, partial cds
3833	16643	29283	0.83	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4144	16886	29517	1.09	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
5585	18382		1.22	2.0E-79	AA312223.1	EST_HUMAN	EST182928 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid B0303.15
5640	18435	31348	0.8	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6149	18826	31896	1.14	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
6864	17941	30577	0.89	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7067	19758	32622	1.7	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 4, mRNA
7067	19758	32623	1.7	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 4, mRNA
7099	20694	33821	1.08	2.0E-79	4508442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1), mRNA

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8415	21108	34247	2.25	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8684	21356	34503	0.58	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8684	21356	34504	0.58	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8902	21593	34734	1.65	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 (H. sapiens) (LOC83981), mRNA
9992	22640	35850	1.44	2.0E-79	S72869.1	NT	H4(D10S170) Putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
9992	22640	35851	1.44	2.0E-79	S72869.1	NT	H4(D10S170) Putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10688	23389	36627	12.34	2.0E-79	U07819.1	NT	Human conifalrin 1 precursor (CNTN1) mRNA, complete cds
10958	23632	36880	4.05	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
10958	23632	36881	4.05	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
11836	17808	30594	2.16	2.0E-79	7682357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12018	24548	31108	5.19	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12238	24690	31075	2.89	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6492	25091	33969	3.76	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA
8143	20837	33969	0.78	1.0E-79	BE394211.1	EST_HUMAN	QV2-HT0540-120600-358-e05 HT0540 Homo sapiens cDNA
11623	24220	37543	2.05	1.0E-79	BF087405.1	EST_HUMAN	601311517F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632909 5'
12047	25333		1.8	1.0E-79	AI460115.1	EST_HUMAN	ar79a04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2161438 3'
3143	15907	28551	2.35	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
3143	15907	28552	2.35	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
9912	22561	35757	1.14	9.0E-80	BE798603.1	EST_HUMAN	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3636081 5'
11245	23907	37189	8.66	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
11245	23907	37200	8.66	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3588	16342		1.31	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7504	20175	33258	3.07	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7504	20175	33258	3.07	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
9302	21969	35142	1.13	8.0E-80	6005921	NT	Homo sapiens triple functional domain (TPPRF interacting) (TRIO), mRNA
9302	21969	35143	1.13	8.0E-80	6005921	NT	Homo sapiens triple functional domain (TPPRF interacting) (TRIO), mRNA
890	13649	26318	1.12	6.0E-80	AI422197.1	EST_HUMAN	ff58d02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR;
1038	14384	27071	2.22	6.0E-80	U84898.1	NT	Homo sapiens NRD convertase mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4252	16993	29820	1.08	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4252	16993	29821	1.08	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
5712	18505	31427	1.79	6.0E-80	11421482	NT	Homo sapiens maleate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
5984	18765	31729	3.37	6.0E-80	AJ404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6135	18913	31882	4.89	6.0E-80	11436738	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6179	18956		1.17	6.0E-80	7682393	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
6230	19004	31980	0.98	6.0E-80	M18533.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
8723	21415	34558	3.22	6.0E-80	11528484	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8723	21415	34559	3.22	6.0E-80	11528484	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8917	21608	34751	1.51	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9259	21938	35113	0.83	6.0E-80	AF181495.1	NT	Homo sapiens HSPC148 mRNA, complete cds
9761	22412	35619	1.48	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
10861	23541	36788	2.83	6.0E-80	11427386	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11187	23852	37138	26.56	6.0E-80	AF226730.1	NT	Homo sapiens Cy19 mRNA, complete cds
11702	24297	37823	1.59	6.0E-80	U76550.1	NT	Human peroxisome targeting signal 2 receptor (Pex7) mRNA, complete cds
11756	24347	37877	1.5	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
11802	24392	37725	2.26	6.0E-80	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11802	24392	37726	2.26	6.0E-80	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11906	13849	26318	1.98	6.0E-80	A1422197.1	EST_HUMAN	t58d02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16785 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
12028	25217		2.42	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12219	24879		5.78	6.0E-80	AB029900.1	NT	Homo sapiens GST gene for cerebroside sulfoltransferase, exon 1, 2, 3, 4, 5
12707	25341		1.94	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
12804	25051	30958	1.35	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
574	13354	25983	0.74	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
815	13588	26253	1.97	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
815	13588	26254	1.97	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1166	13920		2.39	5.0E-80	X91847.1	NT	H. sapiens hox1 gene (exon 12)
1439	14188		2.26	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2361	15083	27821	1.99	5.0E-80	U89358.1	NT	Human (3)mbd protein homolog mRNA, complete cds
2431	15152	27888	1.65	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2797	15502	28242	1.67	5.0E-80	4504292	NT	Homo sapiens H3 Histone family, member J (H3FJ) mRNA
4018	16764	29393	1.37	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4018	16764	29394	1.37	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4900	17627	30244	1.28	5.0E-80	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8255	20949	34086	1.04	5.0E-80	9910293	NT	Mus musculus keratin complex 2, gene 6g (K12-5g), mRNA
8157	21888	35056	8.77	4.0E-80	F25915.1	EST_HUMAN	HSPD13155 Hm3 Homo sapiens cDNA clone s4000045F03
211	13023		8.96	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4861	17395	30030	1.7	3.0E-80	BF085009.1	EST_HUMAN	PMO-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA
4850	17580		3.77	3.0E-80	BE817485.1	EST_HUMAN	QV4-BN0263-040600-241-q10 BN0263 Homo sapiens cDNA
5730	18522	31443	2.68	3.0E-80	A091675.1	EST_HUMAN	cc23e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to TR:O35790 O35790 PIG-L
1790	14530	27238	5.08	2.0E-80	R35321.1	EST_HUMAN	yg55a08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38060 5'
1853	14591	27307	1.18	2.0E-80	A1444821.1	EST_HUMAN	RET487 subtracted retina cDNA library Homo sapiens cDNA clone RET487
2049	14782	27509	5.82	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1323 5'
6708	18823	32667	0.83	2.0E-80	AA582952.1	EST_HUMAN	nm80d01.s1 NCI CGAP_C08 Homo sapiens cDNA clone IMAGE:1090177 3'
6813	19474	32498	1.71	2.0E-80	11421930	NT	Homo sapiens Golgi transport complex protein (90 kDa) (GTC90), mRNA
7151	19838	32808	1.48	2.0E-80	T75215.1	EST_HUMAN	yc88112.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22851 5' similar to
9057	21746	34805	1.41	2.0E-80	AW964270.1	EST_HUMAN	SP-K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B :
9688	22320	36518	1	2.0E-80	AJ007378.1	NT	ES1376343 IMAGE resequences, MAGH Homo sapiens cDNA
10780	23463	36705	4.48	2.0E-80	AA939362.1	EST_HUMAN	Homo sapiens GGT gene, exon 6
331	13132		2.25	1.0E-80	AL163303.2	NT	z70f12.r1 Soares testis 1N1T Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
782	13554	26215	1.37	1.0E-80	AF231920.1	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
1947	14882		2.44	1.0E-80	AJ732686.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
5080	17779	30397	0.99	1.0E-80	4557610	NT	Homo sapiens chromosome 21 unknown mRNA
5244	18050		6.43	1.0E-80	BE386615.1	EST_HUMAN	nm0112.x5 NCI CGAP_C09 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR repetitive element ;
5881	18667	31808	6.58	1.0E-80	L10347.1	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
6406	19175	32174	1.36	1.0E-80	5174540	NT	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3816433 5'
7106	19764	32859	0.95	1.0E-80	AJ224172.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
7472	20145	33237	2.53	1.0E-80	A948731.1	EST_HUMAN	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
7472	20145	33238	2.53	1.0E-80	A948731.1	EST_HUMAN	Homo sapiens mRNA for lipophilin B
							wq25c05.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3'
							wq25c05.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8130	20824	33060	2.84	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
8601	21293	34435	1.72	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
8601	21293	34436	1.72	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9185	21855	35019	1.21	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
9185	21855	35020	1.21	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10325	22972	36192	0.95	1.0E-80	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10548	23244	36479	5.25	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
10548	23244	36480	5.25	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
12289	24719	31051	1.57	1.0E-80	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12498	24853	31034	3.08	1.0E-80	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
10583	23278	36515	1.46	8.0E-81	A1251752.1	EST_HUMAN	q190g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854286 3'
10583	23278	36516	1.46	8.0E-81	A1251752.1	EST_HUMAN	q190g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854286 3'
11102	23772	37048	8.46	8.0E-81	BE394525.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
7152	19839	32909	3.58	7.0E-81	A1822115.1	EST_HUMAN	zaf1c08.x3 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:289618 3'
4354	17092	29726	5.26	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4354	17092	29727	5.26	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5201	18009	30630	2.1	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5201	18009	30631	2.1	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7489	20161	33253	0.97	6.0E-81	AF038660.1	NT	Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
9136	21824	34989	1.36	6.0E-81	AA360017.1	EST_HUMAN	EST169129 Fetal lung II Homo sapiens cDNA 5' end
11800	24390	37723	1.81	6.0E-81	BE396092.1	EST_HUMAN	601312522F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3659284 5'
12430	24803	31041	2.29	6.0E-81	BF679022.1	EST_HUMAN	602153366F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294801 5'
12430	24803	31042	2.28	6.0E-81	BF679022.1	EST_HUMAN	602153366F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294801 5'
2214	14942	27682	2.8	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8311	21005	34143	1.83	5.0E-81	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8311	21005	34144	1.83	5.0E-81	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9548	22201	35383	0.77	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9548	22201	35384	0.77	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11577	24178	37491	2.23	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
11839	24423	37764	1.3	5.0E-81	11526341	NT	Homo sapiens armadillo repeat gene deletions in velocardiofacial syndrome (ARVCF), mRNA
866	13461	26109	2.03	4.0E-81	A1521435.1	EST_HUMAN	h80a12.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85590 Q85590
1815	14555	27270	1.31	4.0E-81	AW779812.1	EST_HUMAN	h89d02.x1 NCI_CGAP_Cot4 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:COGP_BOVIN P53620 COATOMER GAMMA SUBUNIT;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3168	15931	28580	3.58	4.0E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3619	16372	29013	0.98	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815
4139	16881	29509	2.26	4.0E-81	AF263306.1	NT	STRIATIN 1
4139	16881	29510	2.26	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4360	17098	29733	1.33	4.0E-81	8923209	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
7177	19863	32934	1.11	4.0E-81	4757893	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
7298	19862	33058	0.57	4.0E-81	11420544	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2), mRNA
8185	20879	34016	3.59	4.0E-81	X06989.1	NT	Homo sapiens ets variant gene 1 (ETV1), mRNA
8443	21135	34271	3.43	4.0E-81	U20197.1	NT	Human mRNA for amyloid A4(751) protein
8443	21135	34272	3.43	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9128	21814	34980	6.1	4.0E-81	AB018001.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
10001	22649	35891	1.53	4.0E-81	11425281	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10070	22718	35935	0.71	4.0E-81	11439065	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10070	22718	35936	0.71	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11140	23807	37088	3.2	4.0E-81	4759085	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11140	23807	37087	3.2	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B), mRNA
11828	25280	30731	3.63	4.0E-81	11417862	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B), mRNA
11828	25280	30732	3.63	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12463	24831	31030	1.53	4.0E-81	11417871	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12463	24831	31031	1.53	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12597	24911	31004	4.82	4.0E-81	11417874	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
1244	13963	26658	12.36	3.0E-81	Y18000.1	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1244	13963	26659	12.36	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2371	15083	27832	1.23	3.0E-81	AF07188.1	NT	Homo sapiens NF2 gene
2889	15755	28400	5.83	3.0E-81	4506280	NT	Homo sapiens cullin 4A (CUL4A), mRNA, complete cds
2889	15755	28401	5.83	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
2837	15605	28254	2.97	2.0E-81	BE784636.1	EST_HUMAN	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
2837	15605	28255	2.97	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3755	16507	29144	0.71	2.0E-81	AW611542.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
7857	20552	33678	0.6	2.0E-81	8923839	NT	Hg85d01.x1 NCL_CGAP_Ki6711 Homo sapiens cDNA clone IMAGE:2952384 3'
							Homo sapiens hypothetical protein (LOC55596), mRNA

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1402	14149	28829	1.13	1.0E-81	W26539.1	EST_HUMAN	3373 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
3644	16397	29037	1.07	1.0E-81	AW606658.1	EST_HUMAN	EST1372728 IMAGE resequences, MAGF Homo sapiens cDNA
4479	17214	29839	3.56	1.0E-81	AA040370.1	EST_HUMAN	zk45h09.r1 Soares_pregnant_uterus_Nb1HPU Homo sapiens cDNA clone IMAGE:485825 5' similar to
4600	17335	29964	6.99	1.0E-81	BE047896.1	EST_HUMAN	PIR:S52437 S52437 ODP-diacylglycerol synthase - fruit fly;
5157	17890	37795	4.69	1.0E-81	U87928.1	NT	tz45c04.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2281526 5'
5269	18075	30704	4.1	1.0E-81	11432966	NT	Human acetylcholinesterase (AChE) gene, exon 3
5269	18075	30705	4.1	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5415	18214	30922	0.85	1.0E-81	AA255569.1	EST_HUMAN	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5568	18365	31273	3.47	1.0E-81	U52351.1	NT	zr85d06.r1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:682475 5' similar to SW:PR12_HUMAN
5568	18365	31274	3.47	1.0E-81	U52351.1	NT	P49843 DNA PRIMASE 58 KD SUBUNIT ;
6054	18834	31796	1.81	1.0E-81	BF674641.1	EST_HUMAN	Homo sapiens arm-repeat protein NPRAP/neurigin (CTNND2) mRNA, partial cds
6453	19221	32218	0.59	1.0E-81	11420965	NT	Homo sapiens arm-repeat protein NPRAP/neurigin (CTNND2) mRNA, partial cds
6453	19221	32219	0.59	1.0E-81	11420965	NT	602137854F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
6639	19401	32416	0.87	1.0E-81	AJ133269.1	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7669	20333	33444	8.45	1.0E-81	11432966	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
9676	22328	35523	5.09	1.0E-81	BE958278.1	EST_HUMAN	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
9676	22328	35524	5.09	1.0E-81	BE958278.1	EST_HUMAN	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
9669	22519	35715	5.06	1.0E-81	BE564367.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
							601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
							601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
							601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
							ac14406.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:856427 3' similar to
							SW:YB36_YEAST P38126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION. ;
10003	22651	35863	1.59	1.0E-81	AA630784.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10005	22653	35865	3.27	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10005	22653	35866	3.27	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10405	23051	36269	1.59	1.0E-81	AW697550.1	EST_HUMAN	CM3-NN0055-140400-147-a12 NN0055 Homo sapiens cDNA
10860	23540	36787	2.59	1.0E-81	8923988	NT	Homo sapiens golgin-like protein (GLP), mRNA
11029	23700	36966	1.87	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11029	23700	36967	1.87	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11240	16397	29037	1.72	1.0E-81	AW606658.1	EST_HUMAN	EST1372728 IMAGE resequences, MAGF Homo sapiens cDNA
11507	24108	37421	1.99	1.0E-81	BF204263.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
12132	24622	31069	4.13	1.0E-81	11418138	NT	Homo sapiens phospholipase B mRNA editing protein (DJ742C19.2), mRNA
12	12839	25452	3.8	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
104	12839	25452	2.45	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
257	13065	25704	1.1	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
795	13567	26227	2.83	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
867	13636	26308	0.84	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1474	14221	26807	1.42	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1654	14400	27089	1.43	8.0E-82	671560.1	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4219	16960	29585	0.8	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1433	14180		1.7	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
2769	15474	28216	1.2	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
11759	24350	37682	1.71	7.0E-82	AA663747.1	EST_HUMAN	aa68a04.s1 Stratagene echizo brain S11 Homo sapiens cDNA clone IMAGE:968342 3'
4104	16847	29473	0.71	5.0E-82	AA575512.1	EST_HUMAN	nt69e11.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:325196 3'
1666	14412	27103	49.82	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5409	18208	30915	0.8	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-f08 HT0540 Homo sapiens cDNA
5409	18208	30916	0.8	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-f08 HT0540 Homo sapiens cDNA
5671	18466	31381	0.65	4.0E-82	M25833.1	NT	Human von Willebrand factor gene, exon 9
11716	24310	37633	11.61	4.0E-82	AB937300.1	EST_HUMAN	wp75e09.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR-O75276
12374	24773		5.05	4.0E-82	AF029701.2	NT	O75276 PKD1 :
						NT	Homo sapiens presenilin-1 gene, exons 1 and 2
271	13079	25721	21.65	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
687	13462	26110	3.11	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-R02 BN0120 Homo sapiens cDNA
770	13542	26203	5.7	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
						NT	
850	13620	26290	10.65	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1039	13799		18.58	3.0E-82	AA725848.1	EST_HUMAN	ai23a05.e1 Soares_testis NHT Homo sapiens cDNA clone 1343648 3'
1333	14082	26758	1.25	3.0E-82	AW875079.1	EST_HUMAN	RC8-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1450	14197	26881	3.44	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1894	14631	27341	1.91	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
						NT	
2000	14735	27459	1.53	3.0E-82	4501922	NT	Homo sapiens adenylyl cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA
3266	16028		2.52	3.0E-82	545381.1	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA

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4864	17593	30216		0.98	AA135979.1	EST_HUMAN	zn93b04.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565711 5' similar to SW:PAGT_BOVIN Q07537 POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE ;
8052	20746	33878	3.14	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8454	21146	34287	0.88	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8454	21146	34288	0.88	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
9724	22375	35575	3.23	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
9724	22375	35576	3.23	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
583	13363	25990	2.55	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
583	13363	25991	2.55	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1881	14425	27121	1.21	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434M117 5'
3827	16578	29210	1.25	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4208	16949	29575	1.17	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4521	17256	29890	1.01	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4521	17256	29891	1.01	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4816	17547	30172	2.85	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5021	17742	30352	1.46	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5021	17742	30353	1.46	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5384	18184	30874	5.65	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6082	18861	31827	4.73	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
7581	25426		0.91	2.0E-82	AI478428.1	EST_HUMAN	tm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
7705	20369	33482	0.85	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8204	20898	34035	2.16	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
8568	21280	34397	0.45	2.0E-82	7657340	NT	Homo sapiens microtubule (mouse) homolog (MORC), mRNA
8568	21260	34398	0.45	2.0E-82	7657340	NT	Homo sapiens microtubule (mouse) homolog (MORC), mRNA
10009	22657	35870	1.84	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10009	22657	35871	1.84	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11237	23900	37187	1.27	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11237	23900	37188	1.27	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11279	23940	37233	4.45	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11279	23940	37234	4.45	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11750	24341	37670	1.91	2.0E-82	5031680	NT	Homo sapiens EGF-like repeats and disocidin-like domains 3 (EDIL3), mRNA
11957	24508		1.58	2.0E-82	N94950.1	EST_HUMAN	z531d10.s1 Soares_parathyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:305203 3'

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12485	24844		3.47	2.0E-82	AA011278.1	EST_HUMAN	201g09.r1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
12775	25029		1.95	2.0E-82	11418097	NT	Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA
578	13358	25085	1.14	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1186	13938		0.77	1.0E-82	BE865106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1283	14012	26679	3.1	1.0E-82	BE865386.1	EST_HUMAN	RCA-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
1284	14013	26680	1.26	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
8841	21533	34678	1.13	1.0E-82	AB037838.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
9553	22206	35390	0.59	1.0E-82	AB014562.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
10145	22793		1.17	1.0E-82	BF515938.1	EST_HUMAN	U1-H-BW1-acca-f-03-0-U1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
10646	23337	36576	2.34	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8615	21307	34449	4.51	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
10174	22822	36039	0.53	9.0E-83	BE253347.1	EST_HUMAN	601117160F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357734 5'
1392	14139	26816	3.33	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1676	15523	27115	5.63	8.0E-83	N66951.1	EST_HUMAN	z448f12.s1 Scores_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:295823 3'
1335	14084	26759	0.97	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-271299-068-111 LT0016 Homo sapiens cDNA
2868	15635		1.88	7.0E-83	AA584655.1	EST_HUMAN	no12h01.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4785	17497		6.68	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI CGAP_Py28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316
5960	18742	31702	0.58	7.0E-83	11426657	NT	DJ207H1.1 ;
11717	24311	37834	1.4	7.0E-83	5729753	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
11717	24311	37635	1.4	7.0E-83	5729753	NT	Homo sapiens transcription factor CA150 (CA150) mRNA
394	13179	25826	1.98	6.0E-83	M3320.1	NT	Homo sapiens transcription factor CA150 (CA150) mRNA
1779	14520	27224	1.5	6.0E-83	AW573088.1	EST_HUMAN	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
3017	15783	28432	0.71	6.0E-83	AW819405.1	EST_HUMAN	h31h03.x1 Scores_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2933525 3' similar to SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN HI0034. ;
3046	18812		1.08	6.0E-83	AF231918.1	NT	QV4-ST0234-181189-037-405 ST0234 Homo sapiens cDNA
5211	18019	30641	2.02	6.0E-83	4507866	NT	Homo sapiens chromosome 21 unknown mRNA
5933	18716	31674	1.52	6.0E-83	AJ010770.1	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
7401	20079	33160	2.27	6.0E-83	11422024	NT	Homo sapiens hypoxanthine phosphoribosyl transferase gene, exons 1-50
9575	22226	35413	2.85	6.0E-83	4505314	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
9669	22321	35517	2.34	6.0E-83	11430647	NT	Homo sapiens myomesin (M-protein) 2 (16kD) (MYOM2), mRNA
9689	22321	35518	2.34	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA

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11517	24117		2.53	6.0E-83	AA488105.1	EST_HUMAN	ab14e10.s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element ;
11908	24472		4.27	6.0E-83	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
925	13692		2.03	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2043	15526		1.55	5.0E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3629	16382	29022	1.18	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
3886	16636	29275	0.77	5.0E-83	4885190	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
5020	17741	30350	11.53	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5020	17741	30351	11.53	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5093	17812	30428	1.07	5.0E-83	5031660	NT	Homo sapiens EGF-like repeats and discordin like domains 3 (EDIL3), mRNA
5093	17812	30429	1.07	5.0E-83	5031660	NT	Homo sapiens EGF-like repeats and discordin like domains 3 (EDIL3), mRNA
625	13404	26039	1.72	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
977	13742		4.9	3.0E-83	AA368311.1	EST_HUMAN	EST79542 Placenta 1 Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9 repetitive element ;
2780	15485		1.33	3.0E-83	AA632654.1	EST_HUMAN	np87c07.s1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR12 THR repetitive element ;
6483	19250		0.82	3.0E-83	A1217223.1	EST_HUMAN	qf73e06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755682 3'
1792	14532	27240	1.86	2.0E-83	AA993492.1	EST_HUMAN	qf84g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92814
1792	14532	27241	1.86	2.0E-83	AA993492.1	EST_HUMAN	qf84g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92814
1918	14655	27365	4.07	2.0E-83	N66951.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216. ;
2856	15624	28268	1.1	2.0E-83	BE828694.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216. ;
3263	16025		1.89	2.0E-83	11430834	NT	Q92614 MYELOBLAST KIAA0216. ;
3756	16508		0.7	2.0E-83	AL163202.2	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
4302	17041	29668	4.11	2.0E-83	AF202879.1	NT	Homo sapiens chromosome 21 segment HS21C002
4604	17339	29668	6.14	2.0E-83	7706398	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4604	17339	29668	6.14	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5189	17997	30620	0.9	2.0E-83	U06679.1	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5755	18547	31468	0.85	2.0E-83	11428081	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5875	18682	31603	1.31	2.0E-83	BE885401.1	EST_HUMAN	Human carcinoembryonic antigen gene family member 18 (CGM18) gene, exons A1 and B1
6847	19408	32423	1.12	2.0E-83	AF129533.1	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7335	20017	33095	6.36	2.0E-83	AF129533.1	NT	801507482F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909068 5'
							Homo sapiens F-box protein FB3b (FBL3B) mRNA, partial cds
							Homo sapiens F-box protein FB3b (FBL3B) mRNA, partial cds

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7704	20367	33490	0.64	2.0E-83	BF105097.1	EST_HUMAN	601822090F1 NIH_MGC.75 Homo sapiens cDNA clone IMAGE:4042318 5'
7742	20438	33560	0.78	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7742	20438	33561	0.78	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7888	20581	33710	1.79	2.0E-83	U68707.1	NT	Rattus norvegicus densin-180 mRNA, complete cds
8213	20907	34042	2.05	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8213	20907	34043	2.05	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
9494	22147	35328	0.48	2.0E-83	5453381	NT	Homo sapiens phosphatase kinase, gamma 1 (muscle) (PHKG1) mRNA
9494	22147	35329	0.48	2.0E-83	5453381	NT	Homo sapiens phosphatase kinase, gamma 1 (muscle) (PHKG1) mRNA
9934	22582	35780	4.01	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
9934	22582	35781	4.01	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10018	22804	35881	1.39	2.0E-83	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
10089	22737	35952	0.77	2.0E-83	AW505800.1	EST_HUMAN	UJ-HF-BN0-amd-h-07-0-UI,1 NIH_MGC.50 Homo sapiens cDNA clone IMAGE:3081852 5'
10753	23438	36882	0.64	2.0E-83	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
10845	23527	36770	2.19	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
10845	23527	36771	2.19	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
12522	24869		3.85	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-9, complete cds
1390	14137	26813	2.18	1.0E-83	4504326	NT	Homo sapiens hydroxyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1390	14137	26814	2.18	1.0E-83	4504326	NT	Homo sapiens hydroxyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1442	14189	26873	0.98	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1442	14189	26874	0.98	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
3179	15942	28593	1.18	1.0E-83	7882349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
3850	16600	29237	3.93	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4220	16981	29586	1.99	1.0E-83	Z25822.1	NT	H. sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
4831	17562	30184	3.36	1.0E-83	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
6598	19359	32373	1.65	1.0E-83	AI027614.1	EST_HUMAN	019908.01 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM PROTEIN (HUMAN);
3776	16528	29187	3.8	7.0E-84	BE901209.1	EST_HUMAN	601876023F1 NIH_MGC.21 Homo sapiens cDNA clone IMAGE:3958853 5'
1272	14021	26687	3.5	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-q05 FN0119 Homo sapiens cDNA
1272	14021	26688	3.5	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-q05 FN0119 Homo sapiens cDNA
2398	15117	27854	8.26	6.0E-84	AA776574.1	EST_HUMAN	ae68a03.s1 Stratigene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5160	17892		3.33	6.0E-84	AL042863.2	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5431	18230	30943	1.87	6.0E-84	AA897339.1	EST_HUMAN	al47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
5574	18371	31282	1.04	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA
5574	18371	31283	1.04	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA
7373	20553	33134	2.94	6.0E-84	BE810371.1	EST_HUMAN	PMO-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA
7591	20259	33367	0.97	6.0E-84	AF038391.1	NT	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
7972	20667	33789	2.37	6.0E-84	BE770199.1	EST_HUMAN	PM4-F T0054-160600-004-e10 F70054 Homo sapiens cDNA
897	13472	26121	0.71	5.0E-84	AA382811.1	EST_HUMAN	EST196094 Testis 1 Homo sapiens cDNA 5' end
3013	15779		1.82	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
6015	18786	31758	0.59	5.0E-84	AA167678.1	EST_HUMAN	zq39e07.1 Stratagene hMT neuron (#937233) Homo sapiens cDNA clone IMAGE:832100 5' similar to TR:G483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q.;
11533	24133	37438	3.17	5.0E-84	11426740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11652	24249	37570	1.77	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11652	24249	37571	1.77	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11813	24401	37738	1.44	5.0E-84	11433550	NT	Homo sapiens tropomodulin 2 (neuronal) (TMOD2), mRNA
1389	14136	26812	2.19	4.0E-84	AI885321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN_043847 NARDILYSIN PRECURSOR;
4897	17624	30242	1.79	4.0E-84	AF069801.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5475	18274	31168	1.36	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5475	18274	31169	1.36	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6175	18952	31925	1.88	4.0E-84	AF059650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7547	20217	33319	14.38	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
8809	21501	34647	1.21	4.0E-84	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8809	21501	34648	1.21	4.0E-84	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
10835	23517	36759	4.51	4.0E-84	AB032856.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
308	13112	25752	1.24	3.0E-84	AF028200.1	NT	Homo sapiens Becl1 protein homolog mRNA, partial cds
1953	14688	27401	1.15	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2001	14736	27460	2.41	3.0E-84	AL096860.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3578	18333	28977	1.07	3.0E-84	AB028898.1	NT	Homo sapiens DNA, DLG1 to ORCTL4 gene region, section 1/2 (DLG1, ORCTL3, ORCTL4 genes, complete cds)
3731	18483	29121	5.2	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA, complete cds

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10790	23473		3.55	3.0E-84	A1983801.1	EST_HUMAN	wu2d05.x1 Soares Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:1.05093.60S RIBOSOMAL PROTEIN L18A (HUMAN);
2098	14829	27563	6.94	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190800-272-b08 BT0795 Homo sapiens cDNA
2098	14829	27564	6.94	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190800-272-b08 BT0795 Homo sapiens cDNA
2944	15710	28362	9.31	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
2982	15728	28378	0.77	2.0E-84	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
5439	18238	30952	0.92	2.0E-84	BF511575.1	EST_HUMAN	U1H-B14-act-a-02-0-UIs1 NCL CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
5439	18238	30953	0.92	2.0E-84	BF511575.1	EST_HUMAN	U1H-B14-act-a-02-0-UIs1 NCL CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
6540	19305	32310	0.75	2.0E-84	H63370.1	EST_HUMAN	yr56e11.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:209324 3'
7956	20651		1.35	2.0E-84	A1298674.1	EST_HUMAN	qm87c09.x1 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1895728 3'
8284	20978	34118	0.49	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8284	20978	34119	0.49	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9245	21924	35094	0.81	2.0E-84	AU120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
9631	22283	35476	0.61	2.0E-84	H22841.1	EST_HUMAN	ym49e11.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:51383 5' similar to SP-APOH_RAT P26844 BETA-2-GLYCOPROTEIN I;
12159	24643	31100	3	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_synthetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1;
12159	24643	31101	3	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_synthetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1;
304	13108	25748	1.89	1.0E-84	AF114488.1	NT	Homo sapiens tyrosine 3-monooxygenase/hypoxanthine 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
536	13319	25953	20.64	1.0E-84	4507952	NT	Homo sapiens complement component 5 (C5), mRNA
703	13478		1	1.0E-84	11427631	NT	am85b11.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1829885 3'
1270	14019	26685	3.17	1.0E-84	AA984379.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5'
2048	14781	27608	1.92	1.0E-84	BE392137.1	EST_HUMAN	Homo sapiens pericentriolar material 1 (PCN1), mRNA
2220	14948	27686	1.13	1.0E-84	11427197	NT	nm12a08.s1 NCL CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
3733	16486	29123	2.46	1.0E-84	AA720851.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4383	17120	29752	5.01	1.0E-84	AJ229041.1	NT	DKFZp434N0323 r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4651	17385	30017	3.53	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323 r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4651	17385	30018	3.53	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323 r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4855	17120	29752	2.67	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5153	17870	30483	1.15	1.0E-84	7656998	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
5830	18619	31551	0.98	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA

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6097	18875	31844	1.41	1.0E-84	S73482.1	NT	uterine water channel=28 kda erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
6781	19525	32552	1.66	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
6781	19525	32552	1.66	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7007	19659	32753	2.32	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7389	20049	33130	1.26	1.0E-84	8898994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7501	20137	33229	2.42	1.0E-84	11430846	NT	Homo sapiens NGF1-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
9435	22113		3.05	1.0E-84	5031884	NT	Homo sapiens nuclear transport factor 2 (placental protein 16) (PP16) mRNA
9670	22322	35519	0.53	1.0E-84	AF224511.1	NT	Homo sapiens Ca2+-binding protein CABP3 (CABP3) gene, exon 6 and partial cds
9890	17900	30588	3.05	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9890	17900	30589	3.05	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10496	23142	36368	1.08	1.0E-84	11437356	NT	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4), mRNA
12046	24566		2.34	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RX1), mRNA
12151	24638	31096	3.2	1.0E-84	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
946	13712		1.06	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1051	13810	26469	2.39	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1051	13810	26470	2.39	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1360	14108	26783	0.95	9.0E-85	4758669	NT	Homo sapiens leupaxin (LDPL), mRNA
1572	14319	27004	1.23	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1572	14319	27005	1.23	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1870	14415	27108	3.6	9.0E-85	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4225	16968	29591	0.96	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4824	17555	30177	0.96	9.0E-85	5801979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4856	17585	30208	1.12	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1114	13871	26530	1.45	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11842	24239		4.32	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11392	23968	37300	3.35	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11392	23968	37301	3.35	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11766	24357	37690	1.29	6.0E-85	AA403053.1	EST_HUMAN	z62601.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
2332	15056	27792	1.49	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084

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4399	17138		0.8	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
5364	18166	30851	1.4	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
5364	18166	30852	1.4	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
11063	23733	37005	2	5.0E-85	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12743	17136		5.28	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
6056	18836	31797	1.51	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6056	18836	31798	1.51	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
10472	23118		1.3	4.0E-85	BE079283.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
1276	14026	26694	2.98	3.0E-85	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1773	14515	27215	3.51	3.0E-85	T97495.1	EST_HUMAN	yes5g09.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:121504 5'
4280	17019	29646	6.53	3.0E-85	BE267189.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4841	17571	30194	1.45	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4841	17571	30195	1.45	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5316	18120	30777	1.07	3.0E-85	11436001	NT	Homo sapiens lactrin-like protein rich protein (LPRP), mRNA
5994	18775	31737	0.63	3.0E-85	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6043	18823	31783	5.71	3.0E-85	7662309	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6043	18823	31784	5.71	3.0E-85	7662309	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6853	19553		7.79	3.0E-85	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7295	19978	33055	0.91	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0621 protein (KIAA0621), mRNA
7771	20467	33591	1.89	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
8406	21089	34235	0.74	3.0E-85	11525828	NT	Homo sapiens CGI-81 protein (LOC51109), mRNA
8877	21568	34712	3.8	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9206	22085	35257	0.96	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B" (SNRPB2), mRNA
9206	22085	35258	0.96	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B" (SNRPB2), mRNA
10361	23027	36242	0.56	3.0E-85	AF089642.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
10730	23418	36859	1.88	3.0E-85	BE150392.1	EST_HUMAN	RC1-HT0268-031299-012-409 HT0268 Homo sapiens cDNA
11490	24091	37403	2.25	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
11824	24408	37742	1.79	3.0E-85	AB029030.1	NT	Homo sapiens mRNA for KIAA1107 protein, partial cds
11824	24408	37743	1.79	3.0E-85	AB029030.1	NT	Homo sapiens mRNA for KIAA1107 protein, partial cds
12840	24837		1.98	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1017	13777	26438	2.34	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1383	14130	26803	0.97	2.0E-85	7706205	NT	Homo sapiens CGL-201 protein (LOC51340), mRNA
1399	14146	26824	8.28	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1399	14146	26825	8.28	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2226	14954	27692	1.53	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2826	14963		5.28	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
3022	15788	28435	1.18	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4300	17039	29666	4.51	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4527	17262	29896	1.22	2.0E-85	4826977	NT	Homo sapiens resilin (RELN) mRNA
4854	17584	30207	0.97	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9173	21843	35009	3.18	2.0E-85	A1760820.1	EST_HUMAN	w67h08.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element
9549	22022	35385	1.08	2.0E-85	A914459.1	EST_HUMAN	MSR1 repetitive element
10162	22810	36029	1.32	2.0E-85	A1866384.1	EST_HUMAN	wd49d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331461 3'
2285	15010		2.86	1.0E-85	BE794306.1	EST_HUMAN	wm94d12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
2392	15113	27850	8.42	1.0E-85	BE618392.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945618 5'
2392	15113	27851	8.42	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
9681	22333	35528	4.38	1.0E-85	BE257917.1	EST_HUMAN	601109738F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350553 5'
10842	23524	36766	2.77	1.0E-85	AA776785.1	EST_HUMAN	Z45f03.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10842	23524	36767	2.77	1.0E-85	AA776785.1	EST_HUMAN	Z45f03.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10919	23599	36847	1.73	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
10919	23599	36848	1.73	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
10997	23670	36927	1.28	1.0E-85	Y00052.1	NT	Human mRNA for T-cell cyclophilin
11773	24364	37690	2.41	1.0E-85	A1198420.1	EST_HUMAN	q156e07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1860468 3'
12050	24722	31053	4.4	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12295	24722	31053	4.74	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1409	14156		11.19	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
11698	24203	37818	1.57	8.0E-86	4503224	NT	Homo sapiens cyclochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
916	13683	26345	2.34	7.0E-86	AA860801.1	EST_HUMAN	q88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
916	13683	26346	2.34	7.0E-86	AA860801.1	EST_HUMAN	q88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6103	18881	31848	1.02	7.0E-86	9966888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6103	18881	31849	1.02	7.0E-86	9966888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6890	17956	30553	6.95	7.0E-88	11421737	NT	Homo sapiens Text (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
8643	21335	34479	3.08	7.0E-86	L38557.1	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
9699	22252		1.39	7.0E-86	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9658	22310	35508	2.27	7.0E-86	11526307	NT	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA
10882	23562	36809	1.72	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
10882	23562	36810	1.72	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
1271	14020	26686	2.88	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (liponamide) (OGDH), mRNA
5105	17823	30440	2.64	6.0E-86	Y19138.1	NT	Homo sapiens enteropeptidase gene, exons 20 and 21
5107	17825	30442	1.07	6.0E-86	6005833	NT	Homo sapiens 24 kDa intrinsic membrane protein (PMP24), mRNA
206	13018	25660	4.98	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
5944	18726	31684	12.1	4.0E-86	BE295843.1	EST_HUMAN	601178665F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631953 5'
11205	13018	25660	2.18	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
5509	18307	31208	6.97	3.0E-86	AW340946.1	EST_HUMAN	x92h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
8160	20854	33985	1.05	3.0E-86	AV723239.1	EST_HUMAN	AV723239 HTB Homo sapiens cDNA clone HTB8SD04 5'
10120	22768	35981	3.37	3.0E-86	BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
10120	22768	35981	3.37	3.0E-86	BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11413	23180	36408	5.14	3.0E-86	AI659240.1	EST_HUMAN	tu18b02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2251371 3'
11708	24303	37628	1.6	3.0E-86	11037056	NT	Homo sapiens myosin X (MYO10), mRNA
260	13068	25706	2.02	2.0E-86	AA306264.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
405	13190		2.59	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1168	13922	26584	3.21	2.0E-86	N58877.1	EST_HUMAN	yz19e08.r1 Soares_multiple_sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:283478 5'
1478	14225	26910	1.93	2.0E-86	4758827	NT	Homo sapiens neuritin III (NRXN3), mRNA
1478	14225	26911	1.93	2.0E-86	4758827	NT	Homo sapiens neuritin III (NRXN3), mRNA
2188	14917	27651	5.09	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
2266	14992	27732	1.55	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3410	16168	28817	1.3	2.0E-86	AW966142.1	EST_HUMAN	EST1378215 MAGE resequences, MAGI Homo sapiens cDNA
3729	16481	29118	3.54	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3729	16481	29119	3.54	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4019	16765		2.84	2.0E-86	AW515742.1	EST_HUMAN	hd87g08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2916542 3'
4737	17469	30106	3.28	2.0E-86	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A), partial cds
5782	18573	31501	1.52	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5782	18573	31502	1.52	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
						NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
6974	25098	32476	0.69	2.0E-86	11419429	NT	Human Chediak-Higashi syndrome protein short isoform (LYST), mRNA, complete cds
7908	20603	33733	0.69	2.0E-86	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST), mRNA, complete cds
8414	21107		0.47	2.0E-86	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8472	21164	34307	2.31	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8472	21164	34308	2.31	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8801	21493	34640	0.65	2.0E-86	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9218	21897	35067	1.95	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
10345	22992	36210	2.91	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10345	22992	36211	2.91	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10400	23046	36262	1.15	2.0E-86	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10400	23046	36262	1.15	2.0E-86	AB037832.1	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 6 (RPS6KA6) mRNA
10820	23503	36742	2.54	2.0E-86	475905.1	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12458	24827	31027	3.07	2.0E-86	11418189	NT	Homo sapiens gene for AF-6, complete cds
12821	24926		4.26	2.0E-86	AB011399.1	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
1592	14338	27027	2.28	1.0E-86	4826855	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3160	15923	28569	1.5	1.0E-86	5453649	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3229	15992	28645	2.7	1.0E-86	L20492.1	NT	Homo sapiens chromosome 21 segment HS21C009
3290	16051	28699	1.32	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3290	16051	28700	1.32	1.0E-86	AL163209.2	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3926	16676	29318	0.88	1.0E-86	7706181	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3926	16676	29319	0.88	1.0E-86	7706181	NT	Homo sapiens chromosome 21 segment HS21C100
4233	16974	29599	5.2	1.0E-86	AL163300.2	NT	Homo sapiens synaptobrevin 1 (SYNU1), mRNA
4578	17313	29941	1.23	1.0E-86	4507334	NT	Homo sapiens chromosome 21 segment HS21C084
5465	18284	31155	2	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11608	18284	31155	1.37	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5272	18078		1.81	9.0E-87	AI150703.1	EST_HUMAN	cb77c09.x1 Soares fetal heart N14-119W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE_P02535 KERATIN, TYPE I CYTOSKELETAL 10.
7348	20029	33105	1.7	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7348	20029	33106	1.7	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
467	13252	25893	15.93	8.0E-87	X62245.1	NT	O. carinatus mRNA for elongation factor 1 alpha
2294	15019	27755	1.79	7.0E-87	BF063211.1	EST_HUMAN	7n8502.x1 NCL CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2294	15019	27756	1.79	7.0E-87	BF063211.1	EST_HUMAN	7n8502.x1 NCL CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6307	19079	32084	0.57	7.0E-87	AF090336.1	EST_HUMAN	MR0-NT0039-020500-004-a11 NT0039 Homo sapiens cDNA
8089	20783	33913	3.4	7.0E-87	BF352778.1	EST_HUMAN	IL3-HT0818-060700-198-D10 HT0818 Homo sapiens cDNA
8354	20425	33544	1.15	7.0E-87	BE712981.1	EST_HUMAN	IL5-HT0702-160600-103-d08 HT0702 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9971	22819	35822	3.85	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
9971	22819	35823	3.85	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
10366	23129		0.51	7.0E-87	AI081565.1	EST_HUMAN	α59h01.s1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1660857 3'
10806	23489	36724	6.65	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
10806	23489	36725	6.65	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
3517	18273	28927	0.99	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5128	17846	30463	0.69	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
6327	19097	32085	2.02	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
10825	23318		4.13	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
11351	13891	26551	1.42	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
12297	13891	26551	1.56	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
945	13711	26376	1.51	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1149	13904	26566	13.58	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
2024	14759	27488	1.53	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2421	15142	27874	1.03	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51826), mRNA
2421	15142	27875	1.03	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51826), mRNA
3457	18213	28866	1.8	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23) (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
5360	18162	30846	2.77	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5954	18736	31895	4.53	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
7670	20334	33445	0.72	4.0E-87	L48524.1	NT	Homo sapiens tuberin (TSC2) gene, exon 10
11118	23788	37065	3.44	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
12396	25266	30721	1.5	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12396	25266	30722	1.5	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12541	24831		2.25	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2769	15484	28223	2.77	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
3764	16516	26154	0.83	2.0E-87	AU116835.1	EST_HUMAN	Homo sapiens HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
4857	17566	30209	1.26	2.0E-87	BF376311.1	EST_HUMAN	CMO-TN0039-150900-552-h08 TN0038 Homo sapiens cDNA
4907	17634	30249	1.47	2.0E-87	BE175478.1	EST_HUMAN	RCS-HT0580-200300-031-Q04 HT0580 Homo sapiens cDNA
5575	18372	31284	10.34	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3849730 5'
5575	18372	31285	10.34	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3849730 5'
6234	19008		9.81	2.0E-87	BE567183.1	EST_HUMAN	601341383F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683348 5'

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6589	18362	32375	0.69	2.0E-87	N48128.1	EST_HUMAN	wy21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
6883	19800	32638	0.81	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLC Homo sapiens cDNA clone GLCDSG04 3'
7073	19764	32828	1.58	2.0E-87	BE284432.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
7126	19814	32882	0.94	2.0E-87	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7353	20034	33112	39.61	2.0E-87	N48128.1	EST_HUMAN	wy21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
7587	20255	33362	35.45	2.0E-87	N48128.1	EST_HUMAN	wy21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
8294	20988	34127	17.42	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
9685	22337		5.72	2.0E-87	BE531136.1	EST_HUMAN	601278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'
1159	15521		2.09	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1411	14158	26840	1.1	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1411	14158	26841	1.1	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3697	16451	28090	6.23	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3717	16470	29108	2.43	1.0E-87	4758827	NT	Homo sapiens neurixin III (NRX3) mRNA
5095	17814	30431	0.99	1.0E-87	AF114487.1	NT	Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds
5149	12933	25570	1.04	1.0E-87	AF114487.1	NT	Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds
6132	18910	31878	1.91	1.0E-87	A004091.1	EST_HUMAN	o650d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1620199 3'
6132	18910	31879	1.91	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7077	19768	32832	0.82	1.0E-87	AF039517.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7077	19768	32833	0.82	1.0E-87	AF039517.1	NT	Homo sapiens corticotropin-releasing factor type 1 receptor gene, exon 8
7083	19773	32838	1.18	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7298	19981	33057	1.23	1.0E-87	11431580	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
8015	20710	33840	12.93	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8807	21499	34644	0.97	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
8807	21499	34645	0.97	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9533	22186	35371	2.85	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
9533	22186	35372	2.85	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
10272	22920	36131	0.67	1.0E-87	M34426.1	NT	Human L-plastin mRNA, 5' end
10633	23325	36562	1.55	1.0E-87	5729887	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
10921	23801		1.92	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10965	23941	36893	1.68	1.0E-87	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
10965	23941	36894	1.68	1.0E-87	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
12393	25404		3.54	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
12809	25240		3.94	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1084	13842	26500	10.24	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1327	14076	26750	2.76	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1327	14076	26751	2.76	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2115	14846	27675	1.57	9.0E-88	7661701	NT	Homo sapiens DKFZP586P1522 protein (DKFZP586P1522), mRNA
3617	16370	29012	1.35	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4236	16977	29602	2.73	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
4236	16977	29603	2.73	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
4943	17670	30279	1.05	9.0E-88	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8919	21610	34754	3.82	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1820	14559		1.02	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2845	15355	28100	3.76	5.0E-88	N89399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3000	15766	28414	0.9	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3384	16143		2.28	5.0E-88	AI693217.1	EST_HUMAN	wd88h08.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336798 3' similar to contains Alu repetitive element/contains element MER22 MER22 repetitive element;
4687	17421	30056	0.83	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
6672	19589	32625	3.19	5.0E-88	H10932.1	EST_HUMAN	ym06b10.1 Scores infant brain INIB Homo sapiens cDNA clone IMAGE:47129 5'
7830	20525	33650	1.8	5.0E-88	AL163264.2	NT	Homo sapiens chromosome 21 segment HS21C084
9211	21890	35057	0.45	5.0E-88	BF680206.1	EST_HUMAN	602154958F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285775 5'
1306	14055	26729	1.42	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1306	14055	26730	1.42	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
7143	19830	32899	1.43	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68KD (TGFB1), mRNA
10827	23509	36749	1.8	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
11471	24072	37380	1.89	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11471	24072	37381	1.89	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
715	13489	26140	1.85	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1805	14545		1.96	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2948	15714	28367	4.11	3.0E-88	N66951.1	EST_HUMAN	za48f12.a1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:296823 3'
4216	16957	29579	1.24	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4216	16957	29580	1.24	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4444	17180		4.06	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5216	18024	30648	2.85	3.0E-88	11429637	NT	Homo sapiens valosin-containing protein (VCP), mRNA

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5498	18296	31194	4.13	3.0E-88	9968888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5618	18414	31327	3.56	3.0E-88	11420697	NT	Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6069	18848	31812	0.61	3.0E-88	11417370	NT	Homo sapiens interleukin 13 (IL13), mRNA
6319	25088	32078	1.18	3.0E-88	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6319	25088	32077	1.18	3.0E-88	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6865	18447	32465	14.59	3.0E-88	AF29285.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7440	20117	33206	8.15	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
7821	20516	33642	9.58	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8086	20790	33921	1.35	3.0E-88	AF034374.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds
9334	20405	33521	1.99	3.0E-88	11526262	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
9828	22479	35680	0.58	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9828	22479	35681	0.58	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9857	22507	35705	1.28	3.0E-88	11430065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12139	24628		5.97	3.0E-88	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1013	13773	28432	3.32	2.0E-88	7305188	NT	Homo sapiens Caldesin, presenilin-binding protein, EF hand transcription factor (CSENI), mRNA
1620	14387	27056	1.38	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1744	14486	27185	3.13	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3458	16214	28867	1.52	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4391	17128	29760	2.13	2.0E-88	5031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
5821	18610	31639	5.63	1.0E-88	AW139585.1	EST_HUMAN	U1-H-B1-aaa-4-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
5821	18610	31540	5.63	1.0E-88	AW139585.1	EST_HUMAN	U1-H-B1-aaa-4-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6548	19313	32317	23.81	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6548	19313	32318	23.81	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7022	19714	32771	1.4	1.0E-88	AI669034.1	EST_HUMAN	wg70a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2476806 3'
7084	19774	32838	4.42	1.0E-88	AA488981.1	EST_HUMAN	ae54a11.s1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2 CE00851
9141	21872	35037	0.6	1.0E-88	AA190368.1	EST_HUMAN	zp87c02.f1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:827170 5' similar to SW:P011 HUMAN P10266 RETROVIRUS-RELATED POLYPROTEIN
9478	22131	35311	2.97	1.0E-88	AL043314.2	EST_HUMAN	DKFZp434N0323 J1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'
11422	23189	36420	2.99	1.0E-88	AA991479.1	EST_HUMAN	os91g03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
12356	24760		3	1.0E-88	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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2739	15445	28184	1.33	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
8833	19495	32519	1.2	8.0E-89	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
424	13210	25856	1.72	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
424	13210	25857	1.72	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4828	17559	30181	2.86	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
4878	17605	30228	3.35	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E246 5'
5345	18148	30827	1.34	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete CDS
5345	18148	30828	1.34	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete CDS
6250	19024	31997	0.57	7.0E-89	7549808	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
6250	19024	31998	0.57	7.0E-89	7549808	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
7398	20076	33156	2.06	7.0E-89	11420754	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
7779	20474	33598	0.57	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7779	20474	33599	0.57	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9584	22237	35421	0.6	7.0E-89	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
10429	23075	36296	1.11	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10429	23075	36297	1.11	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10445	23091	36320	2.33	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10445	23091	36321	2.33	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
11203	23867	37154	1.45	7.0E-89	M59783.1	NT	Human aldose reductase (AR) gene, segment 2
12774	25028		1.7	7.0E-89	U87927.1	NT	Human ascorbate hydratase (ACO2) gene, exon 2
1002	13762	26423	0.73	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2210	14938	27676	1.27	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2434	15155	27888	1.06	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2434	15155	27889	1.06	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
3515	16271	28925	0.88	6.0E-89	7861817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4593	17328	29954	3.02	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4593	17328	29955	3.02	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5100	17819	30436	0.81	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5100	17819	30437	0.81	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5018	17737	30345	2.74	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5018	17737	30346	2.74	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383

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7487	20159	33251	1.95	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-080800-219-g03 NT0022 Homo sapiens cDNA
11088	23758	37034	1.56	4.0E-89	AI798672.1	EST_HUMAN	wa91c03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2348452 3'
2879	15646	28289	1.51	3.0E-89	AW976181.1	EST_HUMAN	EST388290 IMAGE resequences, MAGN Homo sapiens cDNA
7040	19731	32780	1.26	3.0E-89	AI217359.1	EST_HUMAN	qh17b08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1844915 3'
10502	23148	36374	0.48	3.0E-89	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
							yw86e11.1 Soares_placenta_8to9weeks_2NBP860W Homo sapiens cDNA clone IMAGE:259148 5'
10702	23393	36630	2.34	3.0E-89	N57357.1	EST_HUMAN	similar to SW:PI4K_HUMAN P42356 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA ;
123	13184	25832	0.87	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	13184	25833	0.87	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
399	13184	25832	1.55	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
399	13184	25833	1.55	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
517	13301	25933	3.17	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2893	15650	28293	1.53	2.0E-89	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
3540	16296	28946	1.01	2.0E-89	AA759149.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN) contains Alu repetitive element
3540	16296	28947	1.01	2.0E-89	AA759149.1	EST_HUMAN	sh70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4125	16867	29494	1.26	2.0E-89	AF089897.1	NT	sh70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4133	16875	29504	5.16	2.0E-89	X58742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4133	16875	29505	5.16	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4315	17054	29679	0.75	2.0E-89	AL163203.2	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4463	17199	29825	1.1	2.0E-89	AJ007378.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
5259	18065	30886	0.66	2.0E-89	BE541744.1	NT	Homo sapiens GGT gene, exon 5
5393	18193	31086	2.9	2.0E-89	AB007546.1	NT	Homo sapiens GGT gene, exon 5
5702	18496	31418	1.61	2.0E-89	U03985.1	NT	Homo sapiens gene for LECT2, complete cds
6116	18894	31961	0.63	2.0E-89	AL163285.2	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
7567	20237	33341	5.33	2.0E-89	U81004.1	NT	Homo sapiens chromosome 21 segment HS21C085
							Human GT24 (GT24) mRNA, partial cds
7835	20530	33657	3.07	2.0E-89	11428801	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8316	21009	34146	1.02	2.0E-89	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
9152	21883	35052	0.6	2.0E-89	AB037754.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
9710	22361	35557	0.68	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
9710	22361	35558	0.68	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5

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11346	24036	37339	2.83	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11448	23215	36447	2.3	2.0E-89	5729867	NT	Homo sapiens heci domain and RLD 2 (HERC2), mRNA
11562	24161	37472	5.03	2.0E-89	11433673	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
11718	24312	37636	2.11	2.0E-89	U10692.1	NT	Human IMAGE-7 antigen (IMAGE7) pseudogene, complete cds
11570	24169	37483	5.97	1.0E-89	BF196052.1	EST_HUMAN	hr81d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN ;
11570	24169	37484	5.97	1.0E-89	BF196052.1	EST_HUMAN	hr81d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN ;
8126	20820	33956	1.57	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8126	20820	33957	1.57	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1041	13801	26459	2.23	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1042	13801	26459	2.9	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1307	15565	26731	3.78	8.0E-90	BE670561.1	EST_HUMAN	7a36f08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1307	15565	26732	3.78	8.0E-90	BE670561.1	EST_HUMAN	7a36f08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8458	21150	34293	0.55	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-120400-022-608 HT0598 Homo sapiens cDNA
10599	23293	36531	1.52	8.0E-90	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
10599	23293	36532	1.52	8.0E-90	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
10963	23639	36889	1.32	8.0E-90	AA705222.1	EST_HUMAN	2f82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
10963	23639	36890	1.32	8.0E-90	AA705222.1	EST_HUMAN	2f82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
816	13587		4.12	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CAGNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8323	21016		2.08	7.0E-90	AA782977.1	EST_HUMAN	af63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
8863	21556	34701	1.62	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
8865	21556	34702	1.62	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10036	22684	35901	1.9	7.0E-90	H68849.1	EST_HUMAN	y88e04.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TEITRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10036	22684	35902	1.9	7.0E-90	H68849.1	EST_HUMAN	y88e04.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TEITRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10352	22999	36216	1.17	7.0E-90	BF526089.1	EST_HUMAN	502071208F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214257 5'
4201	16942	29568	9.12	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4201	16942	29569	9.12	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
5994	18679	31625	3.27	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
5994	18679	31626	3.27	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8225	20919	34056	2.75	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8225	20919	34057	2.75	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
151	12966		19.84	5.0E-90	AB035344.1	NT	Homo sapiens TCL6 gene, exon 1-10b
1170	13924	26586	3.08	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1813	14553	27267	1.47	5.0E-90	A1222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb.J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
1813	14553	27268	1.47	5.0E-90	A1222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb.J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
2560	15274	28011	2.79	5.0E-90	AF114487.1	NT	Homo sapiens intercalin long isoform (ITSN) mRNA, complete cds
4503	17238	29871	2.05	5.0E-90	4506364	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4622	17357	29992	0.98	5.0E-90	AL135549.1	EST_HUMAN	DKF7p762P1616_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKF7p762P1616 5'
5504	18302	31203	2.94	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5606	18402	31316	1.31	5.0E-90	AB015617.1	NT	Homo sapiens ELKS mRNA, complete cds
5679	18302	31203	2.36	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6631	19393	32407	0.74	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6631	19393	32408	0.74	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7114	19802	32866	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7114	19802	32867	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7463	20138	33228	9.01	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
7790	20485	33609	0.44	5.0E-90	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
8192	20886	34025	5.08	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
9096	21784	34950	0.56	5.0E-90	4826670	NT	Homo sapiens cadherin 18 (CDH18) mRNA
							Homo sapiens similar to ecdysiotocidic pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
9579	22232	35416	1.06	6.0E-90	114149429	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10181	22829	36044	0.56	5.0E-90	AF123303.1	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10312	22959	36175	0.5	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10312	22959	36178	0.5	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10344	22981	36209	9.16	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10402	23048	36284	0.54	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10402	23048	36266	0.54	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
11731	24324	37848	2.41	5.0E-90	7662047	NT	Homo sapiens KIAA0305 gene product (KIAA0305), mRNA
12591	24948		2.08	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12641	24938		4.43	5.0E-90	A1523368.1	EST_HUMAN	ar78h05.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2128761 3'
295	13101	25742	1.93	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
295	13101	25743	1.93	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1064	13822	26482	3.26	4.0E-90	4505318	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1684	14428	27125	8.09	4.0E-90	X99033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
2892	15758	28405	0.98	4.0E-90	AF007544.1	NT	Homo sapiens prostate-specific membrane antigen (PSM) gene, complete cds
3023	15789	28436	1.07	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3023	15789	28437	1.07	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4608	17343	29975	7.66	4.0E-90	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4743	17476	30109	2.17	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4768	17500	30123	2.33	4.0E-90	M95987.1	NT	Human prothormone converting enzyme (NEC2) gene, exon 8
7751	20447	33570	1.08	3.0E-90	BF516168.1	EST_HUMAN	U1H-BW1-any-b-04-Q-UI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
7751	20447	33571	1.08	3.0E-90	BF516168.1	EST_HUMAN	U1H-BW1-any-b-04-Q-UI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11630	24227	37551	17.81	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3453834 5'
208	13020	25662	4.71	2.0E-90	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3689147 5'
1150	13905	26567	2.67	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1150	13905	26568	2.67	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3826	16577	28209	1.7	2.0E-90	AI138213.1	EST_HUMAN	qc54c02.x1 Soares_placenta_81cdweeks_2NkHP8at9W Homo sapiens cDNA clone IMAGE:1713410 3'
4840	17374	30008	1.06	2.0E-90	AB006627.1	NT	similar to SW:OLF3 MOUSE P23275 OLFACTORY RECEPTOR OR3.;
4853	17563	30206	7.31	2.0E-90	5728855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5695	18489	31410	4.86	2.0E-90	AW672686.1	EST_HUMAN	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
9689	22441	35534	4.78	2.0E-90	11427320	NT	ba49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2898881 5' similar to TR:075208 075208
9689	22441	35535	4.78	2.0E-90	11427320	NT	HYPOTHETICAL 35.6 KD PROTEIN.;
9689	22441	35535	4.78	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
9689	22441	35535	4.78	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
9860	22510	35706	1.37	2.0E-90	AU118885.1	EST_HUMAN	AU118885 HEMBA1 Homo sapiens cDNA clone HEMBA1004756 5'

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9860	22510	35707	1.37	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11447	23214	36446	2.8	2.0E-90	110247711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
270	13078	25720	4.55	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
365	15516	25805	1.38	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
366	15516	25805	1.43	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
679	13454	26098	2.32	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
679	13454	26098	2.32	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
713	13487	26137	13.22	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
713	13487	26138	13.22	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1088	13846	28703	2.47	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1283	14033	28704	5.56	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1283	14033	28704	5.56	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1662	14408	27342	1.23	1.0E-90	BE379884.1	EST_HUMAN	601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511118 5'
1895	14632	27342	3.33	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
2858	15626	28271	6.46	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
4389	17126	29758	1.29	1.0E-90	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 8 and complete cds, alternatively spliced
5589	18385	31295	2.58	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5746	18538	31460	0.96	1.0E-90	11426910	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6473	19240	32240	0.57	1.0E-90	11419406	NT	Homo sapiens cytochrome P450, 51 (steroid 14-alpha-demethylase) (CYP51), mRNA
6973	19455	32475	0.66	1.0E-90	U91834.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7204	19889	32965	0.84	1.0E-90	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7571	20240	33345	2.77	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
8720	21412	34555	3.73	1.0E-90	11422088	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9193	21863	35062	0.96	1.0E-90	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9215	21894	35063	1.53	1.0E-90	11422109	NT	Homo sapiens CGI-16 protein (LOC51006), mRNA
9215	21894	35063	1.53	1.0E-90	R25886.1	EST_HUMAN	Homo sapiens CGI-16 protein (LOC51006), mRNA
10557	23253	36490	1.5	1.0E-90	J04474.1	NT	yg44411.2 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35477 5'
10967	23843	36896	1.76	1.0E-90	AB002059.1	NT	Human branched chain alpha-keto acid dehydrogenase mRNA, 3' end
12580	24904	31001	1.49	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12580	24904	31002	1.49	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4172	16912	29542	6	8.0E-91	D12234.1	EST_HUMAN	HUM0003381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'

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1427	14174	26859	1.06	7.0E-91	AF053768.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds
8205	20899	34036	1.8	7.0E-91	11419234	NT	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA
10198	22846	36062	0.88	7.0E-91	AI904151.1	EST_HUMAN	CM-B1043-090299-075 BT043 Homo sapiens cDNA
3467	16223	28877	1.93	5.0E-91	AA702794.1	EST_HUMAN	z90b04.s1 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:448016 3'
4480	17215	29840	11.73	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4480	17215	29841	11.73	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4757	17489	30116	0.97	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4757	17489	30117	0.97	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6519	19285	32289	1.25	5.0E-91	AI879995.1	EST_HUMAN	au49R09.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to
8105	20799	33931	1.2	5.0E-91	BF314682.1	EST_HUMAN	SW-ASPQ_FLAME Q47898 N4-(BETA-N-ACETYL-GLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR ;
8658	21350	34495	1.52	5.0E-91	AV849878.1	EST_HUMAN	601901624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
8658	21350	34496	1.52	5.0E-91	AV849878.1	EST_HUMAN	AV849878 GLC Homo sapiens cDNA clone GLC8YF08 3'
12612	24919		1.74	5.0E-91	AI183566.1	EST_HUMAN	q670H11.x1 Soares_fetal_Jung_NHLL18W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains
3197	15960	28611	1.69	4.0E-91	AF156776.1	NT	MIR.b2 MIR MIR repetitive element ;
3197	15960	28612	1.69	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
10848	23530	36775	4.48	4.0E-91	AL163284.2	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
12094	24596	31082	1.96	4.0E-91	M77694.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
12094	24596	31127	1.96	4.0E-91	M77694.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to
1613	14360	27049	3.07	3.0E-91	11430183	NT	Retrovirus-related gag polyprotein
1613	14360	27050	3.07	3.0E-91	11430183	NT	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to
3334	16084	28746	1.62	3.0E-91	AL163283.2	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3455	16211	28863	3.39	3.0E-91	AB033104.1	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3455	16211	28864	3.39	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3768	16520	29159	1.45	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4551	17286	29915	3.79	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5600	18395	31305	1.27	3.0E-91	11434664	NT	Homo sapiens epidermal secretory protein (19.5kD) (HE1), mRNA
6212	18987		2.48	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 8 (CDK8) mRNA
6488	19255	32256	5.82	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA

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6488	19255	32257	5.82	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7538	20208	33306	4.97	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7538	20208	33307	4.97	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8669	21361	34508	2.58	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9188	21858	35023	2.83	3.0E-91	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10803	23486	36723	1.41	3.0E-91	AB032179.2	NT	Homo sapiens EHM2 mRNA, complete cds
11160	23827	37105	1.66	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11160	23827	37106	1.66	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
12335	24749	31057	2	3.0E-91	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12667	17898	30489	4.35	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
12667	17898	30490	4.35	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
47	12876	25501	5.06	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1223	13973	26845	6.31	1.0E-91	AW449746.1	EST_HUMAN	UH-BIG-aks-q-01-q-U1.s1 NCL CGAP Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
5328	18131	30790	0.97	1.0E-91	11434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
6743	19577	32610	2.26	1.0E-91	BF348182.1	EST_HUMAN	602022089F1 NCL CGAP Bm67 Homo sapiens cDNA clone IMAGE:4157804 5'
6743	19577	32611	2.26	1.0E-91	BF348182.1	EST_HUMAN	602022089F1 NCL CGAP Bm67 Homo sapiens cDNA clone IMAGE:4157804 5'
12245	25340		1.35	1.0E-91	H15212.1	EST_HUMAN	ym30603.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:49587 5'
1219	13970	26639	9.06	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1219	13970	26640	9.06	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5120	17838	30454	0.9	9.0E-92	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5376	18176	30867	4.86	9.0E-92	J03007.1	NT	Human Na ⁺ /K ⁺ ATPase alpha-subunit mRNA, partial cds
5518	18316	31217	2.83	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
6362	19132	32127	4.03	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7756	20452	33576	7.17	9.0E-92	AJ250566.1	NT	Homo sapiens partial TMAS2F2 gene for tetraspanin protein, exon 5
7756	20452	33577	7.17	9.0E-92	AJ250566.1	NT	Homo sapiens partial TMAS2F2 gene for tetraspanin protein, exon 5
8272	20966	34107	0.92	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8272	20966	34108	0.92	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9174	21844	35010	1.95	9.0E-92	11422068	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
11161	23828		1.95	9.0E-92	7706898	NT	Homo sapiens RNBB (RNBB), mRNA
91	12917	25554	2.25	8.0E-92	W26367.1	EST_HUMAN	263 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
278	13086	25728	3.29	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814687 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5041	17760	30374	0.96	8.0E-92	AW157571.1	EST HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
5308	18113	30771	0.65	8.0E-92	AB046820.1	NT	TR:060302 O60302 KIAA0565 PROTEIN, contains element MER22 repetitive element;
							Homo sapiens mRNA for KIAA1600 protein, partial cds
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
5411	18210	30918	0.97	8.0E-92	AF264717.1	NT	Homo sapiens MCP-4 gene
6451	19219	32217	1.31	8.0E-92	AJ000979.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
6455	19223	32222	0.92	8.0E-92	AF179428.1	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
7990	20885		0.55	8.0E-92	11416961	NT	Homo sapiens membrane protein (mp19) gene, exon 11
8324	21017	34152	3.91	8.0E-92	L04193.1	NT	Human lens
8324	21017	34153	3.91	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8422	21115	34253	0.58	8.0E-92	11426569	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
8950	21651	34801	2.82	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
9825	22573	35771	1.18	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
10707	23397	36636	3.2	8.0E-92	AF074993.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
							Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
11333	24024	37329	1.61	8.0E-92	4503340	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
23	12851	25466	1.62	7.0E-92	AB031007.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
64	12892	25525	1.01	7.0E-92	AB06076.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
230	15538	25680	0.87	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
230	15538	25681	0.87	7.0E-92	AB018301.1	NT	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds
577	13357		1.34	7.0E-92	AF007822.1	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
1257	14006	26675	1.99	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2184	14913	27645	2.27	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2184	14913	27646	2.27	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2568	15282	28020	1.46	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2728	15435	28171	2.2	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2757	15462	28205	1.23	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3340	17877	28750	1.06	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3340	17877	28751	1.06	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
							N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4547	17282	29812	2.59	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4547	17282	29913	2.59	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4944	17671	30280	0.98	7.0E-92	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5180	17989	30504	6.05	7.0E-92	AA446206.1	EST_HUMAN	z666d12.1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'
1582	14328		1.29	5.0E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805018 5'
2768	15473	28215	1.8	3.0E-92	BE3909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902889 5'
5786	18577	31506	2.6	3.0E-92	AA378336.1	EST_HUMAN	EST191020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
10664	23355	36594	2.72	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
10664	23355	36595	2.72	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
24	12852	25487	1.66	2.0E-92	4501898	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
174	12988	25625	3.57	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (D.J462023.2), mRNA
174	12988	25626	3.57	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (D.J462023.2), mRNA
732	13506	26162	1.33	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
732	13506	26163	1.33	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1709	14452		2.22	2.0E-92	S78653.1	NT	mitg-mas-related [human, Genbank, 2418 nt]
1928	14685	27378	2.36	2.0E-92	A1818119.1	EST_HUMAN	wk27d07.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1928	14685	27379	2.36	2.0E-92	A1818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2041	14775	27504	5.58	2.0E-92	4508880	NT	wk27d07.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2664	15374	28113	19.2	2.0E-92	6812457	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
3600	16353	28992	2.61	2.0E-92	AF231919.1	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
3600	16353	28993	2.61	2.0E-92	AF231919.1	NT	Homo sapiens calcitriol binding protein 1 (KIAA0330), mRNA
3600	16353	28993	2.61	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3674	16427	29068	5.57	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4256	16997	29626	1.23	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4936	17664		2.51	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0414 5'
5673	18468	31363	0.64	2.0E-92	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6209	18984		0.6	2.0E-92	4504756	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
6517	19292	32285	3.03	2.0E-92	AB028991.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7364	20045		0.81	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7387	20045		0.78	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
8754	21446	34594	1.69	2.0E-92	AW340174.1	EST_HUMAN	h002h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711
10656	23350	38587	4.93	2.0E-92	11434800	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
							Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA

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10930	23610	38859	1.48	2.0E-92	11434759	NT	Homo sapiens zinc finger protein 188 (ZNF198), mRNA
10978	23653	38906	2.54	2.0E-92	5803103	NT	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA
12439	24809	31048	2.69	2.0E-92	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12697	15374	28113	2.51	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1842	14580	27295	1.13	1.0E-92	R78078.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:145574 5'
1842	14580	27295	1.13	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta Nb2Lp Homo sapiens cDNA clone IMAGE:145574 5'
2066	14798	27525	8.83	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA
8146	20839	33971	1.29	1.0E-92	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
							tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN
9062	21751	34910	3.82	1.0E-92	A1380356.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1; contains Alu repetitive element; contains element
							MER17 repetitive element;
9062	21751	34911	3.82	1.0E-92	A1380356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN
2023	14758	27487	3	9.0E-93	AU121681.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1; contains Alu repetitive element; contains element
							MER17 repetitive element;
2035	14770		5.48	9.0E-93	AA316723.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
							EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2653	15363		1.45	9.0E-93	AF223391.1	NT	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
3602	16355	28995	1.11	9.0E-93	BE388571.1	EST_HUMAN	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
11645	24242		9.71	9.0E-93	11418526	NT	UI-HB10-aah-h-06-0-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
6351	19121	32112	0.58	8.0E-93	AW014042.1	EST_HUMAN	UI-HB10-aah-h-06-0-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
6351	19121	32113	0.58	8.0E-93	AW014042.1	EST_HUMAN	601490521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
6496	19262	32263	2.51	8.0E-93	BF036384.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
239	13048	25687	9.92	7.0E-93	AF231919.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
3073	15839	28482	0.94	6.0E-93	11526178	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6581	18344	32358	1.02	6.0E-93	AB033093.1	NT	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds
6817	19478	32501	1.12	6.0E-93	AF095771.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
1359	14107	26782	3.51	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
1386	14133	26807	7.28	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1386	14133	26808	7.28	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
3227	15990	28643	2.88	6.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
5710	18503	31425	1.01	5.0E-93	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds

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6018	18799		1.02	5.0E-93	AF045555.1	NT	Homo sapiens wbscr1 (WBSR1) and wbscr5 (WBSR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7614	20280	33388	3.6	5.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8503	21195	34338	1	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8503	21195	34339	1	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9523	22176	35360	2.16	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9707	22358	35554	1.25	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
9970	22818	35821	1.9	5.0E-93	AF068313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
10727	23415	36656	2.25	5.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12343	25052	30959	2.15	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
12805	25052	30959	1.44	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
86	12912		6.52	4.0E-93	AA459833.1	EST_HUMAN	z50e09.s1 Soares' tests, NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW-CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM:
432	13218	25863	1.39	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
432	13218	25864	1.39	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
755	13527	26186	1.67	4.0E-93	7657454	NT	Homo sapiens pscadillo (zebrafish) homolog 1, containing BRC1 domain (PES1), mRNA
755	13527	26187	1.67	4.0E-93	7657454	NT	Homo sapiens pscadillo (zebrafish) homolog 1, containing BRC1 domain (PES1), mRNA
1160	13914	26577	1.53	4.0E-93	8823858	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
1970	14706	27424	4.3	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2241	14969	27707	0.98	4.0E-93	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2397	15118	27855	1.65	4.0E-93	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3553	16308	28958	0.73	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4026	16771	29403	1.67	4.0E-93	4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5557	18354	31264	4.9	4.0E-93	T48864.1	EST_HUMAN	y094c12.r1 Stratagene liver (#637224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP-A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN
11078	23748	37023	6.17	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKC Homo sapiens cDNA clone GKCDR07 5'
3643	16396	29035	7.35	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332036 5'
3643	16396	29036	7.35	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332036 5'
4210	16951		1.31	3.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
6697	18491	31412	0.79	3.0E-93	AI553853.1	EST_HUMAN	t29g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2169076 3'
6697	18491	31413	0.79	3.0E-93	AI553853.1	EST_HUMAN	t29g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2169076 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6468	19235	32236	1.21	3.0E-93	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog) like 2 (GCN5L2), mRNA
10703	23394	36631	4.27	3.0E-93	AB24829.1	EST_HUMAN	w602405.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2304489 3'
185	12998	26637	7.51	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
185	12998	26638	7.51	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
315	13119	25758	9.36	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
316	13119	25758	9.48	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1610	14357	27046	1.33	2.0E-93	AF225998.1	NT	Homo sapiens lensin mRNA, complete cds
2126	14857	27587	1.33	2.0E-93	U40763.1	NT	Human CLK-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2490	15207	27849	1.66	2.0E-93	BE262982.1	EST_HUMAN	60117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5332	18135	30784	5.42	2.0E-93	AW964385.1	EST_HUMAN	EST376458 MAGe resequences, MAGH Homo sapiens cDNA
5342	18145	30824	0.66	2.0E-93	4758153	NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5455	18254		1.04	2.0E-93	BF351459.1	EST_HUMAN	QV3-HT0513-280300-126-h04 HT0513 Homo sapiens cDNA
5550	18347	31256	1.13	2.0E-93	11430033	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
5565	18362	31270	0.65	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-86
6584	19347	36946	1.1	2.0E-93	AW502002.1	EST_HUMAN	ULHF-BN0-aks-g-08-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
11014	23686	36947	1.27	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
11014	23686	36947	1.27	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
12233	24686		2.64	2.0E-93	AA126735.1	EST_HUMAN	z126c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3'
12614	24736		2.17	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12671	24899		10.79	2.0E-93	BF035327.1	EST_HUMAN	601459531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
101	12827	25564	2.29	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
101	12827	25565	2.29	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
505	13289	26923	4.25	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (D328E19.C1.1), mRNA
586	13366	25994	4.57	1.0E-93	AI148755.1	EST_HUMAN	cy84p08.x1 NCL CGAP_G11.1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384
852	13622	26292	8.91	1.0E-93	D87675.1	NT	ZINC FINGER PROTEIN. ;
1144	13899	26560	2.9	1.0E-93	4503872	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1215	13965	26632	7.65	1.0E-93	8923270	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD67, mRNA
1215	13965	26633	7.65	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1322	14071	26744	1.5	1.0E-93	AB046783.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1324	14073	26746	0.99	1.0E-93	AF167706.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
2337	15081	27798	1.33	1.0E-93	AF231981.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
							Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2466	15184	27924	1.7	1.0E-93	AF05068.1	NT	Homo sapiens MHC class 1 region
2511	15228		0.98	1.0E-93	AL137200.1	NT	Novel human gene mapping to chromosome 1
2825	14022	26689	1.47	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2825	14022	26690	1.47	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2834	15700	28349	7.48	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3210	15973		1.27	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4395	17132	29763	2.6	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5479	18278	31173	2.38	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5479	18278	31174	2.38	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5678	18472	31389	0.96	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor, T2R14 gene, complete cds
5825	18614	31546	10.32	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6104	18882	31850	1.4	1.0E-93	7682241	NT	Homo sapiens KIAA0872 gene product (KIAA0872), mRNA
6694	19611	32650	2.01	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7150	19837	32907	3.49	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon1, complete cds
8158	20852	33984	2.54	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8441	21133	34289	1.2	1.0E-93	Y10183.1	NT	H. sapiens mRNA for MEK1D protein
8547	21239	34382	1.38	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9352	20423	33542	1.79	1.0E-93	AB040918.1	NT	Homo sapiens Trisoform mRNA, complete cds
9356	20427	33546	1.26	1.0E-93	AF091395.1	NT	Homo sapiens Trisoform mRNA, complete cds
9488	22141	35319	8.29	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9488	22141	35320	8.29	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9625	22278	35467	0.79	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10045	22693	35910	0.82	1.0E-93	11433846	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
12487	24846		1.94	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12568	24896		2.64	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12739	25391		1.49	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10492	23138		1.03	8.0E-94	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3944	16694	28333	1.63	8.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
5283	18088	30747	4.23	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5283	18088	30748	4.23	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5957	18739	31698	4.22	5.0E-94	AA722434.1	EST_HUMAN	z887g08.s1 Soares_fetal_heart_NH-H19W Homo sapiens cDNA clone IMAGE:409594 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6910	19648	32693	1.29	5.0E-94	AI015800.1	EST_HUMAN	cl83d05.e1 Soares_tet1 Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623369 3'
8537	21229	34371	1.11	5.0E-94	BF529115.1	EST_HUMAN	602042163F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180023 5'
12209	25394	30619	9.99	5.0E-94	T89398.1	EST_HUMAN	yc888504.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1162239 3'
12756	25017		1.5	5.0E-94	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12761	25021		1.86	5.0E-94	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (GPSF1), mRNA
1834	14573		2.64	4.0E-94	LO5094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2662	15372	28111	0.92	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3661	16414	29053	1.38	4.0E-94	AW197851.1	EST_HUMAN	xi88f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3661	16414	29054	1.38	4.0E-94	AW197851.1	EST_HUMAN	xi89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4669	17403	30038	2.87	4.0E-94	AI591312.1	EST_HUMAN	hw11f10.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE
6376	19145	32143	1.82	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6376	19145	32144	1.82	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6812	19473		1.18	4.0E-94	L27386.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
11431	23198	38429	1.5	4.0E-94	11545782	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
597	13375	26005	1.44	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
704	13478	26127	0.89	3.0E-94	4502508	NT	Homo sapiens complement component 5 (C5) mRNA
1733	14475	27173	1.19	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1765	14507	27208	2.61	3.0E-94	4557553	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2073	14805	27534	1.27	3.0E-94	11427779	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2073	14805	27535	1.27	3.0E-94	11427779	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4168	16906	29534	0.83	3.0E-94	AA464805.1	EST_HUMAN	Homo sapiens hepatic leukemia factor (HLF), mRNA
5595	18390	31301	3.47	3.0E-94	11496268	NT	Homo sapiens hepatic leukemia factor (HLF), mRNA
6059	18839	31800	1.33	3.0E-94	AB011538.1	NT	zmv63g08.r1 Soares_tet1 Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:774782 5'
6360	19130	32125	4	3.0E-94	11526228	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
7696	20359	33473	1.7	3.0E-94	4826863	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8098	20792	33923	1.18	3.0E-94	AF152309.1	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
8488	21178	34322	4.35	3.0E-94	AB014579.1	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
9492	22145	35326	5.23	3.0E-94	AF087942.1	NT	Homo sapiens protocadherin alpha 13 (PODH-alpha13) mRNA, complete cds
11043	23713	36983	3.26	3.0E-94	4757821	NT	Homo sapiens mRNA for KIAA0678 protein, partial cds
11878	24274	37598	1.94	3.0E-94	U28711.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
							Homo sapiens exonal transport of synaptic vesicles (ATSV) mRNA
							Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9653	22305	35501	0.7	2.0E-94	A1910393.1	EST_HUMAN	w130h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
9653	22305	35502	0.7	2.0E-94	A1910393.1	EST_HUMAN	w130h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
144	12959	25601	1.94	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3086	15851	28492	2.07	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3086	15851	28493	2.07	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4326	17065	29694	1.7	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
5982	18763	31727	0.64	1.0E-94	AE000269.1	NT	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6173	18950	31922	0.73	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G0314 5'
6182	18959	31933	0.72	1.0E-94	H08270.1	EST_HUMAN	y8702.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:45053 5'
8426	19194	32190	0.58	1.0E-94	AV725992.1	EST_HUMAN	AV725992 HTC Homo sapiens cDNA clone HTCBEF05 5'
8012	20707	33836	0.63	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8012	20707	33837	0.63	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9155	21886	35054	2.76	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
9687	22339	35533	2.04	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872099 5'
11000	23873	36929	3.08	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11288	23949	37245	2.82	1.0E-94	A1272244.1	EST_HUMAN	ap22e02.x1 Schiller oligodendrogloma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR-Q62845
11754	24345	37875	1.72	1.0E-94	11418871	NT	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. ;
12330	12959	25601	1.45	1.0E-94	BE295714.1	EST_HUMAN	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
12608	12959	25601	1.51	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1459	14206	28892	1.93	9.0E-95	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3153	15916	28561	1.45	9.0E-95	7662027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3153	15916	28562	1.45	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5320	18123	30781	1.33	9.0E-95	X82569.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5320	18123	30782	1.33	9.0E-95	X82569.1	NT	Musculus glyt1 gene (exons 1c and 2)
8150	20844	33974	1.77	9.0E-95	AF274753.1	NT	Musculus glyt1 gene (exons 1c and 2)
4499	17235	29866	3.18	8.0E-95	A1700998.1	EST_HUMAN	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4499	17235	29867	3.18	8.0E-95	A1700998.1	EST_HUMAN	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
6849	19549	32579	0.76	8.0E-95	11419378	NT	w609e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340806 3' similar to gb:K00558
7141	19828	32897	1.76	8.0E-95	11426529	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7141	19828	32898	1.76	8.0E-95	11426529	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
							w609e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340806 3' similar to gb:K00558
							TUBULIN ALPHA-1 CHAIN (HUMAN);
							w609e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340806 3' similar to gb:K00558
							TUBULIN ALPHA-1 CHAIN (HUMAN);
							Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
							Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
							Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
							Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA

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8097	20791	33922	1.97	8.0E-95	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
9265	22019	35187	2	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9265	22019	35188	2	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9748	22399	35604	3.1	8.0E-95	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
9779	22430		2.94	8.0E-95	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10135	22793	35994	0.8	8.0E-95	9845523	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
10613	23307	36546	1.3	8.0E-95	AF112152.1	NT	Homo sapiens development arteries and neural crest EGF-like protein mRNA, complete cds
11466	24069	37377	1.86	8.0E-95	10864024	NT	Homo sapiens HGF-binding transcription factor Zhangfei (ZF), mRNA
12535	24879		12.4	8.0E-95	AA629056.1	EST_HUMAN	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.H L1 repetitive element ;
269	13077	25718	32.81	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
269	13077	25719	32.81	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4333	17072	26701	5.18	7.0E-95	M95708.1	NT	Homo sapiens Ly-8-like protein (CD59) mRNA, complete cds
4380	17117		1.3	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
9117	21805	34971	1.31	4.0E-95	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
5356	18159	30842	1.58	3.0E-95	BF526041.1	EST_HUMAN	60207146F NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214147 5'
5588	25071	31294	0.83	3.0E-95	4503354	NT	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA
7268	19952	33027	1.51	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGE resequences, MAGE Homo sapiens cDNA
7268	19952	33028	1.51	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGE resequences, MAGE Homo sapiens cDNA
8278	20972	34113	0.55	3.0E-95	AW157233.1	EST_HUMAN	au83508.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR-O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
8278	20972	34114	0.55	3.0E-95	AW157233.1	EST_HUMAN	au83508.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR-O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
9255	21934	35107	1.89	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9255	21934	35108	1.89	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9647	22298	35495	0.73	3.0E-95	BF213446.1	EST_HUMAN	601845212F1 NIH MGC 55 Homo sapiens cDNA clone IMAGE:4070451 5'
10792	23475	36716	1.48	3.0E-95	R83190.1	EST_HUMAN	yp87g1.11 Soares fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:194468 5'
1639	14385	27072	2.31	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1639	14385	27073	2.31	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
							Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
1834	14659	27384	2.51	2.0E-95	4507512	NT	601312181F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE:3658862 5'
1937	14672	27388	1.92	2.0E-95	BE393873.1	EST_HUMAN	Homo sapiens G protein-coupled receptor 18 (GPR18) mRNA
2426	15147	27880	2.22	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 18 (GPR18) mRNA
2426	15147	27881	2.22	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 18 (GPR18) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2488	15186	27925	3.28	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2517	15233	27973	1.85	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
3155	15918	28564	1.96	2.0E-95	AF016452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3552	16307	28956	3.07	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3552	16307	28957	3.07	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3605	16358	28998	1.29	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3732	16485	29122	0.68	2.0E-95	AI280264.1	EST_HUMAN	qtm02.x1 Scores_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705:
4328	17057	29695	1.32	2.0E-95	7657185	NT	Homo sapiens hypodermal protein (HS322B1A), mRNA
4978	17701	30308	2.72	2.0E-95	7651979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5392	18192	30884	4.21	2.0E-95	7705764	NT	Homo sapiens CGL-48 protein (LOC51096), mRNA
5392	18192	30885	4.21	2.0E-95	7705764	NT	Homo sapiens CGL-48 protein (LOC51096), mRNA
5611	18407	31319	1.27	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5611	18407	31320	1.27	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5651	18446	31360	0.7	2.0E-95	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6051	18831	31794	5.04	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6358	19128	32122	1.16	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6358	19128	32123	1.16	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6478	19243	32243	2.45	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6666	19583	32617	1.82	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9041	21731	34886	1.06	2.0E-95	11421795	NT	Homo sapiens rhophorin II (RPN2), mRNA
10280	22928	36142	0.84	2.0E-95	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10624	23317	36567	2.46	2.0E-95	4757853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRIA) mRNA
11700	24295	37620	3.02	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11700	24295	37621	3.02	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12299	24724	31055	2.3	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12688	24980	30994	4.66	2.0E-95	11418164	NT	Homo sapiens adenylsuccinate lyase (ADSL), mRNA
5527	18325	31226	8.41	1.0E-95	AA284651.1	EST_HUMAN	z23h04.r1 Scores ovary tumor NthOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F5642.6;
5527	18325	31227	8.41	1.0E-95	AA284651.1	EST_HUMAN	z23h04.r1 Scores ovary tumor NthOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F5642.6;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7414	20091	33175	4.3	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
7414	20091	33176	4.3	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
8094	20788	33920	1.49	9.0E-96	BE897259.1	EST_HUMAN	S01437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922423 5'
5424	18223		2.77	8.0E-96	AW836047.1	EST_HUMAN	PMO-LT0019-090300-002-409 LT0019 Homo sapiens cDNA
3889	18639	29278	0.74	7.0E-96	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
3476	16232	28888	20.13	6.0E-96	M28873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
5552	18349	31258	0.74	6.0E-96	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
11534	24134	37439	3.36	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11534	24134	37440	3.36	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11584	24183	37498	2.05	6.0E-96	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11769	24380	37692	1.83	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11769	24380	37693	1.83	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
312	13116	25754	2.74	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
822	13592	26280	4.08	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
822	13592	26281	4.08	5.0E-96	AB032998.1	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2624	15336		1.43	5.0E-96	X60812.1	NT	H. sapiens DNA for monomine oxidase type A (7) (partial)
4846	17576		1.39	5.0E-96	X60812.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6553	19318	32324	1.15	5.0E-96	AF149773.1	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6684	19501	32639	5.18	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6684	19501	32640	5.18	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6823	19659	32706	0.71	5.0E-96	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7415	20092	33177	1.98	5.0E-96	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8005	20700	33828	1.35	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8005	20700	33829	1.35	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
11793	24383	37715	1.4	5.0E-96	7661973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4168	16908		12.32	3.0E-96	H68656.1	EST_HUMAN	Y87H12.1 Soares fetal liver spleen TNF- α mRNA (melanoma-associated) (CSP4), mRNA
408	13191		4.24	2.0E-96	4503098	NT	Homo sapiens chromosome 21 segment HS21C048
730	13504	28159	0.91	2.0E-96	AL183248.2	NT	Homo sapiens cDNA
4708	17440	30072	1.89	2.0E-96	BE148074.1	EST_HUMAN	RC3-H10230-040500-110-g02 H10230 Homo sapiens cDNA
7361	20042	33120	0.62	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
7361	20042	33121	0.62	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
8879	21570		5.63	2.0E-96	AV689461.1	EST_HUMAN	AV689461 GKC Homo sapiens cDNA clone GKCFMD07 5'
12009	24543		2.81	2.0E-96	AW249440.1	EST_HUMAN	2819351 Sprinter NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819351 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
608	13386	26016	2.6	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
608	13386	26017	2.6	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
656	13433	26074	3.38	1.0E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1774	14516	27216	2.56	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
1774	14516	27217	2.56	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
2262	15527	27729	1.06	1.0E-96	U51472.2	NT	Felis catus superfast myosin heavy chain (sMYHC) mRNA, complete cds
6869	17946	30541	1.3	1.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6949	19431	32447	0.67	1.0E-96	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8111	20805	33938	1.24	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8111	20805	33939	1.24	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8816	21308	34450	20.66	1.0E-96	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
8749	21441	34588	2.09	1.0E-96	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10059	22707	35924	1.24	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
10059	22707	35925	1.24	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
11999	13386	26016	1.97	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
11999	13386	26017	1.97	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
7457	20131		2.6	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA
8832	21524	34670	0.69	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
8832	21524	34671	0.69	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
10497	23143	36369	0.57	6.0E-97	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
10497	23143	36370	0.57	6.0E-97	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
11382	23989	37290	1.46	6.0E-97	X15804.1	NT	Human mRNA for alpha-actinin
7913	20608	33739	1.91	5.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
8042	20736	33869					z697e12.at Scores_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
9574	22227	35412	11.73	5.0E-97	AA418026.1	EST_HUMAN	G1304125 PMS4 MRNA
11535	24135	37441	2.66	5.0E-97	BE154912.1	EST_HUMAN	RCO-BT0812-250900-032-a08 BT0812 Homo sapiens cDNA
11535	24135	37442	1.98	6.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
11535	24135	37442	1.98	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
918	13985	26349	1.59	4.0E-97	BE004436.1	EST_HUMAN	CNO-BN0108-170300-283-a08 BN0108 Homo sapiens cDNA
928	13995	26359	1.04	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
928	13995	26360	1.04	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
1903	14640	27349	1.07	4.0E-97	5453572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA

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5478	18277	31172	0.61	4.0E-97	4557326	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
5765	18556	31482	0.95	4.0E-97	U09002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (NMR2A) mRNA; complete cds
5765	18556	31483	0.95	4.0E-97	U09002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (NMR2A) mRNA; complete cds
6725	19559	32590	6.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
6725	19559	32591	6.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
6921	19657	32703	1	4.0E-97	7710125	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
6968	19450	32468	1.05	4.0E-97	11422155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8036	20731	33863	0.57	4.0E-97	4557708	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8256	20950	34087	2.63	4.0E-97	11421793	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
8518	21210	34353	0.75	4.0E-97	11423233	NT	Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA
9147	21878	35043	1.23	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9147	21878	35044	1.23	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11116	23786	37062	1.88	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11116	23786	37063	1.88	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11412	23179	36407	3.61	4.0E-97	AB042557.1	NT	Homo sapiens mRNA, similar to rat myomeslin, complete cds
11415	23182	36411	1.62	4.0E-97	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
11415	23182	36412	1.62	4.0E-97	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
12180	24652		7.76	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
236	13046	25085	1.14	3.0E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
854	13624	26294	29.53	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
854	13624	26295	29.53	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1422	15569	26855	1.29	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2440	15529	27895	1.68	3.0E-97	U36255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3254	16016	28667	1.3	3.0E-97	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
4729	17461	30098	12.99	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6333	18103	32091	2.48	1.0E-97	BE563486.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5'
9344	20415	33534	1.16	1.0E-97	AW379978.1	EST_HUMAN	RCO-HT0258-211199-011-g05 HT0258 Homo sapiens cDNA
9344	20415	33535	1.16	1.0E-97	AW379978.1	EST_HUMAN	RCO-HT0258-211199-011-g05 HT0258 Homo sapiens cDNA
9664	22316	35513	1.6	1.0E-97	R10887.1	EST_HUMAN	Y98c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
10604	23298	36538	3.44	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
10604	23298	36539	3.44	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA

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11280	23041	37235	2.03	1.0E-97	AA553781.1	EST_HUMAN	h29g02.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014962 3'
11445	23212	36443	14.01	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11445	23212	36444	14.01	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
881	13650	26319	3.52	9.0E-98	BE090973.1	EST_HUMAN	PMA-B107/24-010400-008-s12 BT0724 Homo sapiens cDNA
1253	14002	26670	1.12	9.0E-98	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6210	18985		0.71	9.0E-98	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
7190	19876	32949	0.67	9.0E-98	7661871	NT	Homo sapiens leucyl-tRNA synthetase, mitochondrial (KIAA0028), mRNA
7286	19669	33046	0.6	9.0E-98	11419408	NT	Homo sapiens A kinase (PRKA) anchor protein (xtlaa) 9 (AKAP9), mRNA
7825	20520	33646	4.79	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7825	20520	33647	4.79	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9014	21704	34854	6.28	9.0E-98	X06989.1	NT	Human mRNA for amyloid A4(751) protein
9124	21812	34977	1.5	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9192	21862	35027	1.59	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9238	21917		0.96	9.0E-98	AF057726.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9267	22021	35190	1.14	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 3 (SMARCA3) mRNA
9267	22021	35191	1.14	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 3 (SMARCA3) mRNA
10160	22808	36026	0.45	9.0E-98	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
10926	23606	36856	2.63	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
10926	23606	36857	2.63	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11004	23676	36932	1.39	9.0E-98	11418982	NT	Homo sapiens mitogen-activated protein kinase kinase 7 (MAP3K7), mRNA
11850	24434	37776	1.39	9.0E-98	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11850	24434	37777	1.39	9.0E-98	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
1351	14099	26774	0.92	8.0E-98	AB033768.1	NT	Homo sapiens RPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
1719	14462	27161	2.7	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1719	14462	27162	2.7	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3775	19527	29166	6.89	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
5991	18772	31735	0.99	5.0E-98	BE868873.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909097 5'
2176	14905	27638	1.14	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2913	15324	28087	0.99	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2753	15458		2.9	3.0E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
6847	19547	32576	1.9	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6847	19547	32577	1.9	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8649	21341	34485	2.73	3.0E-98	H46898.1	EST_HUMAN	yo17g09.r1 Soares adult brain N2b5fHB55Y Homo sapiens cDNA clone IMAGE:178240 5'
9197	21868	35030	0.48	3.0E-98	8922096	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
9783	22434	35639	1.42	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone J8
9783	22434	35640	1.42	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone J8
10371	23017	36233	0.96	3.0E-98	BE900454.1	EST_HUMAN	601873686F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3956517 5'
10872	23552	36799	4.11	3.0E-98	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
11863	24447	37788	1.56	3.0E-98	L26405.1	NT	Homo sapiens (huc) mRNA, complete cds
12688	25262		1.47	3.0E-98	BE382519.1	EST_HUMAN	601297955F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:3628213 5'
12751	25013		3.56	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
2071	14803	27531	2.66	2.0E-98	BE294281.1	EST_HUMAN	601172658F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3528134 5'
2231	14959	27699	1.53	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4284	17005	29637	0.8	2.0E-98	AF032897.1	NT	Homo sapiens poliovirus channel subunit (HERG-3) mRNA, complete cds
4306	17045	29670	3.21	2.0E-98	4758331	NT	Homo sapiens fatty acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4776	17508	30129	1.34	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4776	17508	30130	1.34	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5131	17849	30466	1.39	2.0E-98	4758975	NT	Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA
5292	18097	30757	4.03	2.0E-98	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6557	19322	32329	1.15	2.0E-98	4505708	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7523	20194	33286	1.07	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7523	20194	33287	1.07	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8508	21198	34342	4.94	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8508	21198	34343	4.94	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8591	21283	34421	0.58	2.0E-98	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
8591	21283	34422	0.58	2.0E-98	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
9437	22115	35260	1.48	2.0E-98	X12694.1	NT	H. sapiens arginase gene exon 3 (EC 3.5.3.1)
10313	22960		1.37	2.0E-98	7705888	NT	Homo sapiens AIM-1 protein (LOC511151), mRNA
11155	23822	37103	1.42	2.0E-98	U22028.1	NT	Human cytochrome P450 (CYP2A13) gene, complete cds
398	13181	25829	16.4	1.0E-98	AI862007.1	EST_HUMAN	W36804.X1 NC1 CGAP_U1 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN
442	13228	25871	2.12	1.0E-98	AW998611.1	EST_HUMAN	P29316 60S RIBOSOMAL PROTEIN L23A ;
1789	14529	27237	11.24	1.0E-98	N49818.1	EST_HUMAN	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA W23105.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5234	18040	30668	3.4	1.0E-98	AA195854.1	EST_HUMAN	z98c09.r1 Striatogene muscle 637209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562
5482	18281	31178	1.1	1.0E-98	BE390027.1	EST_HUMAN	G806562 NEBULIN ;
5482	18281	31179	1.1	1.0E-98	BE390027.1	EST_HUMAN	601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
8896	21587	34726	2.7	1.0E-98	AF141349.1	NT	601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
8896	21587	34727	2.7	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5728	18520	31441	0.88	9.0E-99	A1905004.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
5728	18520	31442	0.88	9.0E-99	A1905004.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
5949	18731	31691	4.21	9.0E-99	AW968635.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
11086	23736	37009	2.75	9.0E-99	AI479829.1	EST_HUMAN	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
11086	23736	37010	2.75	9.0E-99	AI479829.1	EST_HUMAN	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
11390	23996	37298	2.13	9.0E-99	AA134604.1	EST_HUMAN	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
8627	21319	34461	1.96	8.0E-99	9635487	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
5743	18535	31458	10.03	7.0E-99	AF035808.1	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
11610	24208	37532	2.99	7.0E-99	AF001886.1	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
459	13244	25886	1.89	6.0E-99	U10991.1	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
3868	16618	29258	1.15	6.0E-99	AW976364.1	EST_HUMAN	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
4698	17433	30064	1.21	6.0E-99	4502660	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
6503	19268	32270	0.72	6.0E-99	7706136	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
6578	19341	32354	1.01	6.0E-99	L43610.1	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
6578	19341	32355	1.01	6.0E-99	L43610.1	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
8003	20698	33826	1.18	6.0E-99	X99101.1	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
8022	20717	33849	0.53	6.0E-99	8601589	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
8663	21355	34502	2.28	6.0E-99	AB036429.1	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
8762	21454	34602	3.33	6.0E-99	AF080255.1	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
8762	21454	34603	3.33	6.0E-99	AF080255.1	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
8821	21513	34657	0.6	6.0E-99	11431994	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
8821	21513	34658	0.8	6.0E-99	11431994	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
10620	23313	36553	3.89	6.0E-99	11526299	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
11433	23200	36431	2.01	6.0E-99	9910279	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
11433	23200	36432	2.01	6.0E-99	9910279	NT	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA

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1957	14693	27406	1.38	5.0E-99	Y11355.1	NT	H. sapiens IMPA gene, exon 8
4826	17261	29895	1.56	5.0E-99	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12208	24674		2.81	5.0E-99	BE890177.1	EST_HUMAN	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
8220	20914		4.88	3.0E-99	M95588.1	NT	Human E2AFHLA fusion protein (E2AFHLF) mRNA, complete cds
1217	13968		6.88	2.0E-99	AW274792.1	EST_HUMAN	XP0906.x1 NCI CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3253	16015	28566	1.29	2.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4506	17241	29874	1.04	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7574	20243	33348	0.58	2.0E-99	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8608	21300	34444	9.55	2.0E-99	W23507.1	EST_HUMAN	zb4606.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306835 5' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
9050	21739	34897	0.76	2.0E-99	R78254.1	EST_HUMAN	y81b09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145625 5'
11049	23719	36990	3.39	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
11788	24378	37708	1.46	2.0E-99	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
307	13111	25751	1.63	1.0E-99	AF114487.1	NT	Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds
370	13166	25809	1.02	1.0E-99	11526150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60KD) (GABPA), mRNA
1400	14147	26826	2.09	1.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1549	14295	26981	2.64	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1549	14295	26982	2.64	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1920	14657	27367	1.41	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36KD) (FKBP6) mRNA, and translated products
1920	14657	27368	1.41	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36KD) (FKBP6) mRNA, and translated products
3083	15848	28489	1.36	1.0E-99	J03171.1	NT	Human Interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4347	17086	29715	2.82	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4347	17086	29716	2.82	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5658	18453	31367	0.68	1.0E-99	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
6707	19622	32665	1.28	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6707	19622	32666	1.28	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7039	25104	32789	0.76	1.0E-99	X98022.1	NT	H. sapiens E8-AP gene exon 2
9099	21787		1.49	1.0E-99	11418721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
9420	22098	35270	1.71	1.0E-99	AW340174.1	EST_HUMAN	h02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
11084	23754	37029	2.01	1.0E-99	7427514	NT	O02711 PRO-POLYUTPASE POLYPROTEIN;
11084	23754	37030	2.01	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11084	23754	37030	2.01	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA

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11141	23808	37088	1.8	1.0E-99	5901879	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11350	24040	37343	2.77	1.0E-99	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11984	24525		6.68	1.0E-99	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	12830	25443	0.95	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	12830	25443	1.53	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
66	12894	25526	1.54	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
68	12894	25527	1.54	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
85	12911	25550	0.69	1.0E-100	AW1275237.1	EST_HUMAN	x78b11.x1 NCI_CGAP_Brm53 Homo sapiens cDNA clone IMAGE:2824605 3'
165	12979	25618	1.24	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
309	13113	25753	0.83	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
334	13135	25770	3.06	1.0E-100	TG5087.1	EST_HUMAN	EST:2975 Fetal brain, Stragene (cat#938206) Homo sapiens cDNA clone HFBOR32
427	13213		1.28	1.0E-100	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
477	13263		7.19	1.0E-100	X89631.1	NT	G-protin DNA for ZNF80 gene homolog
496	13280	25915	1.33	1.0E-100	BE180608.1	EST_HUMAN	RC3-HT0625-040500-022-509 HT0625 Homo sapiens cDNA
998	13758	26418	3.22	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
998	13758	26419	3.22	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1415	14163	26846	3.14	1.0E-100	BF530735.1	EST_HUMAN	G02072094F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4215039 5'
1538	14285		1.14	1.0E-100	AW207555.1	EST_HUMAN	U1-H-B11-afk-c-07-0-J1 s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1543	14289	26976	1.81	1.0E-100	AI200857.1	EST_HUMAN	q162109.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA
1856	14594	27309	1.41	1.0E-100	AB032994.1	NT	P81061 CYSTATIN;
2238	14988		1.39	1.0E-100	D83349.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2439	15159	27894	1.33	1.0E-100	X62468.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2710	15417	28165	2.36	1.0E-100	D11078.1	NT	H sapiens mRNA for IFN-gamma (pK-C)
3018	15784		5.5	1.0E-100	D11078.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4186	16927	29558	1.52	1.0E-100	AF057354.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4211	16952	29578	2.14	1.0E-100	4503762	NT	Homo sapiens myoblastin-related protein 1a mRNA, partial cds
4418	17154	29785	1.03	1.0E-100	AF036943.1	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5031	17751	30362	2.68	1.0E-100	5032104	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
5031	17751	30363	2.68	1.0E-100	5032104	NT	Homo sapiens small optic tubules (Drosophila) homolog (SOLH) mRNA
5207	18015	30637	1.62	1.0E-100	BF244218.1	EST_HUMAN	Homo sapiens small optic tubules (Drosophila) homolog (SOLH) mRNA

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5421	18220	30931	0.59	1.0E-100	AW075983.1	EST_HUMAN	ya8201.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433
5614	18410	31323	1.33	1.0E-100	AU118182.1	EST_HUMAN	PROTEIN PHPS1-2 (HUMAN);
5660	18455	31369	1.26	1.0E-100	AF135116.1	NT	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5747	18539	31461	0.8	1.0E-100	X14690.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6071	18850	31814	0.94	1.0E-100		NT	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
6071	18850	31814	0.94	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6343	19113		1.67	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6405	19174	32173	5.64	1.0E-100	AU140214.1	EST_HUMAN	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6457	19224	32224	1.97	1.0E-100	AU136800.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6586	19349	32362	1.37	1.0E-100	R10887.1	EST_HUMAN	AU136800 PLACE1 Homo sapiens cDNA clone PLACE1005089 5'
6670	19587	32622	0.9	1.0E-100	7382479	NT	y38c08.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:129134 3'
6742	19576	32608	1.19	1.0E-100	AA496841.1	EST_HUMAN	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 4, mRNA
6742	19576	32609	1.19	1.0E-100	AA496841.1	EST_HUMAN	ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
6786	19630	32557	1.13	1.0E-100	BF376476.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.;
6786	19630	32558	1.13	1.0E-100	BF376476.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.;
6793	19537	32555	6.76	1.0E-100	X04571.1	NT	MR1-TN0048-060900-004-b05 TN0046 Homo sapiens cDNA
8430	21123	34261	7.17	1.0E-100	BF103853.1	EST_HUMAN	MR1-TN0048-060900-004-b05 TN0046 Homo sapiens cDNA
8466	21158		4.8	1.0E-100	AL163203.2	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
8912	21603	34746	0.68	1.0E-100	AU116951.1	EST_HUMAN	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
8912	21603	34747	0.68	1.0E-100	AU116951.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9132	21820	34986	3.62	1.0E-100	AB040918.1	NT	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9210	22089		2.78	1.0E-100	AI972388.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9333	20404	33520	1.82	1.0E-100	AW98861.1	EST_HUMAN	Homo sapiens mRNA for KIAA1485 protein, partial cds
9386	22048		7.61	1.0E-100	AU127720.1	EST_HUMAN	wt37g09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element MER22 repetitive element;
9483	22138	35316	2.11	1.0E-100	AB046846.1	NT	PMD-BN0066-100300-001-c08 BN0065 Homo sapiens cDNA
9483	22136	35317	2.11	1.0E-100	AB046846.1	NT	AU127720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
9743	22394	35598	1.68	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1628 protein, partial cds
9743	22394	35599	1.68	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1628 protein, partial cds
9905	22554	35749	0.49	1.0E-100	AV732101.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2969398 5'
10388	23014	36230	1.47	1.0E-100	BF347519.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2969398 5'
							AV732101 HTF Homo sapiens cDNA clone HTFBIG01 5'
							602020564F1 NCI_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4166165 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10458	23104		2.2	1.0E-100	Y10391.1	NT	Human endogenous retrovirus HERV-K, pol gene
10658	23349	36596	6.27	1.0E-100	BF327292.1	EST_HUMAN	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
11326	24017	37319	4.52	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11326	24017	37320	4.52	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11358	12830	25443	2.11	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11633	24230		1.59	1.0E-100	AW875484.1	EST_HUMAN	QV2-PT0012-010300-070-d04 PT0012 Homo sapiens cDNA
11681	24276		1.48	1.0E-100	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11749	24340	37668	1.57	1.0E-100	AA115605.1	EST_HUMAN	z189a03.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:489964 5'
11749	24340	37669	1.57	1.0E-100	AA115605.1	EST_HUMAN	z189a03.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:489964 5'
11907	24471	37806	6.67	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12031	25278		1.51	1.0E-100	BF446549.1	EST_HUMAN	7q88h03.x1 NCJ CGAP Lu24 Homo sapiens cDNA clone IMAGE:3' similar to TR:Q21997 Q21997
12200	24668	31071	3.67	1.0E-100	11545732	NT	COSMID R151. [2] TR:Q9UA08
12782	25044	30968	4.62	1.0E-100	11417974	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
75	12902	25539	1.75	1.0E-101	7110714	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
75	12902	25540	1.75	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
671	13447	26087	1.62	1.0E-101	AB007915.2	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
688	13463	26111	5.88	1.0E-101	7110734	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
688	13463	26112	5.88	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
754	13526	26185	1.99	1.0E-101	7657454	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
833	13603	26273					Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
904	13671	26335	1.5	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
964	13728	26396	1.22	1.0E-101	Z20656.1	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
1030	13790	26449	14.26	1.0E-101	BF681218.1	EST_HUMAN	Homo sapiens of cardiac alpha-myosin heavy chain gene
1577	14324	27012	1.63	1.0E-101	AI221878.1	EST_HUMAN	602156474FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5'
1577	14324	27013	1.46	1.0E-101	5921460	NT	qg98c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1740	14482	27182	1.46	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1740	14482	27183	1.52	1.0E-101	7662183	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1938	14673	27389	1.52	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
2050	14783	27510	1.62	1.0E-101	4502896	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
2349	15592	27808	1.79	1.0E-101	BE843070.1	EST_HUMAN	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2620	15332	28076	1.71	1.0E-101	5729892	NT	RC3-ST0281-160600-016-h08 ST0281 Homo sapiens cDNA
			2.8	1.0E-101	X72893.1	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
							H. sapiens EWS gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2747	15452	28192	1.09	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2747	15452	28193	1.09	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2955	15721		13.73	1.0E-101	AJ262312.1	NT	Homo sapiens genomic downstream Rhesus box
3198	15961	28613	1.98	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3235	15997		2.27	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3375	16134	28790	1.93	1.0E-101	AW965556.1	EST_HUMAN	EST377629 IMAGE resequences, MAGI Homo sapiens cDNA
3395	15452	28192	1.49	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3395	15452	28193	1.49	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3857	16607	29245	3.69	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
4974	17697	30304	1.16	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
4974	17697	30305	1.16	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5235	18041	30659	1.22	1.0E-101	AW965139.1	EST_HUMAN	EST377212 IMAGE resequences, MAGI Homo sapiens cDNA
5913	18698	31651	3.68	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
5913	18698	31652	3.68	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6595	19358	32372	1.27	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7173	19859		1.01	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7220	19905	32977	5.57	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7220	19905	32978	5.57	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7376	20056	33136	7.48	1.0E-101	AW008475.1	EST_HUMAN	wv55f12.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2633487 3'
7474	20147		1.79	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349901 5'
7623	20269	33398	7.43	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA
7813	20508	33631	0.94	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
7813	20508	33632	0.84	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
7954	20849	33772	2.88	1.0E-101	BF029174.1	EST_HUMAN	601764686F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5'
8221	20915	34050	0.67	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCI CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143
8221	20915	34051	0.67	1.0E-101	AW630070.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8908	21599	34741	1.08	1.0E-101	AA036800.1	EST_HUMAN	hh74g10.y1 NCI CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143
9229	21908	35080	0.83	1.0E-101	AB037772.1	NT	INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
9229	21908	35081	0.83	1.0E-101	AB037772.1	NT	z129g08.r1 Scores_pregnant_uterus_NHIFU Homo sapiens cDNA clone IMAGE:471998 5' similar to
9362	20432	33553	17.13	1.0E-101	X60069.1	NT	PIR:S54640 S54640 YD3335.03c protein - yeast :
9362	20432	33554	17.13	1.0E-101	X60069.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9362	20432	33554	17.13	1.0E-101	X60069.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9362	20432	33554	17.13	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9362	20432	33554	17.13	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9375	21950	35123	17.01	1.0E-101	9845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
9657	22309	35506	6.24	1.0E-101	BE619687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9657	22309	35507	6.24	1.0E-101	BE619687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9794	22445	35650	0.72	1.0E-101	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10308	22955	36171	1.49	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10447	23093	36323	0.94	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10447	23093	36324	0.94	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10788	23471	36713	1.98	1.0E-101	S38327.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, segment 8 of 9]
11053	23723	36994	2.11	1.0E-101	AB020626.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
11398	24004	37307	2.06	1.0E-101	A1590078.1	EST_HUMAN	Homo sapiens mRNA for KIAA0819 protein, partial cds
11398	24004	37308	2.06	1.0E-101	A1590078.1	EST_HUMAN	Homo sapiens mRNA for KIAA0819 protein, partial cds
11763	24354	37898	1.31	1.0E-101	A1908168.1	EST_HUMAN	tm58c01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162304 3' similar to gb:M13361
11763	24354	37897	1.31	1.0E-101	A1908168.1	EST_HUMAN	tm58c01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162304 3' similar to gb:M13361
12461	24829	25485	13.68	1.0E-102	AF012872.1	NT	HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HUMAN);
38	12866	25485	2	1.0E-102	AF012872.1	NT	HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HUMAN);
332	13133	25767	4.35	1.0E-102	AL163303.2	NT	RC-BT163-290499-085 BT163 Homo sapiens cDNA
759	13530	26190	1.59	1.0E-102	4557534	NT	RC-BT163-290499-085 BT163 Homo sapiens cDNA
1095	13853	26512	2.8	1.0E-102	M10976.1	NT	RC-BT163-290499-085 BT163 Homo sapiens cDNA
1245	13994	26660	1.67	1.0E-102	11437146	NT	RC-BT163-290499-085 BT163 Homo sapiens cDNA
1245	13994	26661	1.67	1.0E-102	11437146	NT	RC-BT163-290499-085 BT163 Homo sapiens cDNA
1261	14010	26678	0.99	1.0E-102	BE408447.1	EST_HUMAN	QV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
1398	14145	26823	119.7	1.0E-102	BE408447.1	EST_HUMAN	QV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
2307	15032	27769	1.88	1.0E-102	A1124689.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2307	15032	27770	1.88	1.0E-102	A1124689.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3061	15927	28472	1.32	1.0E-102	7661979	NT	Homo sapiens chromosome 21 segment HS21C103
3130	15895	28538	4.76	1.0E-102	AU141005.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3130	15895	28539	4.76	1.0E-102	AU141005.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4207	16948	29574	1.57	1.0E-102	AL163207.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4378	17115	29748	2.17	1.0E-102	BE251310.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
2307	15032	27770	1.88	1.0E-102	A1124689.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
2307	15032	27770	1.88	1.0E-102	A1124689.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3061	15927	28472	1.32	1.0E-102	7661979	NT	Homo sapiens chromosome 21 segment HS21C103
3130	15895	28538	4.76	1.0E-102	AU141005.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3130	15895	28539	4.76	1.0E-102	AU141005.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4207	16948	29574	1.57	1.0E-102	AL163207.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4378	17115	29748	2.17	1.0E-102	BE251310.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103

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5287	18092	30753	1.87	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5663	18458		9.17	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5698	18492	31414	2.84	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5698	18492	31415	2.84	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5704	18498	31420	0.81	1.0E-102	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
							ar8209.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137
							Q13137 NDP52.
6200	18976	31954	2.93	1.0E-102	AI459825.1	EST_HUMAN	601561503F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7036	19728	32785	0.75	1.0E-102	BE729323.1	EST_HUMAN	601277215F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618243 5'
7065	19756	32821	1.04	1.0E-102	BE386106.1	EST_HUMAN	Homo sapiens mRNA for Centaurin-alpha2 protein
7255	19939	33014	8.23	1.0E-102	AJ238994.1	NT	Homo sapiens cDNA clone CUAAD093 5'
7524	20195	33288	2.48	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CUAAD093 5'
8122	20816	33952	3.91	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT0025-210600-236-h08 NT0025 Homo sapiens cDNA
8201	20895	34032	1.32	1.0E-102	BE910555.1	EST_HUMAN	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone GKGEE11 5'
8392	21085	34218	2.21	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKGEE11 5'
8392	21085	34219	2.21	1.0E-102	AV694817.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
8501	21183	34335	1.19	1.0E-102	AB007923.1	NT	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
8829	21521	34667	0.63	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
8829	21521	34668	0.63	1.0E-102	BE388063.1	EST_HUMAN	wf63506.x1 NC1_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2397971 3' similar to contains MER4 t1
							MER4 MER4 repetitive element.
9150	21881	35049	0.52	1.0E-102	A1762859.1	EST_HUMAN	AV755842 BM Homo sapiens cDNA clone BMFAUD06 5'
9181	21851	35017	0.81	1.0E-102	AV755842.1	EST_HUMAN	AV755842 BM Homo sapiens cDNA clone IMAGE:67021 5'
9221	21900	35069	2.28	1.0E-102	T70393.1	EST_HUMAN	Yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
9221	21900	35070	2.28	1.0E-102	T70393.1	EST_HUMAN	Yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
9311	21978	35151	3.79	1.0E-102	AU124629.1	EST_HUMAN	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
10281	22929		0.69	1.0E-102	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10367	23013	36228	3.67	1.0E-102	A1905037.1	EST_HUMAN	RC-BT074-260469-014 BT074 Homo sapiens cDNA
10367	23013	36229	3.67	1.0E-102	A1905037.1	EST_HUMAN	RC-BT074-260469-014 BT074 Homo sapiens cDNA
							or57604.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1660823 3' similar to
10428	23074	36295	1.24	1.0E-102	AA970786.1	EST_HUMAN	SW-CAV2_HUMAN P51636 CAVEOLIN-2. [1];
11008	23680	36937	2.56	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11008	23680	36938	2.56	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11260	23951	37248	1.55	1.0E-102	AA868675.1	EST_HUMAN	ak49k10.31 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409347 3'
11360	23987	37287	3.01	1.0E-102	BF359243.1	EST_HUMAN	RC6-E10072-150600-011-F01 E10072 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11710	24305	37631	3.57	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
11911	24475		3.52	1.0E-102	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
12450	24820	31023	4.89	1.0E-102	AW300862.1	EST_HUMAN	x07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'
67	12895	25528	1.19	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
67	12895	25529	1.19	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
98	12924	25561	10.5	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
203	13016	25656	1.45	1.0E-103	5453783	NT	Homo sapiens nucleolar protein (KKEID repeat) (NOP56) mRNA
960	13725	26389	0.79	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1221	13971	26643	10.23	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1591	14337	27026	3.76	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1907	14644	27354	1.75	1.0E-103	7657592	NT	Homo sapiens sing GDS-ASSOCIATED PROTEIN (SMAP), mRNA
1968	14704	27420	1.44	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1968	14704	27421	1.44	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2303	15028	27765	1.15	1.0E-103	AU134991	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2452	15170	27909	1.33	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2603	15316	28055	1.23	1.0E-103	BF529379.1	EST_HUMAN	602041882F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179429 5'
2603	15316	28056	1.23	1.0E-103	BF529379.1	EST_HUMAN	602041882F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179429 5'
3064	15830		2.68	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3374	16133	28789	4.1	1.0E-103	AW298245.1	EST_HUMAN	U1-HBW0-elt-h-11-0JL.s1 NCI_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2733165 3'
3433	16189	28837	0.99	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3737	16490		8.55	1.0E-103	AF023961.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3774	16526	29165	1.23	1.0E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element
3810	16562	29195	1.72	1.0E-103	11430876	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
3985	16733	29367	3.47	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cat109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cat109+10-Bio-7 3'
5844	18632	31567	0.96	1.0E-103	BF569527.1	EST_HUMAN	602186023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310573 5'
5852	18639	31577	2.62	1.0E-103	AF176995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6174	18951	31923	0.89	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6174	18951	31924	0.89	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6368	19137	32132	0.75	1.0E-103	AW954566.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6368	19137	32133	0.75	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6498	25092	32265	1.53	1.0E-103	AA781442.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6535	19301	32304	0.94	1.0E-103	AF053490.1	NT	aj26e03.s1 Soares_basili NIH Homo sapiens cDNA clone 1391452 3'
							Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6618	19380	32396	1.48	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6618	19380	32397	1.48	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6747	17916	30578	1.53	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6747	17916	30580	1.53	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6872	17949	30544	1.27	1.0E-103	11431100	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
6935	19670	32716	0.99	1.0E-103	AJ289880.1	NT	Homo sapiens KIA0851 gene (partial), X13 gene and LZ1FL1 gene
7127	19815	32883	1.63	1.0E-103	AW965776.1	EST_HUMAN	EST1377849 MAGE resequences, MAGI Homo sapiens cDNA
7233	19918	32990	6.93	1.0E-103	BE748158.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
7871	20335	33446	4.21	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
7871	20335	33447	4.21	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
8187	20881	34019	0.77	1.0E-103	T31080.1	EST_HUMAN	EST127193 Human Brain Homo sapiens cDNA 5' end similar to None
8519	21211	34354	2.22	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8519	21211	34355	2.22	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8604	21296	34439	1.1	1.0E-103	BF109244.1	EST_HUMAN	760e03.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525984 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1:
9005	21695	34845	2.86	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9005	21695	34846	2.86	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9046	21738	34891	1.16	1.0E-103	AA581083.1	EST_HUMAN	nd13c02.s1 NCI_CGAP_Ov1 Homo sapiens cDNA clone IMAGE:900162 3' similar to gbl02426 26S PROTEASE SUBUNIT 4 (HUMAN);
9088	21777	34941	5.04	1.0E-103	AA774980.1	EST_HUMAN	ae84d12.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:970871 3' similar to gb-X03747_cds1 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-1 (HUMAN);
9182	21832	34995	0.56	1.0E-103	BE935842.1	EST_HUMAN	QV2-NN0045-230800-322-b03 NN0045 Homo sapiens cDNA
9182	21832	34996	0.56	1.0E-103	BE935842.1	EST_HUMAN	QV2-NN0045-230800-322-b03 NN0045 Homo sapiens cDNA
9958	22808	35811	1.44	1.0E-103	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
9999	22647	35859	1.89	1.0E-103	AW963878.1	EST_HUMAN	EST1375749 MAGE resequences, MAGH Homo sapiens cDNA

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10138	22786	35998	9.2	1.0E-103	A1878958.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518328 5' similar to TR:O15048 O15048 KIAA0338
10634	23326	36563	3.56	1.0E-103	A792759.1	EST_HUMAN	010208.y5 NCL CGAP Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING
10737	23424	36668	2.04	1.0E-103	11424081	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
10737	23424	36669	2.04	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
10748	23434	36677	2.22	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
10748	23434	36678	2.22	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
10793	23476	36717	1.3	1.0E-103	X87831.2	NT	Homo sapiens mRNA for partial OCT/plexin-A2 protein
10793	23476	36718	1.3	1.0E-103	X87831.2	NT	Homo sapiens mRNA for partial OCT/plexin-A2 protein
11347	24037	37340	2.8	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACET Homo sapiens cDNA clone PLACE1003923 5'
11423	23190	36421	10.74	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11748	24339	37687	2.41	1.0E-103	BE644611.1	EST_HUMAN	7e68a10.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.13 MER29 repetitive element
11937	24494		2.11	1.0E-103	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12128	24620	31091	2.83	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
227	13039	25676	3.73	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_j1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
227	13039	25877	3.73	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_j1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1881	14618	27328	2.18	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteoinductive protein 2) (BMP8) mRNA
2190	14919	27653	3.68	1.0E-104	AA132975.1	EST_HUMAN	z02c08.s1 Stratagene codon (#937294) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14118.maf1 CD59 GYCOPROTEIN PRECURSOR (HUMAN);
2201	14929	27666	2.57	1.0E-104	BE744628.1	EST_HUMAN	601577460F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928438 5'
2369	15091	27829	1.38	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2369	15091	27830	1.38	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2438	15158	27893	1.68	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2507	15224	27965	1.11	1.0E-104	7682125	NT	Homo sapiens KIAA00440 protein (KIAA00440), mRNA
2507	15224	27966	1.11	1.0E-104	7682125	NT	Homo sapiens KIAA00440 protein (KIAA00440), mRNA
2874	15641	28285	7.41	1.0E-104	M34671.1	NT	Human lymphocytic antigen CD59/ME43 mRNA, complete cds
2917	15883	16145	2.74	1.0E-104	Y11151.1	NT	H.sapiens gene encoding phenylpyruvate tautomerase II
3386	16145		2.04	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3587	16341	28986	0.79	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3587	16341	28987	0.79	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3924	16874	29315	0.76	1.0E-104	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4344	17083	28712	3.83	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)

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4570	17305	29932	1.23	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4570	17305	29933	1.23	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
5106	17824	30441	1.06	1.0E-104	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
5850	18637	31573	1.26	1.0E-104	U43376.1	NT	Human Down Syndrome region of chromosome 21 DNA
5850	18637	31574	1.26	1.0E-104	U43376.1	NT	Human Down Syndrome region of chromosome 21 DNA
5897	18682	31630	1.12	1.0E-104	AB017332.1	NT	Homo sapiens alk3 mRNA for Aurora/ipl1-related kinase 3, complete cds
6375	19144	32141	9.51	1.0E-104	AI768797.1	EST_HUMAN	w03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q141415 Q14145
6375	19144	32142	9.51	1.0E-104	AI768797.1	EST_HUMAN	KIAA0192 PROTEIN, contains element LTR7 repetitive element;
6551	19316	32322	0.75	1.0E-104	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6706	19621	32663	3.31	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6706	19621	32664	3.31	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7125	19813	32881	2.03	1.0E-104	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8495	21187	34330	0.83	1.0E-104	BF509244.1	EST_HUMAN	UI-H-B14-aw-b-09-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086176 3'
9065	21754	34915	5.23	1.0E-104	BF448230.1	EST_HUMAN	nad16g11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
9163	21833	34997	0.5	1.0E-104	AA682308.1	EST_HUMAN	z98b05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9184	21854		1.31	1.0E-104	T74219.1	EST_HUMAN	yc83102.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22440 5'
9214	21893	35060	4.27	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9214	21893	35061	4.27	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9341	20412	33529	4.4	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9341	20412	33530	4.4	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9654	22306	35503	0.85	1.0E-104	AW103848.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
9654	22306						Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
9847	22497	35698	0.71	1.0E-104	AF113514.1	NT	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
9993	22641	35652	2.83	1.0E-104	BE791713.1	EST_HUMAN	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
9993	22641	35653	2.83	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10299	22946	36160	1.29	1.0E-104	AV728070.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10339	22986	36204	4.51	1.0E-104	AU130765.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
10450	23096	36327	4.41	1.0E-104	U86535.1	NT	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
10464	23110		0.92	1.0E-104		NT	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
11268	23930	37221	2.07	1.0E-104	BE720191.1	EST_HUMAN	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
							RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA

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11268	23830	37222	2.07	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11299	23859	37259	4.96	1.0E-104	BF694288.1	EST_HUMAN	602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
11590	24189	37505	1.75	1.0E-104	BE731978.1	EST_HUMAN	601566806F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841681 5'
11590	24189	37508	1.75	1.0E-104	BE731978.1	EST_HUMAN	601566806F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841681 5'
11791	24381	37712	1.42	1.0E-104	11434729	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5), mRNA
12702	24982		2.38	1.0E-104	BE393892.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3656676 5'
272	15514	25722	11.13	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
416	12827	25440	8.99	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
580	13380	25987	1.92	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
580	13380	25988	1.92	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1814	14554	27269	0.91	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1919	14656	27366	1.93	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2188	14915	27649	1.29	1.0E-105	AA318389.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' and similar to autoimmune antigen Ku, p70/p80 subunit
2322	15047		1.44	1.0E-105	BE891768.1	EST_HUMAN	601434491F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919511 5'
3006	15772		2.89	1.0E-105	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3346	16105	28759	0.88	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3346	16105	28760	0.88	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4077	16821	29447	2.07	1.0E-105	AW061688.1	EST_HUMAN	EST373761 IMAGE resequences, MAGG Homo sapiens cDNA
4694	17428	30058	0.74	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4694	17428	30059	0.74	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4886	17613		4.24	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5043	17762	30377	1.16	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
5091	17810	30426	0.94	1.0E-105	AW066016.1	EST_HUMAN	EST378088 IMAGE resequences, MAGI Homo sapiens cDNA
5247	18053	30881	0.96	1.0E-105	AF018704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5312	18116		1.07	1.0E-105	11420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6804	19465	32485	2.16	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
6804	19465	32488	2.16	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
6885	17961	30515	3.65	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6885	17961	30518	3.65	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6927	19663	32709	0.83	1.0E-105	AW951634.1	EST_HUMAN	EST363689 IMAGE resequences, MAGB Homo sapiens cDNA
7184	18870	32944	0.59	1.0E-105	BE002618.1	EST_HUMAN	601677279F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960019 5'
7722	20388	33500	0.65	1.0E-105	8808894	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
7758	20454	33578	0.97	1.0E-105	X12556.1	NT	Human mRNA for dbl proto-oncogene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7927	20622	33750	6.55	1.0E-105	T05087.1	EST_HUMAN	EST02075 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone IMAGE:2500826 3' similar to
8287	20991	34129	1.41	1.0E-105	AW007194.1	EST_HUMAN	SW:ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
8826	21518	34683	0.68	1.0E-105	AW840817.1	EST_HUMAN	RC1-CN0008-070100-011-e05 CN0008 Homo sapiens cDNA
8948	21639	34786	2.82	1.0E-105	AW016879.1	EST_HUMAN	UHL-B10p-ab1-b-12-0-U1.s1 NCI CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9103	21791	34954	0.9	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9103	21791	34955	0.9	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9467	22077	35247	0.88	1.0E-105	BE887793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
9467	22077	35248	0.68	1.0E-105	BE887793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
10850	23531	36776	5.73	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11195	23860	37146	1.59	1.0E-105	D63548.1	NT	Homo sapiens COL4A8 gene for $\alpha 4(\text{IV})$ collagen, exon 31
11250	23912	37204	2.38	1.0E-105	7705936	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11580	24179	37494	2.58	1.0E-105	AW027554.1	EST_HUMAN	w74607.x1 Scars_NHFT11 Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892 P87892 PROTEASE ;
11675	24270	37592	1.43	1.0E-105	BF430921.1	EST_HUMAN	7c18c10.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR:P97880 P97880 RIN1 ;
11831	24415	37763	1.73	1.0E-105	AB004924.1	NT	Homo sapiens gene for Smad3, exon 2 and 3
11831	24415	37754	1.73	1.0E-105	AB004924.1	NT	Homo sapiens gene for Smad3, exon 2 and 3
147	12862	25654	1.39	1.0E-106	AW503208.1	EST_HUMAN	UHF-BNO-akt-g-07-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
200	13013	25654	1.79	1.0E-106	AI565065.1	EST_HUMAN	1q79c01.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2215008 3'
529	13313	25947	2.68	1.0E-106	AW965558.1	EST_HUMAN	EST377829 MAGI resequences, MAGI Homo sapiens cDNA
591	13371	26000	0.75	1.0E-106	J00148.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
592	13371	26000	2.06	1.0E-106	J00148.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
1515	14282	26948	1.33	1.0E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1697	14440	27138	3.48	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1798	14536	27245	4.71	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCI CGAP_Ox3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ;
1798	14536	27246	4.71	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCI CGAP_Ox3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ;
2118	14849	27578	2.31	1.0E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2315	15040	27778	2.89	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2610	15322	28084	1.82	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2761	15466	28210	3.24	1.0E-106	AI276526.1	EST_HUMAN	q78h10.x1 Scars_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2828	14159	26842	1.91	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA

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2828	14159	28843	1.91	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2942	15707	28357	5.23	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2942	15707	28358	5.23	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3176	15939	28588	2.18	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3176	15939	28589	2.18	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3387	16126	28784	0.81	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3434	16190	28838	1.18	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3434	16190	28839	1.18	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4017	16783	29391	7.95	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4017	16783	29392	7.95	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4035	16780	29410	1.05	1.0E-106	5729729	NT	Homo sapiens API5-like 1 (API5L-1), mRNA
4582	17287	29924	1.4	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-J10 HT0165 Homo sapiens cDNA
5135	17853	30469	1.09	1.0E-106	AL050253.1	NT	H. sapiens mRNA similar to D29763 mouse mRNA for seizure-related gene product 6. Shares domains with BMPs, Tolloid, Sushi repeat proteins
5135	17853	30470	1.09	1.0E-106	AL050253.1	NT	H. sapiens mRNA similar to D29763 mouse mRNA for seizure-related gene product 6. Shares domains with BMPs, Tolloid, Sushi repeat proteins
5285	18090	30750	2.81	1.0E-106	AA781155.1	EST_HUMAN	el24009.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:U12433 PROTEIN PHPS1-2 (HUMAN);
5764	18555	31480	0.58	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5764	18555	31481	0.58	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5816	18605	31533	0.58	1.0E-106	AA434168.1	EST_HUMAN	zw28412.s1 Scores ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770815 3'
5904	18689	31637	1.3	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
5904	18689	31638	1.3	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6011	18792	31755	4.89	1.0E-106	BF679574.1	EST_HUMAN	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285067 5'
6303	18892	31860	0.77	1.0E-106	BE897112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924841 5'
6325	19085	32083	17.66	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6326	19085	32084	17.66	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
7271	19955	33031	5.16	1.0E-106	AA863779.1	EST_HUMAN	ee72e07.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:U65873 KINESIN HEAVY CHAIN (HUMAN);
7324	20007	33084	5.33	1.0E-106	11429817	NT	Homo sapiens XPM22 protein (LOC57109), mRNA
7402	20080	33161	1.21	1.0E-106	BE282722.1	EST_HUMAN	801105739F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:2988345 5'
7511	20182	33275	9.29	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7511	20182	33276	9.29	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7714	20378	33491	0.87	1.0E-106	AU118850.1	EST_HUMAN	AU118850 HEMBA1 Homo sapiens cDNA clone HEMBA1000129 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7884	20579	33707	6.44	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
7884	20579	33708	6.44	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8074	20768	33897	1.38	1.0E-106	AI523066.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8527	21219	34361	0.47	1.0E-106	BE387990.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8527	21219	34362	0.47	1.0E-106	BE387990.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8607	21299	34443	3.64	1.0E-106	AI654123.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8950	21641	34788	0.58	1.0E-106	AW838831.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
9045	21735	34889	3.28	1.0E-106	AA825307.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
9045	21735	34890	3.28	1.0E-106	AA825307.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
9186	21856	35021	1.28	1.0E-106	AI760447.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
9329	21986	35169	1.8	1.0E-106	AI479569.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
9329	21986	35170	1.8	1.0E-106	AI479569.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
9802	22551	35746	1.19	1.0E-106	BE389234.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
9884	22632	35841	1.09	1.0E-106	BF027310.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
9884	22632	35842	1.09	1.0E-106	BF027310.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
10141	22789	36003	6.22	1.0E-106	AA604417.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
10185	22833	36047	1.6	1.0E-106	AW363299.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
10358	23005	36222	0.53	1.0E-106	AL039898.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
10478	23125	36354	2.81	1.0E-106	AL163202.2	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
10812	23495	36730	7.1	1.0E-106	BF032755.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
10812	23495	36731	7.1	1.0E-106	BF032755.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
10995	23668	36925	2.22	1.0E-106	J05200.1	NT	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
10995	23668	36926	2.22	1.0E-106	J05200.1	NT	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
11394	23991	37292	1.91	1.0E-106	BE257385.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
11532	24132	37436	1.35	1.0E-106	BE010882.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
11532	24132	37437	1.35	1.0E-106	BE010882.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
11981	25194	31068	6.77	1.0E-106	AW410405.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
12193	24664	31068	3.32	1.0E-106	BE89488.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'

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12193	24664	31069	3.32	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12408	24791		4.6	1.0E-106	BE695905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
228	13040		4.42	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
258	13066		1.29	1.0E-107	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
607	13385		4.03	1.0E-107	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
616	13394	26028	1.89	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
866	13635	26306	1.52	1.0E-107	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
948	13714	26379	11.55	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1255	14004	26673	0.73	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1562	14309	26996	3.77	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1746	14488	27187	1.55	1.0E-107	AF136275.1	NT	Homo sapiens cathapsin Z precursor (CTS2) gene, exon 3
1832	14571	27283	0.99	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1832	14571	27284	0.99	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2205	14933	27671	0.95	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2362	15084	27822	1.45	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2362	15084	27823	1.45	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2535	15250	27991	1.2	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2535	15250	27992	1.2	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
3007	15773	28421	3.89	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3007	15773	28422	3.89	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3096	15861	28502	2.63	1.0E-107	5902087	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3806	16558	29190	5.14	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5537	18335	31242	0.66	1.0E-107	AW969038.1	EST_HUMAN	EST381115 MAGC resequences, MAGK Homo sapiens cDNA
5775	18566	31495	3.2	1.0E-107	BE867469.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848494 5'
6823	19484	32506	1.45	1.0E-107	11431469	NT	Homo sapiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220KD) (GTF3C1), mRNA
6823	19484	32507	1.45	1.0E-107	11431469	NT	Homo sapiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220KD) (GTF3C1), mRNA
7263	19947	33023	1.42	1.0E-107	AW503913.1	EST_HUMAN	UHF-BN0-af-c-08-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7263	19947	33024	1.42	1.0E-107	AW503913.1	EST_HUMAN	UHF-BN0-af-c-08-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7429	20106	33193	1.46	1.0E-107	A1765078.1	EST_HUMAN	W56104.x1 NC1_CGAP_K14111 Homo sapiens cDNA clone IMAGE:2384791 3'
7690	20354	33469	0.6	1.0E-107	AW410981.1	EST_HUMAN	fh09d11.x2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2964524 5'
9287	22041	35213	0.95	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10603	23297	36537	3.18	1.0E-107	A1392850.1	EST_HUMAN	ig10x06.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICDI
10866	23546	36794	14.26	1.0E-107	L49141.1	NT	P05095 ALFA-ACTININ 3, NON MUSCULAR ;
10880	23560	36807	1.71	1.0E-107	BF668511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11293	23954	37252	6.66	1.0E-107	BE540550.1	EST_HUMAN	602123953F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281039 5'
11367	23178	36405	5.97	1.0E-107	11419701	NT	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11367	23178	36406	5.97	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11843	24427	37768	1.36	1.0E-107	4506970	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11843	24427	37769	1.36	1.0E-107	4506970	NT	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA
12043	25328		5.86	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA
935	13702	26367	2.66	1.0E-108	BE296042.1	EST_HUMAN	2e45e01.s1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
1242	13991	26657	1.87	1.0E-108	Y18000.1	NT	THR repetitive element ;
							601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
							Homo sapiens NF2 gene
2428	15149	27883	4.97	1.0E-108	BE206694.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S
3344	16103	28755	0.71	1.0E-108	AF032897.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3344	16103	28756	0.71	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4136	16878	29507	1.14	1.0E-108	AW664438.1	EST_HUMAN	h12a11.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE
4489	17225	29853	2.18	1.0E-108	U72961.1	NT	P55194 SH3-BINDING PROTEIN 3BP-1 ;
4489	17225	29854	2.18	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4752	17484	30113	1.74	1.0E-108	7661979	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4896	17623	30241	2.8	1.0E-108	AJ008005.1	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5391	18191	30883	1.15	1.0E-108	AW384094.1	EST_HUMAN	Homo sapiens PSN1 gene, alternative transcript
5440	18239	30954	1.7	1.0E-108	BE669016.1	EST_HUMAN	RCO-HT0372-241169-031-003 HT0372 Homo sapiens cDNA
5440	18239	30955	1.7	1.0E-108	BE669016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5837	18626		0.99	1.0E-108	AF012623.1	NT	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
6048	18828	31790	6.13	1.0E-108	AF284717.1	NT	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
6048	18828	31791	6.13	1.0E-108	AF284717.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete
							cds
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete
							cds

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6169	18946	31918	1.27	1.0E-108	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6265	18697	31650	0.92	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6521	19287	32290	0.83	1.0E-108	AF016708.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6521	19287	32291	0.63	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7057	19748	32811	5.82	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family G, group 5, member B (GPCRB5), mRNA
7339	20020	33098	3.55	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS5D6) mRNA
7377	20057	33137	1.16	1.0E-108	BE252607.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354064 5'
7405	20082	33164	0.84	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
7405	20082	33165	0.84	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
7963	20658	33838	1.68	1.0E-108	AF033500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8014	20709	33839	0.48	1.0E-108	AW408694.1	EST_HUMAN	UHF-BMD-ads-e-12-0-UJ1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8014	20709	33839	0.48	1.0E-108	AW408694.1	EST_HUMAN	UHF-BMD-ads-e-12-0-UJ1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8945	21636	34781	0.75	1.0E-108	AF203977.1	NT	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
8984	21674	34823	0.54	1.0E-108	N44974.1	EST_HUMAN	y95h10.1 Soares melanocyte ZNbf-HM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIRA45773
10565	20368	33481	1.73	1.0E-108	BE535227.1	EST_HUMAN	A45773 leish protein, long form - fruit fly
10731	17911	30597	1.98	1.0E-108	Y12490.1	NT	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
10988	23671	36928	1.39	1.0E-108	AF223391.1	NT	Homo sapiens mRNA for Gdgl-associated microtubule-binding protein (GMAP-210)
11239	23902	37191	3.82	1.0E-108	AW966185.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11294	23955	37253	2.2	1.0E-108	AV708790.1	EST_HUMAN	EST378258 MAGE resequences, MAGI Homo sapiens cDNA
11294	23955	37254	2.2	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADG Homo sapiens cDNA clone ADCAE03 5'
11343	24033	37359	1.67	1.0E-108	11441465	NT	AV708790 ADG Homo sapiens cDNA clone ADCAE03 5'
11405	24054	37359	1.68	1.0E-108	D63559.1	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
12204	24671	31072	2.41	1.0E-108	AK024447.1	NT	Homo sapiens COL4A6 gene for a(IV) collagen, exon 23
12583	24906	25488	8.32	1.0E-108	BF346356.1	EST_HUMAN	Homo sapiens mRNA for FLJ00037 protein, partial cds
41	12869	25488	0.87	1.0E-109	AW803116.1	EST_HUMAN	Homo sapiens mRNA for FLJ00037 protein, partial cds
62	12890	25523	0.97	1.0E-109	D86974.1	NT	IL2-UJM0077-280400-079-D06 UM0077 Homo sapiens cDNA
220	13031	25667	1.59	1.0E-109	11438391	NT	Human mRNA for KIAA0220 gene, partial cds
454	13240	25878	5.59	1.0E-109	4507712	NT	Homo sapiens telitricopeptide repeat domain 2 (TTC2) mRNA
584	13364	25992	26.8	1.0E-109	AB023216.1	NT	Homo sapiens telitricopeptide repeat domain 2 (TTC2) mRNA
584	13364	25993	26.8	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1180	13933	26598	10.97	1.0E-108	M28699.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
							Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds

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1181	13933	26598	4	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1533	14280	26967	3.31	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
1533	14280	26968	3.31	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
1867	14605	27315	3.3	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2237	14965	27705	1.78	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2248	14976	27714	1.89	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2628	15340	28084	3.98	1.0E-109	A1022328.1	EST_HUMAN	TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ; ow65a01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to
2628	15340	28085	3.98	1.0E-109	A1022328.1	EST_HUMAN	ow65a01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to
2629	15341	28086	2.07	1.0E-109	4504206	NT	TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ; Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3054	15820	28464	2.22	1.0E-109	N85100.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3383	16142	28799	3.14	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150410 NN0009 Homo sapiens cDNA
3383	16142	28800	3.14	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150410 NN0009 Homo sapiens cDNA
3508	16264	28918	1.21	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3548	16303	28953	0.9	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3548	16303	28954	0.9	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3823	16575	29357	2.59	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
3974	16723	29357	1.42	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
3974	16723	29358	1.42	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
4127	16869	29497	3.88	1.0E-109	AI855417.1	EST_HUMAN	Is98606.x1 NCJ_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 CE16100 :
4141	16883	29512	1.02	1.0E-109	AA862274.1	EST_HUMAN	nu93c12.e1 NCJ_CGAP_P722 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN P30712 GLUTATHIONE S-TRANSFERASE THETA 2 :
4141	16883	29513	1.02	1.0E-109	AA862274.1	EST_HUMAN	nu93c12.e1 NCJ_CGAP_P722 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN P30712 GLUTATHIONE S-TRANSFERASE THETA 2 :
4371	17109	29744	2.48	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4561	17296	29923	1.69	1.0E-109	7662083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
4867	17595	30218	1.27	1.0E-109	R15400.1	EST_HUMAN	y448e08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53057 5'
4992	17715	30320	1.39	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
4992	17715	30321	1.39	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
5167	17976	30534	0.81	1.0E-109	AU137282.1	EST_HUMAN	AU137282 PLACE1 Homo sapiens cDNA clone PLACE1008159 5'
5179	17988	30503	1.06	1.0E-109	BF073718.1	EST_HUMAN	602136446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'

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5230	18036	30662	3.09	1.0E-109	5174622	NT	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
5520	18318		1.11	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-404 HT0615 Homo sapiens cDNA
5838	25078	31560	0.64	1.0E-109	BF379688.1	EST_HUMAN	CM1-UT0038-060900-399-h07 UT0038 Homo sapiens cDNA
5907	18318		1.6	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-404 HT0615 Homo sapiens cDNA
7140	19827	32896	0.97	1.0E-109	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7464	20138	33230	3.99	1.0E-109	11432674	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7466	20140	33232	5.28	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
7466	20140	33233	5.28	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
7674	20338	33451	0.67	1.0E-109	BE263297.1	EST_HUMAN	601145017F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160229 5'
8073	20767	33896	1.48	1.0E-109	AL049784.1	NT	Novel human gene mapping to chromosome 13
8183	20877	34014	0.89	1.0E-109	AW749130.1	EST_HUMAN	PM0-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA
8555	21247		2.77	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
8633	21325	34466	8.42	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8633	21325	34467	8.42	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8878	21567	34711	0.56	1.0E-109	BE145672.1	EST_HUMAN	IL0-HT0205-071199-142-g01 HT0205 Homo sapiens cDNA
9137	21825	34990	1.91	1.0E-109	H84860.1	EST_HUMAN	Ys90g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP-A53491
9250	21929	35101	0.63	1.0E-109	BE397088.1	EST_HUMAN	A53491 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER - SPINY ;
9250	21929	35102	0.63	1.0E-109	BE397088.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9384	22046	35218	2.64	1.0E-109	F06804.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
10673	23364	36806	1.71	1.0E-109	BE540909.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
10673	23364	36607	1.71	1.0E-109	BE540908.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
10710	23369	36638	15.79	1.0E-109	BF694631.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
10888	23568	36818	1.55	1.0E-109	7662279	NT	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
10888	23568	36819	1.55	1.0E-109	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
11069	23739	37013	1.8	1.0E-109	AU121370.1	EST_HUMAN	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
11342	24032	37336	2.72	1.0E-109	4502838	NT	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'
11383	23990	37291	11.6	1.0E-109	W16510.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
11685	24280	37602	1.46	1.0E-109	11418618	NT	zb08b12.r1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to
11848	24432	37773	1.27	1.0E-109	BF339540.1	EST_HUMAN	PIR:S43989 S43989 p54-beta stress-activated protein kinases - rat ;
11848	24432	37774	1.27	1.0E-109	BF339540.1	EST_HUMAN	Homo sapiens single-minded (Drosophila) homolog 1 (SIM1), mRNA
12112	14976	27714	2.1	1.0E-109	Y17123.1	NT	602039003F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186753 5'
12328	14976	27714	2.73	1.0E-109	Y17123.1	NT	602039003F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186753 5'
							Homo sapiens SNF5/INI1 gene, exon 6
							Homo sapiens SNF5/INI1 gene, exon 6

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12443	24813	31047	2.08	1.0E-109	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3	12831	25444	1.85	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
36	12884	25482	4.71	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
36	12884	25483	4.71	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
79	12905	25543	0.7	1.0E-110	C04498.1	EST_HUMAN	C04498 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC3467
107	12831	25444	2.26	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
514	13298	25930	1.54	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1157	13912	26575	0.8	1.0E-110	5031820	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1258	14005	26674	0.8	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1914	14651	27361	1.19	1.0E-110	BE379477.1	EST_HUMAN	801237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3089683 5'
2051	14784		1.6	1.0E-110	BF508896.1	EST_HUMAN	UIH-B14-aos-b-05-0-UI-s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2845	15613		1	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3189	15952	28603	1.49	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3189	15952	28604	1.49	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4031	16776	29407	1.09	1.0E-110	BE018556.1	EST_HUMAN	5582a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR:O60312 O60312 KIAA0566 PROTEIN ;
4591	17326	29951	2.14	1.0E-110	A017213.1	EST_HUMAN	au32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to
4606	17341	29972	3.9	1.0E-110	AU117812.1	EST_HUMAN	SW.N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4916	17644		2.7	1.0E-110	7682441	NT	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5212	18020	30642	2.63	1.0E-110	BE209406.1	EST_HUMAN	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5639	18434	31347	0.8	1.0E-110	BE621069.1	EST_HUMAN	801118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
5656	18451	31364	8.61	1.0E-110	11419323	NT	801493677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895795 5'
5656	18451	31365	8.61	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6817	25096	32395	8.08	1.0E-110	M55112.1	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
7002	19694	32746	0.8	1.0E-110	U08888.1	NT	Human cytochrome oxidase subunit II (COX2) gene, exon 2
7002	19694	32747	0.8	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7224	19909	32983	0.74	1.0E-110	A1560288.1	EST_HUMAN	tn12808.x1 NCL_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN
7325	20008	33085	6.9	1.0E-110	AV714276.1	EST_HUMAN	P50549 ETS TRANSLOCATION VARIANT 1 ;
7325	20008	33086	6.9	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCE01 5'
7355	20036	33114	3.21	1.0E-110	AB020875.1	NT	AV714278 DCB Homo sapiens cDNA clone DCBCE01 5'
7469	20143	33235	0.83	1.0E-110	AU137823.1	EST_HUMAN	Homo sapiens mRNA for KIAA0868 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9234	21913	35087	7.88	1.0E-110	BE302594.1	EST_HUMAN	ba68101.yt NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905561 5' similar to TR:077258 077258
9476	22129	35308	2.39	1.0E-110	AW808394.1	EST_HUMAN	EG:114D9.2 PROTEIN. ;
10221	22869	36081	3.45	1.0E-110	11432732	NT	QV2-LT0053-020400-119-e04 LT0053 Homo sapiens cDNA
10648	23339	36578	3.64	1.0E-110	Y12337.1	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
10887	23567	36816	3.75	1.0E-110	BE734357.1	EST_HUMAN	H. sapiens mRNA for myoblastic dystrophy protein kinase like protein
10887	23567	36817	3.75	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
							601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
							zw67g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816
							G1145816 FKBP54 ;
11420	23187	36418	2.45	1.0E-110	AA446529.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
11939	24496		4.54	1.0E-110	BE897218.1	EST_HUMAN	IL0-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
12061	24578		11.71	1.0E-110	AW062258.1	EST_HUMAN	Homo sapiens gene for AF-6, complete cds
12290	24720		1.44	1.0E-110	AB011399.1	NT	qc31c12.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:1711222 3'
12346	24753		1.35	1.0E-110	AI127761.1	EST_HUMAN	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA
12429	25339		3.25	1.0E-110	BF364548.1	EST_HUMAN	UIH-BI4-aos-b-05-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
12701	14784		1.45	1.0E-110	BF508896.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
170	12983		10.84	1.0E-111	U43701.1	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
191	13004	25645	1.05	1.0E-111	4758907	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
718	13492		2.38	1.0E-111	BF035327.1	EST_HUMAN	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
726	13500	26154	5.13	1.0E-111	8393092	NT	Homo sapiens cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
906	13673	26338	3.82	1.0E-111	M25142.1	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
1624	14371	27060	1.43	1.0E-111	7682177	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
2234	14962	27701	1.02	1.0E-111	AF036126.1	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4150	18892	29522	1.08	1.0E-111	K02288.1	NT	Human enkephalin B (enkeB) gene, exon 4 and 3' flank and complete cds
4295	17034	29682	4.38	1.0E-111	K02288.1	NT	Homo sapiens phosphotyrosine kinase, alpha 1 (muscle) (PHKA1), mRNA
4691	17425	30057	8.36	1.0E-111	4505778	NT	601443360F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3847655 5'
5544	18341	31249	1.09	1.0E-111	BE867808.1	EST_HUMAN	qp09g12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1817574 3' similar to gb:M28893 RAS-RELATED PROTEIN RAL-A (HUMAN);
5942	18724	31683	1.98	1.0E-111	A1344678.1	EST_HUMAN	RELATD PROTEIN RAL-A (HUMAN);
6580	19543	32357	1.16	1.0E-111	AL040782.1	EST_HUMAN	DKFZp434C1815_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1815 5'
6708	19624	32668	1.06	1.0E-111	AW294848.1	EST_HUMAN	UI-H-BW0-eil-d-03-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729525 3'
7347	20028	33104	2.98	1.0E-111	BF368228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
							wf68d01.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813
7433	20110	33188	0.92	1.0E-111	A1761228.1	EST_HUMAN	CYTOCHROME P450 11A5 (HUMAN);

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7514	20185	33279	0.6	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
7993	20688	33815	0.73	1.0E-111	AA278888.1	EST_HUMAN	zs79g03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
7993	20688	33816	0.73	1.0E-111	AA278888.1	EST_HUMAN	zs79g03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
8088	20832	33912	0.62	1.0E-111	11431896	NT	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
8139	20783	33967	3.28	1.0E-111	U66533.1	NT	zs79g03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
8579	21271	34409	0.78	1.0E-111	11420516	NT	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
8674	21366	34513	0.73	1.0E-111	AK024453.1	NT	Homo sapiens protein x 0001 (LOC51185), mRNA
8707	21399		1.57	1.0E-111	AF177987.1	NT	Homo sapiens beta4-integrin (ITGB4) gene, exon 13
8708	21400		8.65	1.0E-111	BF214002.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8782	21474	34620	12.9	1.0E-111	X17033.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
8782	21474	34621	12.9	1.0E-111	X17033.1	NT	Homo sapiens mRNA for integrin alpha-2 subunit
8986	21676	34825	2.8	1.0E-111	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9217	21896	35066	0.49	1.0E-111	BF333210.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:U09235
10052	22700	35917	3.21	1.0E-111	AA504160.1	EST_HUMAN	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10080	22728		2.4	1.0E-111	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10172	22820	36038	5.24	1.0E-111	AA131248.1	EST_HUMAN	z31f01.r1 Soares, pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10973	23849	36802	4.25	1.0E-111	U68159.1	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
11465	24068	37376	2.74	1.0E-111	AU751071.1	EST_HUMAN	cn07a11.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn07a11 random
11897	24464	37802	3.72	1.0E-111	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12424	24800	37040	1.51	1.0E-111	AV708482.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCA0808 5'
12672	17914	30699	1.56	1.0E-111	AB035366.1	NT	Homo sapiens mRNA for neurixin F-alpha protein, complete cds
594	13372	26001	1.29	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
596	13374	26003	12.55	1.0E-112	U29103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
596	13374	26004	12.55	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
617	13395	26029	1.86	1.0E-112	BF509039.1	EST_HUMAN	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
617	13395	26030	1.86	1.0E-112	BF509039.1	EST_HUMAN	UIH-B14-act-g-04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
981	13746	26408	8.84	1.0E-112	AF157623.1	NT	UIH-B14-act-g-04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1040	13800	26458	2.2	1.0E-112	P52742	SWISSPROT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
							ZINC FINGER PROTEIN 135

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1679	14423	27117	4.39	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1679	14423	27118	4.39	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2194	14923	27857	1.37	1.0E-112	A1766925.1	EST_HUMAN	w90906.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400611 3'
2512	15229	27969	1.1	1.0E-112	BE866859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3078	15942		1.15	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3355	16115	28770	0.7	1.0E-112	A1826511.1	EST_HUMAN	wk45b12.x1 NCI_CGAP_P222 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81650_mna1
3864	16614	29253	0.74	1.0E-112	BE076073.1	EST_HUMAN	SEMN0GELIN 1 PROTEIN PRECURSOR (HUMAN);
4565	17300	29927	1.39	1.0E-112	4504116	NT	MR2-BT0590-090300-113-109 BT0590 Homo sapiens cDNA
4704	17437	30068	4.9	1.0E-112	AB037832.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4704	17437	30069	4.9	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5581	18378	31291	40.71	1.0E-112	N46046.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
5985	18766	31730	1.04	1.0E-112	AF149773.1	NT	y35d07.1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:273229 5'
6155	18932	31899	1.43	1.0E-112	BE741066.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6369	19138	32134	0.68	1.0E-112	BF672815.1	EST_HUMAN	601594717F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
6539	19304	32308	0.71	1.0E-112	BE273103.1	EST_HUMAN	602152649F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4268420 5'
6539	19304	32309	0.71	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6741	19575	32607	1.13	1.0E-112	BF574235.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
7236	19921	32995	1.97	1.0E-112	11416777	NT	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7236	19921	32996	1.97	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7729	25120	33507	0.56	1.0E-112	BF213358.1	EST_HUMAN	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8063	20787	33919	1.73	1.0E-112	AU118051	EST_HUMAN	601845089F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070302 5'
8856	21547	34694	2.09	1.0E-112	BE867635.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone IMAGE:1002773 5'
8856	21547	34695	2.09	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9793	22444	35949	2.15	1.0E-112	BF111413.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
10677	23368	36611	2.86	1.0E-112	AJ249900.1	NT	780907.x1 Soares NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to
10968	23548	36796	3.37	1.0E-112	AJ249900.1	NT	TR:Q9VW35 Q9VW35 CG8743 PROTEIN ;
11040	23711	36981	1.92	1.0E-112	BE280479.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
11109	23711	37053	1.59	1.0E-112	AJ249900.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
							Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
							601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3198989 5'
							qk24c08.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868902 5' similar to TR:Q64362 Q64362
							FUSED TOES ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11108	23779	37054	1.59	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES:
11139	23806	37085	6.6	1.0E-112	AW377870.1	EST_HUMAN	PMO-C10237-141099-001-h02 C10237 Homo sapiens cDNA
11810	24399	37734	1.92	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES:
11810	24399	37735	1.92	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES:
725	13499	26152	5.37	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
725	13499	26153	5.37	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
921	13688	26352	7.99	1.0E-113	M11965.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1532	14279	26966	2.66	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1932	15524	27382	1.44	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2088	14820	27551	1.02	1.0E-113	BF515218.1	EST_HUMAN	UI-H-BW1-ant-f03-Q-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
2456	15174	27913	28.34	1.0E-113	AJ006976.1	NT	Homo sapiens PLP gene
3127	15892	28536	1.92	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
4986	17691	30300	0.91	1.0E-113	D85606.1	NT	Homo sapiens gene for cholesterylkin type-A receptor, complete cds
6008	17731	30335	2.16	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5008	17731	30336	2.16	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5165	25178	30909	2.97	1.0E-113	BE780858.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5405	18205	30909	7.66	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
5832	18821	31554	4.17	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
5861	18848	31589	1.47	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
5979	18761	31725	2.62	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
6064	18843	31806	0.88	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6064	18843	31807	0.88	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6224	18998	31974	0.8	1.0E-113	8006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6224	18998	31975	0.8	1.0E-113	8006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7221	19008	32979	0.78	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
7221	19008	32980	0.78	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
7573	20242	33347	0.56	1.0E-113	AW958960.1	EST_HUMAN	EST137030 IMAGE resequences, IMAGE Homo sapiens cDNA
8790	21482	34629	0.46	1.0E-113	8922819	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8992	21692	34830	3.06	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
8992	21692	34831	3.06	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9301	21968		0.93	1.0E-113	BE772967.1	EST_HUMAN	RC1-F10134-280600-021-002 F10134 Homo sapiens cDNA
9730	22381	35583	1.4	1.0E-113	11428367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
9830	22481	35683	0.45	1.0E-113	M21535.1	NT	Human erg protein (ets-related gene) mRNA, complete cds
9950	22598	35802	0.81	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9950	22598	35803	0.81	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10514	23160	36386	0.61	1.0E-113	AW500517.1	EST_HUMAN	U1-HF-BNO-ek4-b-10-O-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077322 5'
10515	23161	36387	0.55	1.0E-113	BF691687.1	EST_HUMAN	602247740F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333280 5'
10515	23161	36388	0.55	1.0E-113	BF691687.1	EST_HUMAN	602247740F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333280 5'
11067	23737	37011	1.83	1.0E-113	AW500519.1	EST_HUMAN	U1-HF-BNO-ek4-b-12-O-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
11076	23746	37019	2.84	1.0E-113	AW630291.1	EST_HUMAN	h181a09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN
11076	23746	37020	2.84	1.0E-113	AW630291.1	EST_HUMAN	h181a09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN
11181	18998	31974	1.39	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11181	18998	31975	1.39	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11227	23890	37177	2.81	1.0E-113	BE292968.1	EST_HUMAN	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988366 5'
11481	24082	37393	1.32	1.0E-113	AA580720.1	EST_HUMAN	nc80b03.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN
11481	24082	37394	1.32	1.0E-113	AA580720.1	EST_HUMAN	P39748 FLAP ENDONUCLEASE-1 ; nc80b03.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1 ;
630	13409	26045	6.8	1.0E-114	T70551.1	EST_HUMAN	y15c01.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1049	13808	26468	1.7	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1290	14039	26712	5.09	1.0E-114	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1667	14413	27104	4.27	1.0E-114	6679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2807	12871	25491	1.28	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2807	12871	25492	1.28	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3128	15893	26537	2.75	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3169	15932	26581	1.02	1.0E-114	BF206374.1	EST_HUMAN	60186932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3997	16745	29377	2.61	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4358	17096	29731	0.72	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rcc) mRNA, complete cds

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5064	17783	30400	1.05	1.0E-114	BE275324.1	EST_HUMAN	601122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346099 5'
5315	18119	30775	1.28	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMASA) mRNA
5315	18119	30775	1.26	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMASA) mRNA
5508	18308	31207	0.97	1.0E-114	9257201	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA
6134	18912	31881	0.64	1.0E-114	Z26288.1	NT	H. sapiens isoform 1 gene for L-type calcium channel, exon 20
6898	17974	30531	0.62	1.0E-114	4759163	NT	Homo sapiens speractin, cdcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6977	19458		0.95	1.0E-114	AB041533.1	NT	Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds
7139	19826	32894	1.02	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7139	19826	32895	1.02	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7182	19868	32941	8.3	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7182	19868	32942	8.3	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7792	20487	33610	2.62	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8087	20761	33889	1.92	1.0E-114	A1363139.1	EST_HUMAN	qy68406.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8087	20761	33890	1.92	1.0E-114	A1363139.1	EST_HUMAN	qy68406.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8602	21294	34437	3.81	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
8665	21357	34505	6.93	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8665	21357	34506	6.93	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9081	21770	34833	0.49	1.0E-114	BF109832.1	EST_HUMAN	766g12.x1 Socius NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to TR:Q8UHN6 Q8UHN6 TRANSMEMBRANE PROTEIN 2 ;
9314	21981		6.83	1.0E-114	AW327455.1	EST_HUMAN	dq33f05.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9363	20433	33555	2.8	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
9448	22125		1.03	1.0E-114	MT1358.1	NT	Human ceruloplasmin mRNA
10039	22687	35905	1.08	1.0E-114	BE870004.1	EST_HUMAN	601449752F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10081	22709	35927	1.5	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10439	23085	36313	0.7	1.0E-114	BE171984.1	EST_HUMAN	MRO-HT0559-250200-002-407 HT0559 Homo sapiens cDNA
							be73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
10887	23378		3.15	1.0E-114	BE302666.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10789	23472	38714	1.71	1.0E-114	AF223391.1	NT	

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10789	23472	36715	1.71	1.0E-114	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11145	23812	37094	3	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cDNA Homo sapiens cDNA clone cdABA08 5'
11145	23812	37095	3	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cDNA Homo sapiens cDNA clone cdABA08 5'
11796	24386	37719	1.7	1.0E-114	4758673	NT	Homo sapiens LIM HOX gene 2 (LHX2) mRNA
11834	24418	37759	1.32	1.0E-114	11526317	NT	Homo sapiens diaphrin, heavy polypeptide-like 1 (CLTCL1), mRNA
12334	25402		3.42	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12577	24902		4.93	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12577	24902	30998	4.93	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
21	12849	25464	2.89	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
127	12942	25585	2.03	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A) mRNA
131	12946		2.33	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
286	13092	25733	2.23	1.0E-115	AW804759.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
523	13307	25939	0.99	1.0E-115	AI339206.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
623	13307	25940	0.99	1.0E-115	AI339206.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
769	13541	26201	1.36	1.0E-115	5174702	NT	q0601.x1 NCL CGAP GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536
769	13541	26202	1.36	1.0E-115	5174702	NT	TTF-1 INTERACTING PEPTIDE 5:
771	13543	26204	40.4	1.0E-115	4503794	NT	TTF-1 INTERACTING PEPTIDE 5:
1552	14298	26985	1.28	1.0E-115	AF229180.1	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
1552	14298	26986	1.28	1.0E-115	AF229180.1	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
1833	14572	27285	1.01	1.0E-115	U78027.1	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
2078	14810	27541	0.96	1.0E-115	AB007902.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
2298	15023	27758	2.13	1.0E-115	AF231124.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
2855	15623		1.39	1.0E-115	AW804759.1	EST_HUMAN	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
3113	15878	28518	6.22	1.0E-115	AJ245922.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3113	15878	28519	6.22	1.0E-115	AJ245922.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
3465	16221	28875	1.6	1.0E-115	AJ277892.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
4021	16767	29397	3.87	1.0E-115	AB002348.2	NT	Homo sapiens lesfican-1 mRNA, complete cds
4369	17107	29742	3.27	1.0E-115	6912659	NT	Homo sapiens lesfican-1 mRNA, complete cds
4403	17140	29768	3.6	1.0E-115	4758279	NT	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
4628	17363	29996	2.84	1.0E-115	AL096857.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
						NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
						NT	Homo sapiens partial TTN gene for titin
						NT	Homo sapiens partial TTN gene for titin
						NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
						NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
						NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
						NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
						NT	Homo sapiens EPHA4 (EPHA4) mRNA
						NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

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4628	17363	29997	2.64	1.0E-115	AL098957.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4848	17578	30201	3.51	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4848	17578	30202	3.51	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5263	18069	30698	1.62	1.0E-115	AW970335.1	EST_HUMAN	EST382416 MAGE resequences, MAGK Homo sapiens cDNA
5338	18141	30802	0.78	1.0E-115	BF686387.1	EST_HUMAN	602119346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276738 5'
5454	18253	31143	1.96	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5454	18253	31144	1.96	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5604	18400	31313	1.34	1.0E-115	AI928799.1	EST_HUMAN	eu64q01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb.L07807
5604	18400	31314	1.34	1.0E-115	AI928799.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
6168	18945	31916	0.97	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6168	18945	31917	0.97	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6302	19075	32061	8.84	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA
6434	19202	32198	2.04	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6434	19202	32199	2.04	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6835	19497	32521	0.83	1.0E-115	T86774.1	EST_HUMAN	y48608.11 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to
7178	19864	32935	1.54	1.0E-115	AI076598.1	EST_HUMAN	SP-DPOG_YEAST P15801 DNA POLYMERASE GAMMA ;
7178	19864	32936	1.54	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7308	19991	33068	8.22	1.0E-115	AB023212.1	NT	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
8060	20754	33885	13.71	1.0E-115	BE830187.1	EST_HUMAN	Homo sapiens mRNA for KIAA0995 protein, partial cds
8060	20754	33886	13.71	1.0E-115	BE830187.1	EST_HUMAN	RC8-E10081-130700-011-G01 ET0081 Homo sapiens cDNA
8712	21404	34548	2.15	1.0E-115	11434772	NT	RC8-E10081-130700-011-G01 ET0081 Homo sapiens cDNA
9675	22327	35522	0.6	1.0E-115	BF382029.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
9899	22549	35743	2.25	1.0E-115	AB002336.1	NT	601816332F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050108 5'
9899	22549	35744	2.25	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10418	23064	36284	1	1.0E-115	AI221878.1	EST_HUMAN	Human mRNA for KIAA0338 gene, partial cds
10418	23064	36285	1	1.0E-115	AI221878.1	EST_HUMAN	qg98e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10426	23072	36293	0.82	1.0E-115	AI624687.1	EST_HUMAN	qg98e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10617	23310	36549	7.62	1.0E-115	AW571544.1	EST_HUMAN	tt12a07.x1 NCL_CGAP_CL1 Homo sapiens cDNA clone IMAGE:2118036 3' similar to TR:O16129 O16129
10869	23549	36797	1.33	1.0E-115	9910279	NT	PHENYLALANINE TRNA SYNTHETASE ;
							xx32708.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA
							P10463 CALYPHOSINE ;
							Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA

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11225	23888	37174	1.54	1.0E-115	BE045890.1	EST_HUMAN	h954c10.x1 NCI_CGAP_Par3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378 PRP4 PROTEIN KINASE HOMOLOG ;
11225	23888	37175	1.54	1.0E-115	BE045890.1	EST_HUMAN	h954c10.x1 NCI_CGAP_Par3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378 PRP4 PROTEIN KINASE HOMOLOG ;
11374	23981	37281	2.27	1.0E-115	4502528	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
11775	24366	37699	2.53	1.0E-115	BE255549.1	EST_HUMAN	601111744F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352379 5'
11842	24426	37767	1.63	1.0E-115	AW884375.1	EST_HUMAN	QV3-OT0065-290300-137-h12 OT0065 Homo sapiens cDNA
11920	24481		2.16	1.0E-115	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
559	13341	25069	1.98	1.0E-116	BE275502.1	EST_HUMAN	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988875 5'
783	13555	26216	2.21	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
839	13609		1.76	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1990	14726	27447	2.55	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
1990	14726	27448	2.55	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
2090	15585	27552	2.6	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2090	15585	27553	2.6	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2305	15030	27767	1.95	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2340	15063		1.36	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo olfr17-01 (OR17-01) pseudogene, complete cds
2458	15176	27915	2.84	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2738	15533	28183	1.53	1.0E-116	BE889256.1	EST_HUMAN	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3171	15934	28582	4.87	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3171	15934	28583	4.87	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4345	17084	29713	2.43	1.0E-116	5031854	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4803	17534	30156	1.57	1.0E-116	A1907096.1	EST_HUMAN	PM-BT135-070496-016 BT135 Homo sapiens cDNA
5197	18005	30627	0.87	1.0E-116	A302062.1	EST_HUMAN	q119d04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898695 3' similar to contains element MER25 repetitive element ;
5889	18674	31619	4.4	1.0E-116	W42822.1	EST_HUMAN	zc24d07.r1 Scores_senescent_fibroblasts_NHISF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
6117	18895	31862	1.8	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
6117	18895	31863	1.8	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
6184	18931	31934	0.78	1.0E-116	BE408097.1	EST_HUMAN	601302281F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636764 5'
6421	19189		1.55	1.0E-116	BE158133.1	EST_HUMAN	MR2-HT0379-210200-102-504 HT0379 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6844	19544	32572	1.19	1.0E-116	C02944.1	EST_HUMAN	C02944 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHCO567
7102	19790	32855	5.74	1.0E-116	AV716314.1	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCBBG06 5'
8267	20961	34101	1.37	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
8267	20961	34102	1.37	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
8376	21071	34209	0.98	1.0E-116	AI904151.1	EST_HUMAN	CM-BT043-090299-075 BT043 Homo sapiens cDNA
8836	21528	34874	1.66	1.0E-116	BE565507.1	EST_HUMAN	601338268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680680 5'
8997	21687	34837	1.81	1.0E-116	AI216352.1	EST_HUMAN	qf09c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3680680 5'
9573	22226	35411	1.52	1.0E-116	11418846	NT	gb-X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
10170	22818	36036	0.74	1.0E-116	AJ277441.1	NT	Homo sapiens laminin, alpha 2 (merotin, congenital muscular dystrophy) (LAMA2), mRNA
10170	22818	36037	0.74	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10246	22894	36104	0.78	1.0E-116	BE158913.1	EST_HUMAN	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10586	23281	36519	2.4	1.0E-116	BF335849.1	EST_HUMAN	QV4-HT0401-281299-063-c09 HT0401 Homo sapiens cDNA
11080	23750	37025	2.85	1.0E-116	AI367140.1	EST_HUMAN	CM2-CT0482-300800-349-e06 CT0482 Homo sapiens cDNA
12625	25267		1.86	1.0E-116	AL134889.1	EST_HUMAN	qq41e04.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:B0495.7
545	13328	25959	1.67	1.0E-117	4826836	NT	CE01765:
1055	15559	26474	0.96	1.0E-117	AF124393.1	NT	DKFZp762L1110_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762L1110 5'
1747	14489	27188	1.02	1.0E-117	AF123320.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1823	14562	27274	1.51	1.0E-117	M19816.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1) gene, exons 13a through 15
2208	14936	27674	1.54	1.0E-117	AW957699.1	EST_HUMAN	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
3262	16024	28874	1.64	1.0E-117	AA978114.1	EST_HUMAN	Human apolipoprotein B-100 (apoB) gene, exon 10
3971	16720	29355	2.1	1.0E-117	AA316723.1	EST_HUMAN	EST369769 MAGE resequences, MAGE Homo sapiens cDNA
4310	17049	29674	2.03	1.0E-117	8659554	NT	op32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
4538	17273	29905	2.95	1.0E-117	AL042120.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4674	17408	30043	1.27	1.0E-117	X89670.1	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4674	17408	30044	1.27	1.0E-117	X89670.1	NT	DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4759	17491	30119	10.03	1.0E-117	AF134304.2	NT	H. sapiens mRNA for TPCR16 protein
4759	17491	30120	10.03	1.0E-117	AF134304.2	NT	H. sapiens mRNA for TPCR16 protein
4887	17614	30233	3.57	1.0E-117	AB020673.1	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
5136	17854	30471	0.73	1.0E-117	6912461	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
5284	18070	30689	3.01	1.0E-117	BE730508.1	EST_HUMAN	Homo sapiens mRNA for KIAA0866 protein, complete cds
							Homo sapiens atrophin-1 interacting protein 1; actin receptor interacting protein 1 (KIAA0705), mRNA
							601562657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'

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6860	17937	30574	0.86	1.0E-117	AA323348.1	EST_HUMAN	EST28111 Cerebellum II Homo sapiens cDNA 5' end similar to zinc finger domain
7350	20031	33108	5.01	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7350	20031	33109	5.01	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7446	20122	33212	1.75	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
7446	20122	33213	1.75	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
							wp8607.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2468628 3' similar to TR.O75065
							O75065 KIAA0477 PROTEIN. ;
7878	20573	33699	3.38	1.0E-117	A950145.1	EST_HUMAN	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8210	20904	34039	2.29	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8210	20904	34040	2.29	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8310	21004	34141	0.56	1.0E-117	A1904151.1	EST_HUMAN	GM-BT043-090299-075 BT043 Homo sapiens cDNA
8310	21004	34142	0.56	1.0E-117	A1904151.1	EST_HUMAN	GM-BT043-090299-075 BT043 Homo sapiens cDNA
8310	21004	34142	0.56	1.0E-117	A1904151.1	EST_HUMAN	Human gene for very low density lipoprotein receptor, exon 11
9199	21668	35033	2.25	1.0E-117	D16524.1	NT	601569317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5'
9686	22338	35532	2.07	1.0E-117	BE733922.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid type B receptor 2 (GABABR2) mRNA, complete cds
9846	25127	35697	2.9	1.0E-117	AF099033.1	NT	Homo sapiens Drosophila Kelch like protein (OKELCHL), mRNA
10469	23115	36345	1.11	1.0E-117	11420222	NT	Human mRNA for KIAA0181 gene, partial cds
10765	23449	36691	1.77	1.0E-117	D83778.1	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
10964	23640	36891	2.68	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
10964	23640	36892	2.68	1.0E-117	11424835	NT	Homo sapiens mRNA for MEGF8, partial cds
11243	23905	37196	3.32	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11243	23905	37197	3.32	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11369	23976	37501	14.73	1.0E-117	BE269856.1	EST_HUMAN	601186203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544286 5'
11587	24186	37502	2.02	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11587	24186	37502	2.02	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
68	12896	25530	5.98	1.0E-118	AF161500.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds
94	12920	25577	2.13	1.0E-118	AL045854.1	EST_HUMAN	DKFZp434I056_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I056 5'
504	13288	25922	5.67	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (D328E19.C1.1), mRNA
894	15555	26328	0.96	1.0E-118	5174680	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2227	14955	27693	2.04	1.0E-118	BE369705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2227	14955	27694	2.04	1.0E-118	BE369705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2227	14955	27694	2.04	1.0E-118	BE369705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2227	14955	27695	1.68	1.0E-118	AW951728.1	EST_HUMAN	EST363709 MAGC resequences, MAGB Homo sapiens cDNA
2329	15054	28189	2.61	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2744	15450	28190	2.61	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2744	15450	28190	2.61	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3102	15667		4.64	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7

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3190	15953	28605	4.67	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3190	15953	28606	4.67	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
4067	16811	29439	4.77	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
4659	17393	30028	0.9	1.0E-118	11425793	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
5337	18140	30800	1.87	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5337	18140	30801	1.87	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5543	18340	31247	0.94	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5543	18340	31248	0.94	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5684	18477	31395	1.24	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
5772	18563	31491	0.83	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5772	18563	31492	0.83	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31578	1.49	1.0E-118	11420764	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6592	19355	32368	1.44	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6592	19355	32369	1.44	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6997	19689	32738	1.12	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434O0127 5'
6997	19689	32739	1.12	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434O0127 5'
7500	20172	33264	5.63	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7733	20397	33512	0.86	1.0E-118	BF685272.1	EST_HUMAN	602141620F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302749 5'
7872	20567	33693	2.17	1.0E-118	BE781223.1	EST_HUMAN	601469159F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
8282	20976	34116	6.58	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8282	20976	34117	6.58	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8288	20982	34122	1.37	1.0E-118	AA443024.1	EST_HUMAN	z89d07_r1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8288	20982	34123	1.37	1.0E-118	AA443024.1	EST_HUMAN	z89d07_r1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8573	21265	34404	1.01	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8573	21265	34405	1.01	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8621	21313	34456	2.06	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8621	21313	34456	2.06	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8621	21313	34456	2.06	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8933	21624	34767	4.95	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
8933	21624	34767	4.95	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
8984	21655	34806	0.55	1.0E-118	AL048474.2	EST_HUMAN	DKFZp568K1824_r1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp568K1824
8984	21655	34806	0.55	1.0E-118	AL048474.2	EST_HUMAN	DKFZp568K1824_r1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp568K1824
9493	22146	35327	1.53	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (D1328E19 C1.1), mRNA
9493	22146	35327	1.53	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (D1328E19 C1.1), mRNA
9886	22538	35731	0.98	1.0E-118	AL138321.1	EST_HUMAN	DKFZp547O017_r1 547 (synonym: hbr1) Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW:ZP3A_HUMAN
10274	22922	36134	1.88	1.0E-118	BF195407.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR;

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10365	23012	36227	0.46	1.0E-118	AW271289.1	EST_HUMAN	xs46a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2772666 3' similar to
10431	23077	36300	0.65	1.0E-118	AW266351.1	EST_HUMAN	SW_BODG_HUMAN_075936 GAMMA-BUTYROBETAINE-2-OXOGLUTARATE DIOXYGENASE ;
11206	23869	37155	1.61	1.0E-118	BF685214.1	EST_HUMAN	U1-H-BW6-alo-a-07-QJ.s1 NCI_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2729772 3'
11236	23899	37188	1.8	1.0E-118	11055988	NT	602141529F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302798 5'
11246	23908	37201	10.23	1.0E-118	AA315007.1	EST_HUMAN	Homo sapiens protein with polyglutamine repeat: calcium (ca2+) homeostasis endoplasmic reticulum protein (ERROT213-21), mRNA
11548	24147	37457	1.68	1.0E-118	BE908676.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
11548	24147	37458	1.68	1.0E-118	BE908676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11551	24150	37461	1.81	1.0E-118	BF093687.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11551	24150	37462	1.61	1.0E-118	BF093687.1	EST_HUMAN	QV0-JM0091-120900-385-b12 UM0091 Homo sapiens cDNA
741	13514	26173	0.97	1.0E-119	AF170492.1	NT	QV0-JM0091-120900-385-b12 UM0091 Homo sapiens cDNA
1014	15558	26433	1.61	1.0E-119	7705607	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1926	14662	27374	5.97	1.0E-119	AB023147.1	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
3099	15864	28506	1.57	1.0E-119	8922205	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3234	15906		0.8	1.0E-119	AA916760.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3934	16684	29325	1.42	1.0E-119	4504116	NT	on10605.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2
5253	18059	30688	2.5	1.0E-119	AU133399.1	EST_HUMAN	CE01214 ;
5266	18072	30701	21.82	1.0E-119	M89914.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5270	18076	30706	3.11	1.0E-119	BE936121.1	EST_HUMAN	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001891 5'
5347	18150	30830	1.63	1.0E-119	AV693731.1	EST_HUMAN	Human neurofibromin (NF1) gene, complete cds
5503	18301	31201	0.63	1.0E-119	AL134903.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5503	18301	31202	0.63	1.0E-119	AL134903.1	EST_HUMAN	AV693731 GKC Homo sapiens cDNA clone GKCDH803 5'
6036	18816	31776	7.67	1.0E-119	AI150703.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
6190	18967	31940	0.92	1.0E-119	AF315683.1	NT	DKFZp762M0710_11 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6190	18967	31941	0.92	1.0E-119	AF315683.1	NT	DKFZp762M0710_11 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6239	19013	31987	0.85	1.0E-119	AI476732.1	EST_HUMAN	qb77c09.x1 Soares_fetal_heart_NH9119W Homo sapiens cDNA clone DKFZp762M0710 5'
6370	19139	32135	2.62	1.0E-119	X06292.1	NT	DKFZp762M0710_11 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6380	19149	32148	4.69	1.0E-119	AW974183.1	EST_HUMAN	SW_K1CJ_MOUSE_P02635 KERATIN, TYPE I CYTOSKELETAL 10 ;
7310	19993	33070	1.5	1.0E-119	BE786814.1	EST_HUMAN	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
8560	21262	34390	1.19	1.0E-119	BE615150.1	EST_HUMAN	hm23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9807	22458	35963	1.15	1.0E-119	11036643	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA
10006	22654	35967	0.55	1.0E-119	AI149796.1	EST_HUMAN	qf43a11.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1762764 3' similar to TR:Q13458
10146	22794	36008	3.35	1.0E-119	AA465124.1	EST_HUMAN	Q13458 GUANINE NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO. ;
10401	23047	36263	1.29	1.0E-119	AJ297701.1	NT	as3205.r1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
10443	23089	36317	0.71	1.0E-119	11425837	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10443	23089	36318	0.71	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10517	23163	36390	4.16	1.0E-119	AB032261.1	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10985	23660	36913	2.38	1.0E-119	AJ297701.1	NT	Homo sapiens Scl mRNA for stearoyl-CoA desaturase, complete cds
10985	23660	36914	2.38	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11159	23826		6.31	1.0E-119	BF569571.1	EST_HUMAN	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
12198	25326		2.16	1.0E-119	AW847519.1	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
294	13100	25741	1.43	1.0E-120	4507334	NT	RC3-CT0212-240999-011-403 CT0212 Homo sapiens cDNA
1018	13778	26439	2.49	1.0E-120	AF248540.1	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1018	13778	26440	2.49	1.0E-120	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1405	14152	26832	2.31	1.0E-120	N44873.1	EST_HUMAN	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1597	14343	27033	3.08	1.0E-120	AF167706.1	NT	yy40g12.r1 Scores melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273766 5'
1799	14539	27250	1.21	1.0E-120	4557250	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2100	14831	27565	0.92	1.0E-120	AB011399.1	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2100	14831	27566	0.92	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2831	15247	27985	5.24	1.0E-120	4755124	NT	Homo sapiens gene for AF-6, complete cds
3302	13100	25741	1.59	1.0E-120	4507334	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA
4325	17064	29692	1.95	1.0E-120	AF059490.1	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4325	17064	29693	1.95	1.0E-120	AF059490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4614	17349	29983	2.22	1.0E-120	AF098463.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4614	17349	29984	2.22	1.0E-120	AF098463.1	NT	Homo sapiens stannocalcin (STC) gene, partial cds
5065	17784	30401	1.36	1.0E-120	4504116	NT	Homo sapiens stannocalcin (STC) gene, partial cds
5133	17851	30468	0.9	1.0E-120	AI190903.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5649	18444	31357	16.61	1.0E-120	BF568222.1	EST_HUMAN	q61f03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:173981 3'
5649	18444	31358	16.61	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6350	19120	32110	0.57	1.0E-120	M29428.1	NT	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6350	19120	32111	0.57	1.0E-120	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
7471	20144	33236	1.77	1.0E-120	D34619.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
7795	20480	33612	5.22	1.0E-120	Y00067.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
							Human gene for neurofilament subunit M (NF-M)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7795	20490	33613	5.22	1.0E-120	Y00097.1	NT	Human gene for neurofilament subunit M (NF-M)
8230	20924	34063	2.43	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCI_OGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183333 5'
8303	20997	34135	0.85	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8303	20997	34136	0.85	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8307	21001	34138	2.33	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8307	21001	34139	2.33	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8352	21045	34182	1.17	1.0E-120	AB007934.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds
9401	22063	35233	5.26	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9401	22063	35234	5.26	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9645	22297	35492	3.75	1.0E-120	BF306541.1	EST_HUMAN	601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
9660	22312	35510	8.25	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
9677	22329	35525	0.79	1.0E-120	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
9792	22443	35831	0.54	1.0E-120	AB04151.1	EST_HUMAN	GM-BT043-050299-075 BT043 Homo sapiens cDNA
9876	22624	35831	2.55	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11071	23741	37015	3.72	1.0E-120	BE296387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3332015 5'
11316	24007	37311	2.06	1.0E-120	BE887619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11316	24007	37312	2.06	1.0E-120	BE887619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11550	24247	37567	1.38	1.0E-120	U94774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
71	12898	25534	1.08	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
369	13165	25808	0.83	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLAGE1000899 5'
707	15549	28130	1.31	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1568	14315	27001	2.81	1.0E-121	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
1958	14894	27407	1.33	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
1958	14894	27408	1.33	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
1984	14700	27416	1.18	1.0E-121	M95968.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 9
1984	14700	27416	1.18	1.0E-121	M95968.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 9
2095	14826	27559	1.51	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
3079	15844	28486	3.51	1.0E-121	Y19208.1	NT	Homo sapiens h1b3 gene for hair keratin, exons 1 to 9
3079	15844	28487	3.51	1.0E-121	Y19208.1	NT	Homo sapiens h1b3 gene for hair keratin, exons 1 to 9
3525	16281	28936	1.19	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3525	16281	28937	1.19	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3688	16419	28060	7.35	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4296	17035	29663	2	1.0E-121	A1263294.1	EST_HUMAN	q57b01.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
4919	17647	30259	3.24	1.0E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)
5186	17994	30510	0.97	1.0E-121	BE222250.1	EST_HUMAN	h00908.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119 3'
5474	18273	31167	0.85	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6524	19290	32294	0.91	1.0E-121	M91463.1	NT	Human glucose transporter (GLUT4) gene, complete cds
6788	19532		0.88	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6866	17943	30537	1.78	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA
6866	17943	30538	1.78	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA
7838	20533	33660	2.11	1.0E-121	D84122.1	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
7842	20537	33664	2.45	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
7842	20537	33665	2.45	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
9758	22409	35615	1.21	1.0E-121	AW588858.1	EST_HUMAN	le05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
9758	22409	35616	1.21	1.0E-121	AW588858.1	EST_HUMAN	le05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
10675	23366	36609	2.95	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homodog, cytochrome c oxidase assembly protein (COX11), mRNA
10683	23374	36616	1.28	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
10889	23569	36820	3.48	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
10917	23597	36844	2.53	1.0E-121	N59824.1	EST_HUMAN	y74c01.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:248448 3'
11309	23988	37269	2.83	1.0E-121	AU119320.1	EST_HUMAN	AU119320 HEMBA1 Homo sapiens cDNA clone HEMBA1005538 5'
261	13069	25707	2.28	1.0E-122	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
327	13128	25763	2.63	1.0E-122	AF114498.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
348	13147	25787	2.14	1.0E-122	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
862	13631	26302	3.99	1.0E-122	AF114498.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1188	13950	26614	4.29	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1688	14432	27128	1.28	1.0E-122	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
1707	14450	27150	1.35	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1707	14450	27151	1.35	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1807	14547	27282	4.54	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898358 5'
2495	15212	27954	5.21	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'
2495	15212	27955	5.21	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2844	15612	28260	1.41	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4795	17526	30148	5.04	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nepril-II, Alzheimer disease) (APP), mRNA
4930	17658		1.46	1.0E-122	AW504645.1	EST_HUMAN	UHF-BNO-all-a-03-0-UI-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076948 5'
5476	18275	31170	1.36	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6658	18275	31170	7.1	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7113	19801	32865	0.73	1.0E-122	AA868871.1	EST_HUMAN	ak49h06 s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1409339 3'
8695	21387	34530	0.85	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
8926	21617	34761	1.21	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9223	21902	35073	1.19	1.0E-122	A1359618.1	EST_HUMAN	q42h07 x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;
9223	21902	35074	1.19	1.0E-122	A1359618.1	EST_HUMAN	q42h07 x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;
10034	22682	35899	1.05	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dcl (proto-oncogene)
10908	23588	36834	2.17	1.0E-122	AW955634.1	EST_HUMAN	EST367904 IMAGE resequences, MAGD Homo sapiens cDNA
11358	24046	37349	1.88	1.0E-122	AB024068.1	NT	Homo sapiens gene for B120, exon 10
11958	24509		6.6	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
751	13523	26181	1.74	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
751	13523	26182	1.74	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
992	13754	26415	5.4	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1001	13761	26422	2.5	1.0E-123	58031114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1216	13968	26834	5.58	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1216	13968	26835	5.58	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1438	14185	26871	0.91	1.0E-123	AJ388641.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02
2092	14823	27555	2.7	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2092	14823	27556	2.7	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2092	14823	27557	2.7	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2313	15038		3.82	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
3245	16007	28657	0.95	1.0E-123	6912617	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPCT), mRNA
5361	18163	30847	1.56	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (RALBP) gene, complete cds

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5361	18163	30948	1.56	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5494	18293	31191	1.62	1.0E-123	BE799746.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
6377	19146	32145	2.59	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
6905	19643	32688	1.2	1.0E-123	H53198.1	EST_HUMAN	y84a03.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP-YAK1 YEAST P14680 PROTEIN KINASE YAK1
6915	19652	32698	1.25	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7094	19783	32849	2.87	1.0E-123	U55258.1	NT	Human hBRAYONI-CAM precursor (hBRAYONI-CAM) gene, complete cds
7302	19985	33061	1.62	1.0E-123	11528833	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA
7542	20212	33312	1.3	1.0E-123	11436439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
7551	20221	33324	2.18	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509182 5'
7816	20511	33636	0.67	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
7816	20511	33637	0.67	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8433	21126		1.13	1.0E-123	AW371924.1	EST_HUMAN	RCA-BT0311-251189-012-q07 BT0311 Homo sapiens cDNA
9289	22023	35193	2.43	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9405	22067	35239	15.48	1.0E-123	U08823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefia2) mRNA, complete cds
11720	24314	37637	4.66	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
11720	24314	37638	4.66	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
262	13070	25708	2.19	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
262	13070	25709	2.19	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
268	13076		2.89	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
473	13259	25898	2.84	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C0046
675	13450	26092	2.68	1.0E-124	AA397551.1	EST_HUMAN	z81b04.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
675	13450	26093	2.68	1.0E-124	AA397551.1	EST_HUMAN	z81b04.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
742	13513	26174	7.84	1.0E-124	AF155654.1	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)
790	13562	26223	1.61	1.0E-124	4507500	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)
884	13683	26321	1.94	1.0E-124	7705448	NT	Human putative ribosomal protein S1 mRNA
1325	14074	26747	4.95	1.0E-124	AF274892.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1325	14074	26748	4.95	1.0E-124	AF274892.1	NT	Homo sapiens hypodermal protein (HSPC088), mRNA
1808	14548	27263	2.29	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2034	14786	27512	3.05	1.0E-124	BE879524.1	EST_HUMAN	Homo sapiens mRNA for nuclear RNA-helicase (ncl161 gene)
3368	16118	28774	0.85	1.0E-124	4504116	NT	601491715F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3893954 5'
							Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3482	16239	28895	1.25	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3482	16239	28896	1.25	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3840	16393	29033	1.54	1.0E-124	X13794.1	NT	H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS)
3880	16630	29269	1	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4056	16801	29432	1.34	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4696	17430	30061	1.94	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
4881	17608		1.13	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5215	18023	30847	12.12	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5586	18383	31293	0.92	1.0E-124	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
5797	18588	31514	6.94	1.0E-124	BF686135.1	EST_HUMAN	602124644F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
6077	18856	31823	0.91	1.0E-124	AV711283.1	EST_HUMAN	AV711283 Cu Homo sapiens cDNA clone CuaADF07 5'
6339	19109	32099	0.98	1.0E-124	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
6912	19649	32695	2.95	1.0E-124	Y11717.1	NT	Mimulus mRNAs for hoxa3 gene
7037	19729	32786	0.94	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966885 5'
7037	19729	32787	0.94	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966885 5'
7452	20128	33220	0.92	1.0E-124	AA630331.1	EST_HUMAN	ac08h05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:855897 3'
8156	20850	33982	8.07	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8382	21055	34195	1.26	1.0E-124	AW612108.1	EST_HUMAN	Hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162
8382	21055	34196	1.26	1.0E-124	AW612108.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
9060	21749	34907	0.61	1.0E-124	AI799864.1	EST_HUMAN	Hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162
9060	21749	34908	0.61	1.0E-124	AI799864.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
9390	22052	35223	2.31	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2321428 3'
9390	22052	35224	2.31	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2321428 3'
9477	22130	35309	0.52	1.0E-124	AF022655.1	NT	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9477	22130	35310	0.52	1.0E-124	AF022655.1	NT	Homo sapiens GLC Homo sapiens cDNA clone GLCACE04 3'
9508	22161	35342	7.57	1.0E-124	AI767133.1	EST_HUMAN	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
9508	22161	35343	7.57	1.0E-124	AI767133.1	EST_HUMAN	w63f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
9771	22422	35630	1.57	1.0E-124	AW503755.1	EST_HUMAN	w63f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
10804	23487		1.44	1.0E-124	11432087	NT	UI-HF-BND-alc-b-04-04J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'
10976	23652	36905	1.61	1.0E-124	U94778.1	NT	Homo sapiens leucine-rich, glioma inactivated 1 (LGI1), mRNA
11305	23964	37265	3.51	1.0E-124	AW665663.1	EST_HUMAN	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
							h105c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2880906 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11452	23219	38452	3	1.0E-124	AI448455.1	EST_HUMAN	YKRS PROTEIN.; YKRS PROTEIN.; YKRS PROTEIN.;
11452	23219	38453	3	1.0E-124	AI448455.1	EST_HUMAN	YKRS PROTEIN.; YKRS PROTEIN.; YKRS PROTEIN.;
12029	13450	26092	4.1	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
12029	13450	26093	4.1	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
12454	24823	31026	1.61	1.0E-124	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12706	25279	30729	1.44	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12706	25279	30730	1.44	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
146	12961	25603	1.74	1.0E-125	BE219510.1	EST_HUMAN	h559a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELIN IA;
146	12961	25604	1.74	1.0E-125	BE219510.1	EST_HUMAN	h559a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELIN IA;
311	13115	AB032998.1	5.49	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
417	12828	25441	5.47	1.0E-125	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926886 5'
629	13408	26043	1.18	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
629	13408	26044	1.18	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
711	13485	26134	1.56	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
840	13610	26280	2.29	1.0E-125	AA042813.1	EST_HUMAN	z453c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
978	13743	26405	1.22	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1131	13887	26545	1.76	1.0E-125	7662278	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1668	15575	27105	0.99	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1793	14533	27242	0.91	1.0E-125	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1804	14544	27258	1.59	1.0E-125	AF015450.1	NT	Homo sapiens Uterin-alpha mRNA, complete cds
1804	14544	27259	1.59	1.0E-125	AF015450.1	NT	Homo sapiens Uterin-alpha mRNA, complete cds
2358	15080	27816	1.68	1.0E-125	AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429588 5'
2508	15225	27967	0.99	1.0E-125	AA042813.1	EST_HUMAN	z453c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2604	15317	28057	1.3	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INH) mRNA
2604	15317	28058	1.3	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INH) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor		
3009	17874	28425	0.94	1.0E-125	BE018009.1	EST_HUMAN	bb7406.v1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:Q95604 Q95604 ZINC FINGER PROTEIN.;		
3839	16590	29228	0.92	1.0E-125	AA042813.1	EST_HUMAN	zf3c07.s1 Soares_pregnant_uterus_NH4PU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb-X65857.cd1 OLFATORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);		
4513	17248	29883	2.09	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA		
4513	17248	29884	2.09	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA		
4971	12961	25803	1.48	1.0E-125	BE219510.1	EST_HUMAN	hV69a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN IA;		
4971	12961	25804	1.48	1.0E-125	BE219510.1	EST_HUMAN	hV59a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN IA;		
5783	18574	31503	3.16	1.0E-125	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA		
5802	18592	31517	0.91	1.0E-125	BE175169.1	EST_HUMAN	QV2-HT06577-010500-165-p08 HT0577 Homo sapiens cDNA		
5842	18630	31555	3.76	1.0E-125	BE892660.1	EST_HUMAN	607433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'		
5884	18670	31611	0.74	1.0E-125	AI679904.1	EST_HUMAN	hU67c07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2268108 3' similar to WP:C45G9.2		
6188	18965	31938	0.8	1.0E-125	BE736055.1	EST_HUMAN	CE01854;		
6486	19253	32253	1.53	1.0E-125	BE562526.1	EST_HUMAN	6073055670F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'		
6488	19253	32254	1.53	1.0E-125	BE562526.1	EST_HUMAN	607335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'		
6961	19443	32459	5.26	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5		
6961	19443	32460	5.26	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5		
7706	20370	33483	0.55	1.0E-125	BE515100.1	EST_HUMAN	607236183F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608084 5'		
8444	21136	34273	0.99	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10		
8444	21136	34274	0.99	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10		
9016	21706	34856	6.83	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA		
9016	21706	34857	6.83	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA		
9281	22035	35207	0.96	1.0E-125	AI565996.1	EST_HUMAN	hU52b03.x1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089		
10350	22997	36215	0.53	1.0E-125	BE794576.1	EST_HUMAN	HYPOTHETICAL PROTEIN;		
10391	23037	36253	1.06	1.0E-125	AF043458.1	NT	607590345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944531 5'		
10581	23276	36514	3.23	1.0E-125	AF043458.1	NT	Human mRNA for KIAA0300 gene, partial cds		
10758	23443	36688	1.61	1.0E-125	11425570	NT	Homo sapiens LREL gene, exon 5		
14081	23761	37026	3.94	1.0E-125	AB014567.1	NT	Homo sapiens pyridine receptor 1 (skeletal) (RYR1), mRNA		
							Homo sapiens mRNA for KIAA0687 protein, partial cds		

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11269	23921	37213	1.74	1.0E-125	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11265	23927	37218	4.84	1.0E-125	AF026029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11377	23964	37284	1.92	1.0E-125	AW812899.1	EST_HUMAN	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
11488	24087	37397	3.58	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
11498	24087	37398	3.58	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
787	13529	26189	1.46	1.0E-126	4759007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
899	13667	26331	1.45	1.0E-126	X68735.1	NT	H. sapiens gene for alpha1-antitrypsin, exon 3
2344	15087	27804	1.17	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2344	15087	27805	1.17	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2605	15318	28059	1.48	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3069	15835		0.72	1.0E-126	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3070	15836	28479	7.54	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratiagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3070	15836	28480	7.54	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratiagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3620	16373	29014	1.09	1.0E-126	X53941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3647	16400	29040	1.8	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4783	17515	30137	1.74	1.0E-126	N34078.1	EST_HUMAN	YX78c06.r1 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:287850 5'
5078	17797	30413	0.81	1.0E-126	BE743922.1	EST_HUMAN	601577981F1 NIH MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
5616	18412	31325	0.68	1.0E-126	766998.1	EST_HUMAN	y62b12.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:66527 3'
6139	18917	31887	3.22	1.0E-126	AA460075.1	EST_HUMAN	z066e03.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796444 5' similar to
6197	18973	31949	4.2	1.0E-126	AB040958.1	NT	TR:G1145880 G1145880 TITIN;
6197	18973	31950	4.2	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7399	20077	33157	1.02	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7399	20077	33158	1.02	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7602	20268	33375	0.82	1.0E-126	AU138463.1	EST_HUMAN	AU136463 PLACE1 Homo sapiens cDNA clone IMAGE:1004325 5'
7855	20319	33428	0.69	1.0E-126	AB080483.1	EST_HUMAN	w0807.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350009 3' similar to
7778	20473	33596	0.76	1.0E-126	AB037715.1	NT	SW-MPP2_HUMAN Q14188 MAGUK P55 SUBFAMILY MEMBER 2;
7778	20473	33597	0.76	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
7887	20582	33711	2.55	1.0E-126	X16609.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
						NT	Human mRNA for ankyrin (variant 2.1)
8083	20777	33907	0.99	1.0E-126	AA483368.1	EST_HUMAN	ne74b12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:908983 similar to SW:TSG6_HUMAN
9695	22346	35539	0.87	1.0E-126	4506424	NT	P98068 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR;
						NT	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA

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10893	23384	36824	1.27	1.0E-126	M93198.1	NT	Human macrophage mannose receptor (MRC1) gene, exon 5
10766	23450	36892	2.36	1.0E-126	BF683175.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298240 5'
11501	24102	37414	5.47	1.0E-126	BE261660.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
12490	17797	30413	7.17	1.0E-126	BE743922.1	EST_HUMAN	801577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
168	12982	25622	4.63	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
168	12982	25623	4.63	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
169	12982	25622	4.71	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
169	12982	25623	4.71	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
267	13075	25716	3.54	1.0E-127	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
267	13075	25717	3.54	1.0E-127	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
861	13630	26301	2.03	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
898	13664	26330	1.37	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1886	14430	27128	1.08	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2058	14790	27515	2.44	1.0E-127	5803085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2058	14790	27515	2.44	1.0E-127	5803085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2197	14926	27661	6.02	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L28 (RPL28) mRNA
2341	15064	27801	2.73	1.0E-127	AF245505.1	NT	Homo sapiens edlican mRNA, complete cds
2614	15325	28068	3.04	1.0E-127	X12881.1	NT	Human mRNA for cyclotactin 18
2626	15338	28081	1.1	1.0E-127	AA450131.1	EST_HUMAN	z42a02.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
2626	15338	28082	1.1	1.0E-127	AA450131.1	EST_HUMAN	z42a02.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
							au80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to
							TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-I-RELATED PROTEIN ; contains element MER22 repetitive element ;
3791	18543	29178	1.21	1.0E-127	AW161297.1	EST_HUMAN	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4098	18638	29466	0.7	1.0E-127	AF135188.1	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4227	16968	29592	23.74	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4227	16968	29593	23.74	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4462	17198	29824	0.84	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAL-2 mRNA, complete cds
4564	17299	29928	4.35	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4590	17325		1.92	1.0E-127	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
4625	17360	29983	1.26	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5620	18416	31329	1.37	1.0E-127	W03547.1	EST_HUMAN	z01a10.1 Soares melanocyte 2Nbl1M Homo sapiens cDNA clone IMAGE:291258 5' similar to SW_PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 ;
5650	18445	31359	2.4	1.0E-127	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5713	18506	31428	4.25	1.0E-127	X85764.1	NT	H.sapiens NOS2 gene, exon 6
6070	18849	31813	2.17	1.0E-127	X84060.1	NT	H.sapiens TCF11 gene, exon 3-6
6229	19003	31979	5.28	1.0E-127	4504778	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
6560	19325	32332	0.89	1.0E-127	11421595	NT	Homo sapiens Immunoglobulin superfamily, member 3 (IGSF3), mRNA
6952	19444	32461	0.81	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
7684	20348	33461	1.65	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7684	20348	33462	1.65	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7691	20355	33470	0.64	1.0E-127	AW996292.1	EST_HUMAN	QV3-BN0046-150300-121-h11 BN0046 Homo sapiens cDNA
8785	21477	34625	0.8	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8785	21477	34626	0.8	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9540	22193	35377	4.17	1.0E-127	AF274853.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9540	22193	35378	4.17	1.0E-127	AF274853.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9773	22424	35631	1	1.0E-127	A1288632.1	EST_HUMAN	q9n94h09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1886449 3'
10241	22889	36101	1.34	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11107	23777	37050	7.88	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC83184), mRNA
11107	23777	37051	7.88	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC83184), mRNA
11627	24224	37546	3.25	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
11627	24224	37547	3.25	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
12244	12982	25622	2.25	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12244	12982	25623	2.25	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12444	13982	28623	2.88	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12444	13982	28623	2.88	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
447	13233	25673	3.04	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
2063	14795	27520	5.5	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2063	14795	27521	5.5	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2206	14934	27672	8.76	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2448	15165		1.1	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3389	16148	28802	1.08	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6000	18781	31742	3.73	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQ11 gene
6816	19477	32499	0.56	1.0E-129	BE869993.1	EST_HUMAN	601449740F1 NIH_MGC 85 Homo sapiens cDNA clone IMAGE:3853688 5'
6818	19477	32500	0.56	1.0E-129	BE869993.1	EST_HUMAN	601449740F1 NIH_MGC 85 Homo sapiens cDNA clone IMAGE:3853688 5'
7027	19719	32776	4.15	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQ11 gene
7090	19779	32844	3.93	1.0E-129	AJ006345.1	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
7428	20105	33181	2.49	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
7428	20105	33192	2.49	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8217	20911	35635	0.97	1.0E-129	11437282	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
9979	22627	35836	0.97	1.0E-129	AA682200.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10523	23169	36396	0.57	1.0E-129	AA625526.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
11186	23851	37137	6.57	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
11269	19779	32844	1.38	1.0E-129	AU143115.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
11615	24213	37537	1.38	1.0E-129	AU143115.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
11615	24213	37538	1.38	1.0E-129	AU143115.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
12104	24801		1.79	1.0E-129	HB3155.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
12483	24842		2.66	1.0E-129	AL120739.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
74	12901	25538	1.3	1.0E-130	7705530	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1147	13902	26564	0.69	1.0E-130	AB037835.1	EST_HUMAN	Homo sapiens mRNA for KIAA1414 protein, partial cds
1661	14407	27098	11.38	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3346366 5'
1661	14407	27099	11.38	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3346366 5'
1976	14712		3.08	1.0E-130	X04092.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2773	15478		5.37	1.0E-130	AJ010220.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2881	15948	28290	1.17	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2881	15948	28291	1.17	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
3565	16320	28968	1.09	1.0E-130	AF240698.1	NT	Homo sapiens cDNA clone IMAGE:3685466 5'
3750	15648	28290	5.36	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3685466 5'
3750	15648	28291	5.36	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3685466 5'
3915	16665	28305	1.82	1.0E-130	AW503580.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha RPTM4265-variant, C alpha 1) mRNA
4053	16798	29428	1.5	1.0E-130	M97710.1	NT	Human T-cell receptor (V alpha 22.1, J alpha RPTM4265-variant, C alpha 1) mRNA
4501	17237	29869	6.76	1.0E-130	AW843993.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha RPTM4265-variant, C alpha 1) mRNA
5038	17757	30371	1.07	1.0E-130	AW363289.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha RPTM4265-variant, C alpha 1) mRNA
5038	17757	30372	1.07	1.0E-130	AW363289.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha RPTM4265-variant, C alpha 1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6829	19391	32405	0.55	1.0E-130	X57825.1	NT	Human germ-line immunoglobulin lambda light chain pseudogene (VII.1)
6723	19557	32587	0.81	1.0E-130	AW843875.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6723	19557	32588	0.81	1.0E-130	AW843875.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6736	19570	32602	0.75	1.0E-130	11425448	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7154	19841	32910	2.62	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8582	21274	34553	0.45	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
8718	21410	34553	2.39	1.0E-130	AW958242.1	EST_HUMAN	EST388312 IMAGE resequences, MAGD Homo sapiens cDNA
9114	21802	34987	1.64	1.0E-130	AB037766.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
9833	22484	36340	1.25	1.0E-130	AW103454.1	EST_HUMAN	xd36a06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2895874 3'
10463	23109	36341	0.51	1.0E-130	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
11242	23904	37194	1.72	1.0E-130	8923197	NT	Homo sapiens contactin 6 (CNTN6), mRNA
11242	23904	37195	1.72	1.0E-130	8923197	NT	Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA
11703	24298	37624	2.67	1.0E-130	4504142	NT	Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA
12759	15478		1.56	1.0E-130	AJ010230.1	NT	Homo sapiens glutamate receptor, metabotropic 5 (GRM5) mRNA
							Homo sapiens RET finger protein-like 1 antisense transcript, partial
							zr58c04.1 Soares NIH-MPc S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4	12832	25445	1.9	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.
							zr58c04.1 Soares NIH-MPc S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4	12832	25446	1.9	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.
7	12834	25449	1.02	0.0E+00	4885136	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
14	12841	25454	0.72	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
14	12841	25455	0.72	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
20	12848	25462	6.7	0.0E+00	D83327.1	NT	Homo sapiens DCCR1 mRNA, partial cds
20	12848	25463	6.7	0.0E+00	D83327.1	NT	Homo sapiens DCCR1 mRNA, partial cds
25	12853	25468	17.04	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
33	12861	25478	1.19	0.0E+00	5802987	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
35	12863	25481	0.82	0.0E+00	M58600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
39	12867	25486	4.22	0.0E+00	8857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
55	12884	25512	0.76	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
55	12884	25513	0.76	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
56	12885	25514	3.04	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
56	12885	25515	3.04	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
57	12886	25516	6.76	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
59	12888	25519	12.55	0.0E+00	AW069534.1	EST_HUMAN	cr48a07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48a07 3'
59	12888	25520	12.55	0.0E+00	AW069534.1	EST_HUMAN	cr48a07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48a07 3'
63	12891	25524	1.5	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
65	12893		0.91	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
73	12900	25536	10.36	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
73	12900	25537	10.36	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
76	12900	25536	10.18	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
76	12900	25537	10.18	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	12906	25544	0.78	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
81	12907		15.25	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
90	12916	25553	17.68	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
93	12919	25556	23.26	0.0E+00	U89277.1	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
99	12925	25562	3.51	0.0E+00	A114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
100	12926	25563	1.72	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
105	12928	25566	1.33	0.0E+00	X91213.1	NT	H. sapiens nct1 gene (exon 2)
113	12935	25572	0.89	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
114	12935	25572	1.47	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
115	15513	25573	1.48	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270017 5'
115	15513	25574	1.48	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270017 5'
128	12943	25586	4.38	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
128	12943	25587	4.38	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
136	12950	25593	1.29	0.0E+00	T56045.1	EST_HUMAN	ye83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
136	12950	25594	1.29	0.0E+00	T56045.1	EST_HUMAN	ye83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
149	12964		8.88	0.0E+00		NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
153	12968	25609	2.1	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
155	12970		25.83	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
158	12973	25612	1	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
160	12975	25613	1.15	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
161	12975	25613	0.88	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
162	12976	25614	5.4	0.0E+00	W73973.1	EST_HUMAN	zb62b05.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 6' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
163	12977	25615	0.81	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
163	12977	25616	0.81	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
164	12978	25617	1.42	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
167	12981	25620	28.73	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
167	12981	25621	28.73	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
176	12988	25627	5.95	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
176	12988	25627	5.95	0.0E+00	BE018970.1	EST_HUMAN	CE22631 ;
176	12988	25628	5.95	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
181	12993	25631	3.05	0.0E+00	AB018327.1	NT	CE22631 ;
181	12993	25632	3.05	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
189	13002	25643	67.77	0.0E+00	D50659.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
194	13007	25648	3.74	0.0E+00	AF273045.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
194	13007	25649	3.74	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set14-3 mRNA, complete cds
196	13009	25651	4.81	0.0E+00	AF167174.1	NT	Homo sapiens CTCL tumor antigen set14-3 mRNA, complete cds
196	13009	25652	4.81	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
205	15537	25658	9.26	0.0E+00	AI587308.1	EST_HUMAN	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
205	15537	25659	9.26	0.0E+00	AI587308.1	EST_HUMAN	tt0408.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN);
207	13019	25661	3.08	0.0E+00	AF195658.1	NT	tt0408.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN);
209	13021		23.37	0.0E+00	4506632	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
210	13022		4.72	0.0E+00	AF132000.1	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
214	13026	25664	9.19	0.0E+00	AB018284.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
215	13026	25664	8.34	0.0E+00	AB018284.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
216	13027	25665	3.5	0.0E+00	6678444	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
228	13041	25678	1.23	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
229	13041	25679	1.23	0.0E+00	AB018301.1	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA
231	13042	25682	3.97	0.0E+00	5453805	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
233	13044		6.94	0.0E+00	AL163201.2	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
240	13049	25688	3.85	0.0E+00	AF231919.1	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
242	13051	25691	1.71	0.0E+00	X89772.1	NT	Homo sapiens chromosome 21 segment HS21C001
250	13059		9.14	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
263	13071	25710	1.68	0.0E+00	4507500	NT	H. sapiens mRNA for Interferon alpha/beta receptor (long form)
							Homo sapiens chromosome 21 unknown mRNA
							Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
263	13071	25711	1.68	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
265	13073	25713	3.07	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
276	13083		1.19	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
277	13084	25726	3.28	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
278	13085	25727	3.28	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
287	13093	25734	0.78	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
287	13093	25735	6.65	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
287	13103	25744	4.97	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
298	13104	25745	4.63	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
299	15540		4.23	0.0E+00	4506728	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
300	13105		3.76	0.0E+00	AA480002.1	EST_HUMAN	Homo sapiens ribosomal protein S5 (RPS5) mRNA
301	13106	25746	18.93	0.0E+00	4507152	NT	zvf8c06.r1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:753894 5'
302	13106	25746	16.53	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
306	13110	25750	2.33	0.0E+00	AF114488.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
319	13122	25759	4.97	0.0E+00	7657213	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
320	13122	25759	6.23	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
335	13136	25771	2.98	0.0E+00	5174574	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
338	13139	25775	1.71	0.0E+00	4827057	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
341	13142	25780	1.45	0.0E+00	U71600.1	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
346	13146	25784	2.42	0.0E+00	AF231919.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
346	13146	25785	2.42	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
347	15541	25786	3.84	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
349	13148	25788	2.33	0.0E+00	4507500	NT	Homo sapiens chromosome 21 unknown mRNA
352	13151	25792	0.94	0.0E+00	4503854	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
353	13152	25793	4.1	0.0E+00	D80006.1	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
354	13152	25793	1.9	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
356	13154	25795	1.89	0.0E+00	4507500	NT	Human mRNA for KIAA0184 gene, partial cds
367	13163	25808	1.07	0.0E+00	AU134963.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
378	13203	25849	8.31	0.0E+00	AB028942.1	NT	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
379	13204	25850	1.54	0.0E+00	AI363014.1	EST_HUMAN	Homo sapiens mRNA for KIAA1019 protein, partial cds
383	13170	25813	1.83	0.0E+00	AW754180.1	EST_HUMAN	q61h05.x1 NCL CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN); RC2-CT0320-300100-016-a08 CT0320 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
386	13172	25816	1.58	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
387	13173	25817	2.49	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
387	13173	25818	2.49	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
388	13174	25819	1.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
389	13175	25820	1.39	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
389	13175	25821	1.39	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
390	13176	25822	2.77	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
391	13177	25823	0.84	0.0E+00	4503680	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
392	13178	25824	1.35	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
392	13178	25825	1.35	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
393	13178	25824	1.07	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
393	13178	25825	1.07	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
397	13182	25435	28.13	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
411	12822	25435	1.5	0.0E+00	R17795.1	EST_HUMAN	yg09a02.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31652 5'
419	13205	25851	1.31	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase (GART) mRNA
420	13208	25852	3.18	0.0E+00	4506728	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
421	13207	25852	3.93	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
422	13208	25853	5.45	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
422	13209	25855	4.02	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
423	13209	25855	4.02	0.0E+00	AF193607.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
433	13219	25865	1.99	0.0E+00	4557879	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
438	13224	25865	2.01	0.0E+00	AA324292.1	EST_HUMAN	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
439	13225	25879	0.97	0.0E+00	BE254447.1	EST_HUMAN	EST27054 Carebrilum II Homo sapiens cDNA 5' and
455	13241	25890	3.15	0.0E+00	4504532	NT	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
455	13241	25890	3.15	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
461	13246	25888	1.23	0.0E+00	4557887	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
461	13246	25889	1.23	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
471	13257	25895	2.84	0.0E+00	AL163246.2	NT	Homo sapiens keratin 18 (KRT18) mRNA
472	13258	25896	9.28	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
472	13258	25897	9.28	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
481	13268	25902	3.46	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
483	13268	25904	1.97	0.0E+00	AU132898.1	EST_HUMAN	Homo sapiens NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
491	13276	25910	2.66	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
482	15543	25911	1.11	0.0E+00	AW938825.1	EST_HUMAN	PMO-DT0065-130400-002-c08 DT0065 Homo sapiens cDNA
494	13278	25913	1.33	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
495	13279	25914	1.27	0.0E+00	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
499	13283		0.77	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
506	13290	25924	5.37	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
513	15544	25928	1.29	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-H05 BT0635 Homo sapiens cDNA
518	13302	25934	1.14	0.0E+00	BF028005.1	EST_HUMAN	601764858F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3996998 5'
524	13308	25941	1.88	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
527	13311	25944	27.68	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TGEB1L) mRNA
528	13312	25945	4.33	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
528	13312	25946	4.33	0.0E+00	4504038	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
530	13314	25948	0.97	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
530	13314	25949	0.97	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
535	13318		5.82	0.0E+00	AF003528.1	NT	UI-H-B11-acb-H-04-0-J1.a1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
543	13326	25958	1.89	0.0E+00	AW135324.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
553	13336		8	0.0E+00	D10083.1	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCORF5), nuclear gene encoding mitochondrial protein, mRNA
572	13353	25982	2.63	0.0E+00	5174742	NT	Human apolipoprotein A-1 (ApoA-1) gene, exon 1
585	13365		7	0.0E+00	J04088.1	NT	60182627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
588	13368	25996	1.83	0.0E+00	BF104898.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
590	13370	25998	0.98	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
590	13370	25999	0.98	0.0E+00	8923631	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
595	13373	26002	0.76	0.0E+00	4501854	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
600	13378	26008	1.15	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
600	13378	26009	1.15	0.0E+00	AF221712.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
609	13387	26018	3.18	0.0E+00	AF149773.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	13390	26021	1.2	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
613	13391	26022	3.83	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
613	13391	26023	3.83	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
614	13392	26024	0.92	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
614	13392	26025	0.92	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
620	13399	26034	1.35	0.0E+00	AA3399486.1	EST_HUMAN	z650c07.1 Soares, Isatis, NHT Homo sapiens cDNA clone IMAGE:728732 5'
624	13403	26038	10.1	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
628	13407	26041	0.76	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares fetal liver spleen_TNFRSF_51 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
628	13407	26042	0.76	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares fetal liver spleen_TNFRSF_51 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
631	13410	26043	4.99	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
638	13417	26054	2.98	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
640	13419	26057	1.17	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
643	13422	26061	2.53	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
647	13426	26064	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
647	13426	26065	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
653	13431	26070	4.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
653	13431	26071	4.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
659	15847	26071	1.15	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
667	13443	26084	10.4	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
672	13448	26088	4.49	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
681	13456	26101	2.43	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
693	13468	26115	9.24	0.0E+00	AA614537.1	EST_HUMAN	np49d01.s1 NCL CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
696	13471	26119	4.34	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
696	13471	26120	4.34	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
706	13481	26129	1.71	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
712	13486	26135	4.95	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
712	13486	26136	4.95	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
714	13488	26139	12.29	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
719	13493	26146	2.12	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
739	13512	26170	1.07	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
739	13512	26171	1.07	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
740	13513	26172	2.41	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
743	13516	26175	1.07	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
743	13516	26176	1.07	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
746	13519	26177	1.38	0.0E+00	6812749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
748	15551	26179	1.86	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
748	13521	26180	3.01	0.0E+00	BE669735.1	EST_HUMAN	601445847F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3849803 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
752	13524	26183	3.51	0.0E+00	R48915.1	EST_HUMAN	yf69g08.r1 Soares breast 2NBHBS1 Homo sapiens cDNA clone IMAGE:154046 5'
753	13525	26184	2.4	0.0E+00	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
761	13533	26192	2.07	0.0E+00	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
764	13537	26196	2.34	0.0E+00	7881965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
775	13547	26208	1.18	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
775	13547	26209	1.18	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
780	13552	26213	2.13	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
784	13556	26217	5.97	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
784	13556	26218	5.97	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
788	13560	26222	9.88	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
789	13561	26222	11.63	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
805	13577	26242	1.96	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
806	13578	26243	4.28	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
808	13580	26245	2.81	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
814	13585	26251	1.39	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
814	13585	26252	1.39	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
819	13590	26257	1.58	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
823	13593	26262	2.09	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
823	13593	26263	2.09	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
830	13600	26274	1.32	0.0E+00	AF027153.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
834	13604	26275	4.62	0.0E+00	AB028942.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLCSA3) gene, complete cds
834	13604	26275	4.62	0.0E+00	AB028942.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLCSA3) gene, complete cds
835	13605	26276	9.56	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
836	13606	26277	4.34	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
837	13607	26278	0.8	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
841	13611	26281	2.2	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
841	13611	26282	2.2	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
842	13612	26283	2.45	0.0E+00	AA533272.1	EST_HUMAN	U66407.s1 NCJ_CGAP_P110 Homo sapiens cDNA clone IMAGE:997453
842	13612	26284	2.45	0.0E+00	AA533272.1	EST_HUMAN	U66407.s1 NCJ_CGAP_P110 Homo sapiens cDNA clone IMAGE:997453
843	13613	26285	9.44	0.0E+00	BF677894.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
847	13617	26286	1.94	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
847	13617	26286	1.94	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
848	13618	26287	3.31	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
848	13618	26288	3.31	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
871	13640	26311	0.91	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
878	13647	26316	2.57	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
878	13647	26317	2.57	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
888	13657	26326	6.48	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
888	13666		4.99	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
900	13666		8.49	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
901	13668	26332	1.21	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-enkephalase precursor, mRNA, partial cds
902	13669	26333	1.78	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds
905	13672	26336	1.05	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
905	13672	26337	1.05	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
926	13683	26356	2.98	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0994 protein, partial cds
926	13683	26357	2.98	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0994 protein, partial cds
931	13698	26362	1.19	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
932	13699	26363	9.95	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
933	13700	26364	0.9	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
934	13701	26365	2.18	0.0E+00	4507430	NT	Homo sapiens thyroidal embryonic factor (TEF), mRNA
934	13701	26366	2.18	0.0E+00	4507430	NT	Homo sapiens thyroidal embryonic factor (TEF), mRNA
942	15556	26373	3.38	0.0E+00	A001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
942	15556	26374	3.38	0.0E+00	A001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
943	13709	26375	9.49	-0.0E+00	7857288	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
954	13719	26385	3.18	0.0E+00	AB030568.1	NT	Homo sapiens mRNA for PSP24, complete cds
962	13727	26391	1.11	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
962	13727	26392	1.11	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
962	13727	26393	1.11	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
963	13728	26394	1.69	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
963	13728	26395	1.69	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
972	13737	26402	2.03	0.0E+00	4757668	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL), mRNA
984	13748	26410	1.66	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
985	13749	26411	50.9	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
986	13749	26411	25.17	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
989	13752		5.52	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
990	13752		8.64	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
993	13755	26418	1.17	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
994	13755	26416	1.83	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
995	13755	26416	2.3	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
996	13756	26417	3.78	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
999	13759	26420	3.06	0.0E+00	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1003	13763	26424	2.5	0.0E+00	5803114	NT	Homo sapiens inter membrane protein, mitochondrial (MIMT), mRNA
1004	13764		1.43	0.0E+00	AA458680.1	EST_HUMAN	aa86g07.s1 Striatagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838238 3' similar to SW:PR8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;
1007	13767	26428	1.9	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1007	13767	26429	1.9	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1010	13770		3.55	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
1025	13785	26445	2.49	0.0E+00	4758569	NT	Homo sapiens heat shock 70KD protein 9B (mortalin-2) (HSPA9B), mRNA
1043	13802	26460	1.89	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6), mRNA
1043	13802	26461	1.89	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6), mRNA
1047	13806	26465	3.63	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1047	13806	26466	3.63	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1048	13807	26467	119.02	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1050	13809		1.19	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1052	13811	26471	3.52	0.0E+00	5174384	NT	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA
1060	13818	26480	2.3	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3), mRNA
1074	13832	26490	2.2	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-108 BN0115 Homo sapiens cDNA
1097	13855	26514	6.04	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1097	13855	26515	6.04	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1097	13855	26515	26515	0.9	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1110	13867	26526	26526	0.9	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1110	13867	26527	26527	0.9	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1111	13868	26529	4.27	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A), mRNA
1113	13870	26529	0.96	0.0E+00	8923290	NT	Homo sapiens ribosomal protein S27a (RPS27A), mRNA
1116	13873	26532	23.77	0.0E+00	AB002059.1	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1118	13875	26533	44.3	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1119	13878	26534	5.51	0.0E+00	7657488	NT	Homo sapiens DNA for Human P2XM, complete cds
1119	13878	26535	5.51	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1122	13878	26537	1.1	0.0E+00	7706500	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1123	13878	26538	0.87	0.0E+00	X95826.1	NT	Homo sapiens Npw38-binding protein Npw38 (LOC51729), mRNA
1123	13878	26538	0.87	0.0E+00	X95826.1	NT	Homo sapiens Npw38-binding protein Npw38 (LOC51729), mRNA

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1123	13879	26539	0.87	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1124	13880	26540	0.92	0.0E+00	AI147650.1	EST_HUMAN	qb22d10.x1 Soares_pregnant uterus Nib-IPU Homo sapiens cDNA clone IMAGE:1697011.3'
1126	13882	26542	1.56	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1133	13889	26548	0.71	0.0E+00	475808.1	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1133	13889	26549	0.71	0.0E+00	475808.1	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1133	13889	26550	1.39	0.0E+00	7305076	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1134	13890	26551	6.83	0.0E+00	9666844	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1145	13900	26562	6.83	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1145	13900	26565	1.85	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1148	13903	26574	0.75	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1155	13910	26574	4.54	0.0E+00	AF034996.1	NT	Homo sapiens amphiphysin 1 mRNA, alternative splice isoform, complete cds
1167	13921	26583	1.52	0.0E+00	7657336	NT	Homo sapiens mutL (E. coli) homolog 3 (MLH3), mRNA
1187	13939	26617	1.7	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1201	13953	26620	1.53	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1204	13956	26621	1.53	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1204	13956	26622	1.77	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1205	13957	26623	1.53	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1206	13962	26623	9.12	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1224	13974	26646	1.71	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1225	13975	26647	2.33	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1243	13992	26667	23.59	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1251	14000	26676	3.07	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds
1258	14007	26681	2.07	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1265	14014	26682	2.07	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1265	14014	26682	2.04	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1277	14027	26696	2.04	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1277	14027	26696	2.04	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1277	14027	26697	3.78	0.0E+00	AF096156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1278	14028	26709	1.63	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1286	15564	26710	1.63	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1288	15584	26715	2.03	0.0E+00	5803146	NT	Homo sapiens zinc finger protein 9 (ZNF173) mRNA
1283	14042	26716	0.89	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 9 (ZNF173) mRNA
1284	14043	26716	1.12	0.0E+00	5803148	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1286	14045	26717	0.72	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1297	14046	26718	0.72	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA

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1299	14048	26720	4.71	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1300	14049	26721	2.04	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1301	14050	26722	6.88	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1302	14051	26723	3.01	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1302	14051	26724	3.01	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1314	14062	26737	1.82	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1387	14134	26809	1.38	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyl gene
1393	14140	26817	3.39	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1396	14143	26821	1.59	0.0E+00	AI208756.1	EST_HUMAN	gg38b06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:T27A1.5 CE14213
1397	14144	26822	13.21	0.0E+00	6042206	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1406	14153	26833	5	0.0E+00	4505646	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1406	14153	26834	5	0.0E+00	4505646	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1408	14155	26837	4.08	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1408	14155	26838	4.08	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1410	14157	26839	4.59	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1420	14168	26852	3.02	0.0E+00	AF038280.1	NT	Homo sapiens alpha 1-6 glucosyltransferase (alpha1-6FucT) gene, exon 7
1431	14178	26863	5.39	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1431	14178	26864	5.39	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1436	14183	26868	17.93	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1436	14183	26869	17.93	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1446	14193	26876	2.59	0.0E+00	AL132999.1	NT	Novel human gene on chromosome 20
1447	14194	26877	1.82	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1451	14198	26882	1.73	0.0E+00	DB7077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1454	14201	26885	4.53	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1456	14203	26887	1.55	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1456	14203	26888	1.55	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1460	14207	26893	0.97	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1460	14207	26894	0.97	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1500	14246	26932	1.37	0.0E+00	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51686), mRNA
1516	14263	26949	1.21	0.0E+00	AW959687.1	EST_HUMAN	EST T371757 MAGE sequences, MAGF Homo sapiens cDNA
1517	14264	26950	1.76	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.1 NCJ CGAP_G081 Homo sapiens cDNA clone IMAGE:315116 5'
1522	14269	26953	49.82	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1522	14269	26954	49.82	0.0E+00	AF023860.1	NT	Carcopithecus aethiops cyclophilin A mRNA, complete cds
1524	14271	26957	1.24	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGI resequences, MAGN Homo sapiens cDNA
1524	14271	26958	1.24	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGI resequences, MAGN Homo sapiens cDNA
1525	14272	26959	5.49	0.0E+00	D10894.1	NT	Bovine mRNA for neurocalcin
1527	14274		2.07	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1528	14275	26962	2.1	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1528	14275	26963	2.1	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1530	14277	26965	3.3	0.0E+00	7682405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1531	14278		7.29	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1537	14284	26971	1.84	0.0E+00	M68478.1	NT	Human transglutaminase mRNA, complete cds
1540	14287	26973	3.72	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1540	14287	26974	3.72	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1541	15572		11.72	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1542	14288	26975	11.72	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1553	14300	26988	2.86	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1553	14300	26989	2.86	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1555	14302	26990	11.7	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1563	14310		1.21	0.0E+00	D00333.1	NT	human o-yes-2 gene
1574	14321	27007	1.65	0.0E+00	Z83738.1	NT	H. sapiens HH2B/e gene
1575	14322	27008	1.59	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1575	14322	27009	1.59	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1576	14323	27010	11.18	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1576	14323	27011	11.18	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1579	15573	27014	9.85	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1583	14329	27015	1.83	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1585	14331	27018	9.78	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1585	14331	27019	9.78	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1587	14333	27020	42.75	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1587	14333	27021	42.75	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1589	14335	27023	7.94	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1604	14350	27039	5.85	0.0E+00	H26973.1	EST_HUMAN	ys76c05.e1 Scores adult brain N2b4HB58Y Homo sapiens cDNA clone IMAGE:183848 3'
1614	14361	27051	2	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1614	14361	27052	2	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1659	14405	27095	1.25	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1659	14405	27096	1.25	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1663	14409	27100	1.68	0.0E+00	AI768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2HS2 ZINC FINGER PROTEIN ;
1664	14410	27101	1.2	0.0E+00	4758513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1665	14411	27102	2.61	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1668	14414	27108	1.76	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1669	14414	27107	1.76	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1671	14416	27109	1.35	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1672	14417	27110	1.5	0.0E+00	7657065	NT	Homo sapiens v-e1s avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1675	14420	27113	1.12	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1675	14420	27114	1.12	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1677	14421	27116	3.24	0.0E+00	4557610	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1680	14424	27119	3.18	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NBHb1 Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1680	14424	27119	3.18	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NBHb1 Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1682	14426	27122	1.32	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (HUMAN);
1682	14426	27123	1.32	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (HUMAN);
1685	14429	27133	13.71	0.0E+00	5031748	NT	H. sapiens H2B/h gene
1685	14437	27133	1.11	0.0E+00	AF169963.1	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1685	14438	27136	3.53	0.0E+00	8923841	NT	Homo sapiens WNT16 protein (WNT16) mRNA, complete cds
1702	14445	27145	1.11	0.0E+00	4826973	NT	Homo sapiens FOXJ2 forkhead factor (LOC58910), mRNA
1708	14451	27152	4.08	0.0E+00	AB026542.1	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1710	14453		2.19	0.0E+00	S94400.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1725	15577	27167	1.16	0.0E+00	11545911	NT	TGR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1739	14481	27181	1.93	0.0E+00	AF273841.1	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1778	15578		6.86	0.0E+00	4506718	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1782	14523	27228	3.37	0.0E+00	4557556	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1782	14523	27229	3.37	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1784	14525	27232	1.42	0.0E+00	UG3963.1	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1787	14528		1.2	0.0E+00	W76571.1	EST_HUMAN	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1787	14528		1.2	0.0E+00	W76571.1	EST_HUMAN	zfb6g09.r1 Soares_fetal_NbH19W Homo sapiens cDNA clone IMAGE:345664 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1768	15579	27236	2.74	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1800	14540	27251	5.68	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
1802	14542	27254	2.79	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1803	14543	27255	4.07	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1803	14543	27256	4.07	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1803	14543	27257	4.07	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1812	14552	27265	1.63	0.0E+00	4505328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
1826	14565	27276	5.82	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1826	14565	27277	5.82	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1836	14575	27287	1.12	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1836	14575	27288	1.12	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1840	14578	27290	4.35	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1840	14578	27291	4.35	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1841	14579	27292	5.47	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1841	14579	27293	5.47	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1844	14582	27296	1.46	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-f-07-0-UI st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1844	14582	27297	1.46	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-f-07-0-UI st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1868	14606	27316	3.49	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1868	14606	27317	3.49	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1887	14624	27334	0.93	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0126-200300-012-504 BN0126 Homo sapiens cDNA
1916	14653	27362	2.16	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1916	14653	27363	2.16	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1924	14661	27372	1.22	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1925	15582	27373	1.19	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1925	15582	27373	1.19	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1930	14666	27380	1.53	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1930	14666	27381	1.53	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1933	14668	27383	1.42	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA

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1935	14670		4.27	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1940	14675		1.35	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1949	14684	27396	1.94	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1949	14684	27397	1.94	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1959	14695		1.15	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
1961	14697	27410	1.09	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1961	14697	27411	1.09	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1961	14697	27412	1.09	0.0E+00	8400716	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1962	14698	27413	2.49	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1962	14698	27413	2.49	0.0E+00	4826638	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1973	14709	27427	1.36	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1973	14709	27428	1.36	0.0E+00	AB018333.1	NT	Human TFEF protein mRNA, partial cds
1979	14715	27432	1.69	0.0E+00	M33782.1	NT	Human TFEF protein mRNA, partial cds
1979	14715	27433	1.69	0.0E+00	M33782.1	NT	Human TFEF protein mRNA, partial cds
1981	14717	27434	1.57	0.0E+00	AW193024.1	EST_HUMAN	xi69b01.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2678913 3'
1981	14717	27435	1.57	0.0E+00	AW193024.1	EST_HUMAN	xi69b01.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2678913 3'
1981	14717	27435	1.57	0.0E+00	AW193024.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1982	14718	27436	5.96	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1982	14718	27437	5.96	0.0E+00	6912457	NT	Homo sapiens KIAA0408 gene product (KIAA0408), mRNA
1984	14720	27439	2	0.0E+00	7662095	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1985	14721	27440	1.19	0.0E+00	AB011149.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1986	14722	27441	1.58	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1986	14722	27441	1.58	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1988	14727	27442	3.75	0.0E+00	AB040946.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1993	14729	27451	1.02	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2014	14749	27476	1.02	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2014	14749	27477	1.02	0.0E+00	AF273841.1	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2046	14779	27507	1.64	0.0E+00	7706742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2052	14785	27511	4.13	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone, PLACE400321 5'
2053	14785	26837	1.55	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2053	14785	26838	1.55	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2053	14785	26838	1.55	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2055	14787	27513	2.04	0.0E+00	AA07589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2055	14787	27514	2.04	0.0E+00	AA07589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2055	14787	27514	2.04	0.0E+00	AA07589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2057	14789		2.41	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2059	14791		1.91	0.0E+00	4985863	NT	Homo sapiens phosphodiesterase 9A, cGMP-specific, rod, alpha (PDE9A), mRNA
2060	14792	27517	0.97	0.0E+00	Z42399.1	EST_HUMAN	HS0010021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02

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2062	14794		1.78	0.0E+00	A1244247.1	EST_HUMAN	q90f08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element;
2067	14799	27526	3.46	0.0E+00	BE877225.1	EST_HUMAN	6011485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2069	14801	27528	1.48	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2069	14801	27529	1.48	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2072	14804	27532	3.07	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2072	14804	27533	3.07	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2080	14812	27544	3.71	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2080	14812	27545	3.71	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2085	14817	27549	1.36	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2107	14838		2.06	0.0E+00	BE167964.1	EST_HUMAN	QV1-GN0055-140800-318-c10 GN0055 Homo sapiens cDNA
2108	14839		1.59	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2110	14841	27572	3.76	0.0E+00	BF027562.1	EST_HUMAN	601872066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2111	14842	27573	1.03	0.0E+00	BE072624.1	EST_HUMAN	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2113	14844	27574	1.06	0.0E+00	AF240785.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2116	14847	27576	1.3	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2117	14848	27577	1.47	0.0E+00	L76627.1	NT	Homo sapiens metabotropic glutamate receptor 1 alpha (mGluR1alpha) mRNA, complete cds
2119	14850	27579	6.39	0.0E+00	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2119	14850	27580	6.39	0.0E+00	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2153	14883		1.05	0.0E+00	7657252	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNNMB3L), mRNA
2179	14908		1.22	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2183	14912	27644	1.05	0.0E+00	BE274696.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2185	14914	27647	7.59	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2185	14914	27648	7.59	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2187	14916	27650	1.4	0.0E+00	AA831691.1	EST_HUMAN	cc32e01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2191	14920	27654	5.68	0.0E+00	BF344434.1	EST_HUMAN	602014829F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150734 5'
2192	14921	27655	12.14	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2196	14925	27659	3.55	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2196	14925	27660	3.55	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2200	15588	27665	2.04	0.0E+00	BF313617.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5'
2203	14931	27668	1.93	0.0E+00	BE018750.1	EST_HUMAN	bs84e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-IL-RELATED PROTEIN;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2204	14932	27689	1.55	0.0E+00	AA042813.1	EST_HUMAN	z53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857.cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2204	14932	27670	1.55	0.0E+00	AA042813.1	EST_HUMAN	z53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857.cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2212	14940	27678	3.37	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2212	14940	27679	3.37	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2213	14941	27680	2.3	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2213	14941	27681	2.3	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2218	14946	27681	1.37	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2236	14964	27704	5.71	0.0E+00	4557558	NT	Homo sapiens ETA binding protein p300 (EP300) mRNA
2243	14971	27709	2.03	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2250	14978	27717	1.71	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2253	14981	27720	1.27	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2253	14981	27721	1.27	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2256	14983	27723	2.35	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2299	15024	27759	4.02	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2299	15024	27760	4.02	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2299	15024	27760	4.02	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2300	15025	27761	1.87	0.0E+00	AI076404.1	EST_HUMAN	z058d07.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2302	15027	27763	2.33	0.0E+00	AA429001.1	EST_HUMAN	z778a11.1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2302	15027	27764	2.33	0.0E+00	AA429001.1	EST_HUMAN	z778a11.1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2304	15029	27766	1.75	0.0E+00	BF347039.1	NT	602021848F1 NCL_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4157339 5'
2309	15034	27772	1.52	0.0E+00	L02840.1	NT	Homo sapiens poliovirus channel Kv2.1 mRNA, complete cds
2310	15035	27773	1.81	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2310	15035	27774	1.81	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2311	15038	27775	1.39	0.0E+00	6325468	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2317	15042	27780	1.17	0.0E+00	BE876095.1	EST_HUMAN	722a02.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94839 O94839 KIAA0857 PROTEIN;
2320	15045	27782	4.73	0.0E+00	AF044571.1	NT	Homo sapiens phosphatase kinase alpha subunit (PHKA2) gene, exon 32
2321	15046	27783	1.9	0.0E+00	AI625542.1	EST_HUMAN	1b57c08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2325	15050	27785	1.88	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2325	15050	27786	1.88	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2328	15053	27789	1.95	0.0E+00	5903178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2328	15053	27790	1.95	0.0E+00	5903178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2334	15058	27793	1.24	0.0E+00	7682007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA

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2334	15058	27794	1.24	0.0E+00	7662007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2348	15071	27807	3.2	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1), mRNA
2352	15074	27811	2.39	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2353	15075		4.31	0.0E+00	BE794026.1	EST_HUMAN	601586843F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3941003 5'
2354	15076	27812	1.51	0.0E+00	AW867076.1	EST_HUMAN	MR1-SN0033-120400-002-e04 SN0033 Homo sapiens cDNA
2355	15077	27813	2.99	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2356	15078	27814	2.03	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2356	15078	27815	2.03	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2357	15079		5.25	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2359	15081	27817	7.98	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2359	15081	27818	7.98	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2359	15081	27819	7.98	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2360	15082	27820	0.98	0.0E+00	8923089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2377	15099		0.91	0.0E+00	BE814424.1	EST_HUMAN	MR0-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA
2415	15136	27872	1.06	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1008155 5'
2416	15137		3.74	0.0E+00	AI042035.1	EST_HUMAN	α60b02.x1 Soares, NHMPu, S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:008662
2417	15138	27873	0.98	0.0E+00	8923820	NT	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA
2420	15141		4.44	0.0E+00	BE895605.1	EST_HUMAN	601432608F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918188 5'
2424	15145	27878	1	0.0E+00	BE937632.1	EST_HUMAN	MR1-TN0021-280800-001-H08 TN0021 Homo sapiens cDNA
2433	15154		0.98	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2437	15157	27892	4.5	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2441	15160	27896	2.09	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystikinin type-A receptor, complete cds
2441	15160	27897	2.09	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystikinin type-A receptor, complete cds
2448	15168	27906	1.91	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2454	15172	27911	1.22	0.0E+00	BF345274.1	EST_HUMAN	602018058F1 NCJ CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4153870 5'
2461	15179	27919	4.45	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2465	15183	27922	1.24	0.0E+00	BE831003.1	EST_HUMAN	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2465	15183	27923	1.24	0.0E+00	BE831003.1	EST_HUMAN	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2470	15188	27927	0.93	0.0E+00	U13686.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2470	15188	27928	0.93	0.0E+00	U13686.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2471	15189	27929	2.98	0.0E+00	BF569144.1	EST_HUMAN	602184558T1 NIH_MGC 42 Homo sapiens cDNA clone IMAGE:4300383 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2482	15200	27940	3.34	0.0E+00	AW468922.1	EST_HUMAN	ha04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2484	15202	27941	2.99	0.0E+00	AW501010.1	EST_HUMAN	UI-HF-BPOp-als-c-07-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2498	15215	27958	0.91	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2498	15215	27959	0.91	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2509	15226		1.66	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2514	15231	27971	5.22	0.0E+00	BE795542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2516	14668	27983	1.4	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2516	15232	27972	1.48	0.0E+00	BF509482.1	EST_HUMAN	UI-H-B14-a02-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2518	15234	27974	1.83	0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2520	15236		3.28	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-IIIa (PDGFR.L) mRNA
2522	15238	27977	1.3	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903148 5'
2523	15239	27978	1.96	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POMT21 (POMT21L1), mRNA
2524	15240	27979	2.01	0.0E+00	8923340	NT	Homo sapiens hypothetical protein FLJ20368 (FLJ20368), mRNA
2525	15241	27980	2.21	0.0E+00	U93239.1	NT	Human Sec82 (Sec82) mRNA, complete cds
2530	15246	27984	1.44	0.0E+00	BE886490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2534	15249	27989	5.16	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2534	15249	27990	5.16	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2536	15251	27993	1.19	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2554	15269	28002	1.2	0.0E+00	BE536921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451181 5'
2561	15275	28012	2.97	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2561	15275	28013	2.97	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2562	15276	28014	1.8	0.0E+00	BE292898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2562	15276	28015	1.8	0.0E+00	BE292898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2563	15277	28016	1.07	0.0E+00	BF223041.1	EST_HUMAN	7627h12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3' similar to TR:O00248 O00246
2568	15280	28018	7.94	0.0E+00	AF245505.1	NT	HYPOTHETICAL 9.3 KD PROTEIN ;
2569	15303	28039	2.22	0.0E+00	BE29613.1	EST_HUMAN	Homo sapiens adican mRNA, complete cds
2569	15303	28039	2.22	0.0E+00	BE29613.1	EST_HUMAN	601173031F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528159 5'
2606	15531	28060	2.13	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2606	15531	28061	2.13	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2607	15319		2.47	0.0E+00	BF513835.1	EST_HUMAN	UI-H-BW1-amp-f-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2611	15323	28065	1.36	0.0E+00	BF672818.1	EST_HUMAN	602152853F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289612 5'
2615	15326	28069	1.83	0.0E+00	BF204131.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2615	15326	28070	1.83	0.0E+00	BF204131.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2618	15329	28072	2.08	0.0E+00	A1571737.1	EST_HUMAN	h19b08.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gb:L20977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN); Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF2i) mRNA
2619	15330	28073	2.19	0.0E+00	5032150	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2621	15333	28077	4.95	0.0E+00	AB037859.1	NT	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2622	15334	28078	1.02	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2622	15334	28078	1.02	0.0E+00	BE795445.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2625	15337	28080	2.55	0.0E+00	BE293328.1	EST_HUMAN	601594930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2632	15344		4.92	0.0E+00	BE792472.1	EST_HUMAN	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2641	15352	28098	1.51	0.0E+00	4504698	NT	Homo sapiens Brubn's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP-3 (FTP3) genes, complete cds
2651	15361		1.27	0.0E+00	U78027.1	NT	Homo sapiens quanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2652	15362	28103	6.55	0.0E+00	AF173227.1	NT	Homo sapiens quanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2658	15368	28106	1.22	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2659	15369	28107	1.08	0.0E+00	M69225.1	NT	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2661	15371	28109	2.22	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2661	15371	28110	2.22	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2663	15373	28112	1.71	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-407 OT0086 Homo sapiens cDNA
2666	15376	28115	1.25	0.0E+00	BF000018.1	EST_HUMAN	7h15h05.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:3318089 3'
2667	15377	28116	4.37	0.0E+00	BE383165.1	EST_HUMAN	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2688	15378		2.57	0.0E+00	BE531283.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2725	15432		4.21	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2726	15433	28169	5.57	0.0E+00	BE794884.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2732	15439	28177	3.83	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2733	15440	28178	1.33	0.0E+00	7669517	NT	Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA
2734	15441	28179	1.78	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
2736	15443	28181	1.27	0.0E+00	AB051826.1	EST_HUMAN	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2742	15448	28187	7.77	0.0E+00	BE796376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2745	15604	28191	3.48	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2746	15451		1.16	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2748	15453	28194	2.25	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2748	15453	28195	2.25	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2749	15454	28196	1.21	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2749	15454	28197	1.21	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2750	15455	28198	2.5	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2751	15456		13.89	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'
2752	15457	28199	3.13	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2752	15457	28200	3.13	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2756	15461	28203	33.8	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2756	15461	28204	33.8	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2760	15465	28209	2.58	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2771	15476		1.15	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2772	15477	28219	3.38	0.0E+00	BF514110.1	EST_HUMAN	UHLBW1-amw-07-0.U1.st NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2778	15483		0.99	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2784	15489	28227	2.1	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2784	15489	28228	2.1	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2785	15490	28229	4.67	0.0E+00	BF877694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2791	15496	28237	1.75	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2794	15499	28239	13.56	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCGA03 5'
2794	15499	28240	13.56	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCGA03 5'
2796	15501		7.61	0.0E+00	AI879163.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW-R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2799	15504	28245	5.41	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCL_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4214679 5'
2800	15505	28246	5.55	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2802	15507	28247	1.6	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2802	15507	28248	1.6	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2803	15508	28249	20.25	0.0E+00	BE300344.1	EST_HUMAN	600944784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2803	15508	28250	20.25	0.0E+00	BE300344.1	EST_HUMAN	600944784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2809	12995	25634	4.22	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3088 nt]
2812	15815		4.35	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2818	13491	26144	8.39	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2818	13491	26145	8.39	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2822	13776	26436	3.52	0.0E+00	4503202	NT	Homo sapiens cyclochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2822	13776	26437	3.52	0.0E+00	4503202	NT	Homo sapiens cyclochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2840	15608	28258	3.52	0.0E+00	X85990.1	NT	H.sapiens serine hydroxymethyltransferase pseudogene

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2841	15609		1.34	0.0E+00	AF069824.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
2843	15611		1.22	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2849	15617	28263	2.61	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2852	15620	28265	2.63	0.0E+00	M91803.1	NT	Human sodium channel mRNA
2854	15622	28267	1.94	0.0E+00	M80902.1	NT	Human AHNAC nucleoprotein mRNA, 5' end
2857	15625	28269	1.29	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2857	15625	28270	1.29	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2859	15627		1.18	0.0E+00	X73428.1	NT	H. sapiens l33 gene for HLH type transcription factor
2860	15628		2.59	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C008
2861	15629	28272	1.03	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2861	15629	28273	1.03	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2861	15629	28274	1.03	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2866	15633	28277	18.46	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2866	15633	28278	18.46	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2869	15636	28281	1.69	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2870	15637		7.2	0.0E+00	Y10658.1	NT	H. sapiens mRNA for nuclear DNA Helicase II
2871	15638		1.42	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2872	15639	28282	47.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2872	15639	28283	47.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2882	15649	28292	2.35	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2883	15652	28296	1.06	0.0E+00	AL047599.1	EST_HUMAN	DKFZp566G0621_r1 586 (synonym: lute1) Homo sapiens cDNA clone DKFZp566G0621
2886	15653	28297	0.97	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product Helicase (KIAA0054), mRNA
2886	15653	28298	0.97	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product Helicase (KIAA0054), mRNA
2887	15654		2.96	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2890	15657	28300	5.46	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2890	15657	28301	5.46	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2897	15664	28312	2.09	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
2897	15664	28313	2.09	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
2905	15671		4.18	0.0E+00	Y16210.1	NT	Homo sapiens hhlb5 gene for hair keratin, exons 1 to 9
2907	15673	28321	1.33	0.0E+00	4758276	NT	Homo sapiens EpitA4 (EPHA4) mRNA
2908	15674	28322	20.94	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
							hm16407.x1 NCJ CGAP Bm26 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2909	15675	28323	1.91	0.0E+00	AI561002.1	EST_HUMAN	O16247 F44E7.2 PROTEIN ;

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2909	15675	28324	1.91	0.0E+00	AI561002.1	EST_HUMAN	In18d07.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2187981 3' similar to TR:O16247
2911	15677	28326	1.63	0.0E+00	P52740	SWISSPROT	O16247 F44E7.2 PROTEIN ; ZINC FINGER PROTEIN 132
2912	15678	28327	2.01	0.0E+00	AF152338.1	NT	Homo sapiens protoderm gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2928	15694	28339	1.92	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2928	15694	28340	1.92	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2929	15695	28341	4.56	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2929	15695	28342	4.56	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2932	15698	28345	3.58	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2932	15698	28346	3.58	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2933	15699	28347	3.21	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology); translocated to, 4
2933	15699	28348	3.21	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology); translocated to, 4
2938	15703	28352	1.16	0.0E+00	BF110702.1	EST_HUMAN	740003.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3587028 3' similar to TR:Q9VLN1
2938	15703	28353	1.16	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17283 PROTEIN ;
2946	15712	28364	2.15	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2946	15712	28365	2.15	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2953	15719	28370	1.69	0.0E+00	4758827	NT	Homo sapiens neuron III (NRXN3) mRNA
2954	15720		0.96	0.0E+00	X98494.1	NT	Homo sapiens mRNA for M phase phosphoprotein 10
2957	15723	28373	2.38	0.0E+00	AB033034.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
2958	15724	28374	5.56	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2958	15724	28375	5.56	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2959	15725	28376	7.64	0.0E+00	AF108275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2973	15739		1.13	0.0E+00	AI149880.1	EST_HUMAN	qf43f09.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
2980	15746	28394	1.12	0.0E+00	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
2981	15747	28395	2.85	0.0E+00	AB004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2991	15757	28404	1.52	0.0E+00	7682273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2993	15759	28406	3.75	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2993	15759	28407	3.75	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2967	15763	28412	1.1	0.0E+00	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
3026	15791	28439	1.17	0.0E+00	M74098.1	NT	Human displacement protein (CCAA1) mRNA

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3033	15799	28445	0.71	0.0E+00	4506882	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3039	15805		4.62	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3042	15808	28454	3.74	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3042	15808	28455	3.74	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3044	15810		5.88	0.0E+00	AL359403.1	NT	Isocform 2 of a novel human mRNA from chromosome 22
3049	15815	28480	1.6	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
							Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
3052	15818		1.98	0.0E+00	AF196779.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
3066	15832	28475	1.19	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
3074	15840	28483	2.8	0.0E+00	X03529.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)
3080	15845		1.54	0.0E+00	AF199355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3084	15849	28490	1.72	0.0E+00	AF094589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3104	15869	28509	3.2	0.0E+00	AF285208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3105	15870	28510	7.83	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3110	15875	28514	3.42	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3111	15876	28515	1.21	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
							Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3138	15902	28547	3.74	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3148	15911	28556	26.91	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3151	15914	28559	1.32	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3151	15914	28560	1.32	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
							ye32603.s1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:529539
3158	15921	28567	8.63	0.0E+00	T94870.1	EST_HUMAN	S29539 BASIC PROTEIN, 23K -
3172	15935	28584	0.98	0.0E+00	BF243336.1	EST_HUMAN	S29539 BASIC PROTEIN, 23K -
3178	15941	28591	4.39	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3178	15941	28592	4.39	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3187	15950	28601	1.31	0.0E+00	4758827	NT	Homo sapiens neuramin III (NRXN3) mRNA
3187	15950	28602	1.31	0.0E+00	4758827	NT	Homo sapiens neuramin III (NRXN3) mRNA
3195	15958	28610	8.46	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3211	15974	28626	3.25	0.0E+00	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
							Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3214	15977	28628	1.96	0.0E+00	4502098	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (GREB1) mRNA
3220	15983	28636	0.85	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (GREB1) mRNA

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3220	15983	28637	0.85	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3222	15985	28638	3.07	0.0E+00	AAT74783.1	EST_HUMAN	ae87b11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3230	15993	28646	5.43	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3230	15993	28647	5.43	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3242	16004	28653	1.36	0.0E+00	4557590	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3248	16010	28661	1	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3255	16017		5.8	0.0E+00	M65189.1	NT	Human connectin 43 processed pseudogene
3256	16018	28668	1.26	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
3258	16020	28670	3.96	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3261	16023	28673	1.11	0.0E+00	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3269	17875	28680	2.09	0.0E+00	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3269	17875	28681	2.09	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3285	16046	28695	2.25	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3286	16047	28696	1.17	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3297	16059	28708	1.22	0.0E+00	8923824	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3300	16062	28710	1.09	0.0E+00	7657038	EST_HUMAN	Homo sapiens death receptor 6 (DR6), mRNA
3309	16069	28718	1.18	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3318	16078	28728	1.99	0.0E+00	AJ589294.1	EST_HUMAN	P5121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element
3326	16086	28736	2.33	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3326	16086	28737	2.33	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3327	16087	28738	1.22	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3327	16087	28739	1.22	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3329	16089	28741	1.27	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3329	16089	28742	1.27	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3333	16093	28745	9.77	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3335	16095	28747	1.29	0.0E+00	AB040940.1	NT	Homo sapiens myosin for KIAA1607 protein, partial cds
3342	16101	28753	0.84	0.0E+00	BE779039.1	EST_HUMAN	601464955F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3888248 5'
3352	16112	28767	0.72	0.0E+00	AI632569.1	EST_HUMAN	wb10704.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91929 Q91928
3361	16150	28804	4.44	0.0E+00	AU123664.1	EST_HUMAN	ZINC FINGER PROTEIN ;
3362	16151	28805	4.44	0.0E+00	AU123664.1	EST_HUMAN	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM200735 5'

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3398	16156	28807	0.95	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3398	16156	28808	0.95	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3401	16159	28810	1.36	0.0E+00	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3402	16160	28811	1.42	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-i isoform (CACNA1I) mRNA, complete cds
3406	16164		0.99	0.0E+00	AW867015.1	EST_HUMAN	NR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3418	16175	28824	1.66	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3418	16175	28825	1.66	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3419	16176	28826	1.34	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3421	16178	28827	5.37	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3430	15441	28179	1.75	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3435	16181	28840	2.4	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3438	16194	28844	5.47	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and IncC
3440	16196	28846	1.5	0.0E+00	7427522	NT	Incompatibility determinants
3448	16204	28853	3.54	0.0E+00	AI635159.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR-T), mRNA
3448	16204	28854	3.54	0.0E+00	AI635159.1	EST_HUMAN	wp14d10.X1 NC1 CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3452	16208	28859	2.48	0.0E+00	AJ278120.1	NT	NEURAL CELL ADHESION MOLECULE ;
3459	16215	28868	1.82	0.0E+00	6552332	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3459	16215	28869	1.82	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3464	16220	28874	1.31	0.0E+00	M14123.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3470	16226	28880	5.4	0.0E+00	U43283.1	NT	Human endogenous retrovirus HERV-K10
3475	16231	28884	1.18	0.0E+00	9558718	NT	Human MDSTA (AML1/MDS1 fusion) mRNA, partial cds
3475	16231	28885	1.18	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3479	16235	28890	1.84	0.0E+00	AF045452.1	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3479	16235	28891	1.84	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3484	16241	28898	1.12	0.0E+00	AF231922.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3486	16252	28905	2.21	0.0E+00	BE304791.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3486	16252	28906	2.21	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3489	16255	28909	0.92	0.0E+00	4826795	NT	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3489	16255	28909	0.92	0.0E+00	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3504	16290	28914	0.89	0.0E+00	AI384007.1	EST_HUMAN	te35g12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3507	16293	28917	1.11	0.0E+00	M10976.1	NT	O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3529	16285	28940	1.29	0.0E+00	AV701868.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
3530	16286	28941	0.85	0.0E+00	4506884	NT	AV701869 ADB Homo sapiens cDNA clone ADBDAH06 5'
3531	16287		1.74	0.0E+00	AF078868.1	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3539	16295	28945	1.49	0.0E+00	AL133204.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3542	16297	28948	1.21	0.0E+00	AB040909.1	NT	Novel human gene mapping to chromosome X
3561	16316	28963	1.37	0.0E+00	6997248	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3561	16316	28964	1.37	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3562	16317		0.69	0.0E+00	AI081907.1	EST_HUMAN	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3564	16319	28967	1.04	0.0E+00	6325463	NT	CE13742 ;
3569	16324		4.17	0.0E+00	AW852217.1	EST_HUMAN	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3576	16331		0.78	0.0E+00	AF118946.1	NT	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3577	16332	28976	6.46	0.0E+00	BF676393.1	EST_HUMAN	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3589	16343	28988	0.9	0.0E+00	AW837877.1	EST_HUMAN	602084683F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248566 5'
3603	16356	28996	0.74	0.0E+00	BF672054.1	EST_HUMAN	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3603	16356	28997	0.74	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3604	16357		0.95	0.0E+00	4826987	NT	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3606	16359	28999	1.08	0.0E+00	AW664693.1	EST_HUMAN	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3606	16359	29000	1.08	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3609	16362	29004	1.42	0.0E+00	4826763	NT	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3611	16364	29007	0.93	0.0E+00	7682319	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3621	16374	29015	0.82	0.0E+00	4557752	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3621	16374	29015	0.82	0.0E+00	4557752	NT	Homo sapiens midline 1 (Optic/BBB syndrome) (MID1) mRNA
3638	16391	29030	2.67	0.0E+00	D87327.1	NT	Homo sapiens midline 1 (Optic/BBB syndrome) (MID1) mRNA
3642	16395		33.2	0.0E+00	7689491	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3658	16411	29049	2.6	0.0E+00	AB026542.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3660	16413	29051	3.38	0.0E+00	AF124250.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3660	16413	29052	3.38	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3668	16421	29061	1.85	0.0E+00	AL163204.2	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3688	16421	29062	1.85	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3871	16424	29065	1.62	0.0E+00	AW851714.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
							MR2-CT0222-281099-005-e05 CT0222 Homo sapiens cDNA

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Single Exon Probes Expressed in Brain

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3673	18426	29067	1.53	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3674	18426	29067	1.53	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0706 protein, partial cds
3675	18428	29069	1.81	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3676	18430	29071	1.1	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3677	18430	29072	1.1	0.0E+00	AB020717.1	NT	Homo sapiens KIAA0670 protein/actin (KIAA0670), mRNA
3678	18432	29074	22.21	0.0E+00	7662237	NT	Homo sapiens KIAA0670 protein/actin (KIAA0670), mRNA
3679	18432	29075	22.21	0.0E+00	7662237	NT	Homo sapiens KIAA0670 protein/actin (KIAA0670), mRNA
3680	18432	29075	22.21	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3681	18432	29075	22.21	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3682	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3683	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3684	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3685	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3686	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3687	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3688	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3689	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3690	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3691	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3692	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3693	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3694	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3695	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3696	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3697	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3698	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3699	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3700	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3701	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3702	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3703	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3704	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3705	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3706	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3707	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3708	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3709	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3710	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3711	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3712	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3713	18445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-gis-e-12-0.U1.s1 NC1 CGAP Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3714	18467	29105	1.08	0.0E+00	AA463659.1	EST_HUMAN	SW/KRB4_SHEEP P02445 KERA TIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1];
3715	18467	29105	1.08	0.0E+00	AA463659.1	EST_HUMAN	SW/KRB4_SHEEP P02445 KERA TIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1];
3716	18471	29109	1.14	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3717	18471	29109	1.14	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3718	18471	29109	1.14	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3719	18471	29109	1.14	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3720	18471	29109	1.14	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3721	18471	29111	3.31	0.0E+00	7657468	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3722	18471	29111	3.31	0.0E+00	7657468	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3723	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3724	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3725	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3726	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3727	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3728	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3729	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3730	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3731	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3732	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3733	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3734	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3735	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3736	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3737	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3738	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3739	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3740	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3741	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3742	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3743	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3744	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3745	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3746	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3747	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3748	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3749	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3750	18482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3751	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3752	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3753	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3754	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3755	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3756	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3757	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3758	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3759	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3760	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3761	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3762	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3763	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3764	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3765	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3766	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3767	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3768	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3769	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3770	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3771	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3772	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3773	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3774	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3775	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3776	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3777	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3778	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3779	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3780	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3781	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3782	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3783	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3784	18503	29138	1.08	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3785	18503	29138	1.08</				

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3831	16582	29216	1.12	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3835	16586	29222	6.16	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3835	16586	29223	6.16	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3837	16588	29226	4.04	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3838	16589	29227	0.69	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3841	16592	29229	2.96	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3844	16595	29232	1.05	0.0E+00	AF012815.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3845	16596	29233	1.43	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3847	16598	29235	0.74	0.0E+00	AF098117.1	NT	Homo sapiens amphiphysin gene, partial cds
3856	16606	29244	2.16	0.0E+00	AI894727.1	EST_HUMAN	wk01801.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:043340
3859	16609	29248	4.24	0.0E+00	4506742	NT	O43340 R28830_2, contains element P TR7 repetitive element;
3862	16612	29251	1.35	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3867	16617	29256	1.28	0.0E+00	6005887	NT	DKFZp434N0413_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0413 5'
3867	16617	29257	1.28	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3869	16619	29259	3.22	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3871	16621	29263	1.82	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3875	16625	29263	1.18	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3884	16634	29273	1.2	0.0E+00	4506788	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3888	16638	29277	1.47	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
3886	16646	29286	1.18	0.0E+00	BF355295.1	EST_HUMAN	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA
3898	16648	29286	1.05	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5 Matrix remodeling associated gene 5
3898	16648	29289	1.05	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5 Matrix remodeling associated gene 5
3904	16654	29295	1.82	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein Fb35 (FBL3B) mRNA, partial cds
3907	16657	29298	1	0.0E+00	AW451306.1	EST_HUMAN	UHLH-B13-ah-g-07-Q-J1.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2736949 3'
3912	16662	29303	2.81	0.0E+00	BE378602.1	EST_HUMAN	601236988F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
3920	16670	29311	0.92	0.0E+00	AW580740.1	EST_HUMAN	PM3-LT0031-100100-003-H09 LT0031 Homo sapiens cDNA
3922	16672	29312	2.49	0.0E+00	5360215	NT	Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA
3923	16673	29313	0.98	0.0E+00	BE284998.1	EST_HUMAN	601193827F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3923	16673	29314	0.98	0.0E+00	BE284998.1	EST_HUMAN	601193827F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3952	16702	29339	1.42	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3952	16702	29340	1.42	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
3952	16702	29341	1.42	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
3957	16706	29344	4.69	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3957	16706	29345	4.69	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3966	16715		4.39	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
3968	16717		5.74	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
3975	16724	29359	1.35	0.0E+00	AL118494.1	NT	Novel human gene mapping to chromosome 20
3979	16727	29361	3.22	0.0E+00	AL163294.2	NT	Homo sapiens chromosome 21 segment HS21C084
3987	16735	29369	1.71	0.0E+00	AL163268.2	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
3989	16747		27.98	0.0E+00	4503470	NT	Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:060309 O60309
4003	16750		1.15	0.0E+00	AI657076.1	EST HUMAN	ti55g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:060309 O60309
4005	16751	29382	2.97	0.0E+00	7662183	NT	KIAA0563 PROTEIN
4006	16752	29383	2.65	0.0E+00	U09386.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4013	16759	29387	0.95	0.0E+00	AW339490.1	EST_HUMAN	Human zinc finger protein ZNF133
4024	16769	29401	6.33	0.0E+00	AB015610.1	NT	xz81et10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871594 3'
4033	16778		3.72	0.0E+00	AJ238617.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
4045	16790	29418	1.32	0.0E+00	AB002314.2	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene)
4046	16791	29419	1.04	0.0E+00	AL163203.2	NT	Homo sapiens mRNA for KIAA0316 protein, partial cds
4047	16792	29420	1.18	0.0E+00	AF036943.1	NT	Homo sapiens chromosome 21 segment HS21C003
4048	16793	29421	2.65	0.0E+00	AJ27276.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
4048	16793	29422	2.65	0.0E+00	AJ27276.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4054	16799	29429	6.29	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4054	16799	29430	6.29	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4068	16813	29442	4.7	0.0E+00	4885306	NT	Homo sapiens protein-coupled receptor 21 (GPR21), mRNA
4070	16814	29443	5.98	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4073	16817	29444	1.11	0.0E+00	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4074	16818	29445	5.87	0.0E+00	11419287	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4075	16819	29446	1.94	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4082	16826	29453	2.71	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4091	13867	26525	0.82	0.0E+00	4926947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4091	13867	26526	0.82	0.0E+00	4926947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4097	16840	29466	1.09	0.0E+00	6901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
4099	16842	29469	1.08	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4099	16842	29470	1.08	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60KD) (GABPA), mRNA
4107	16850	29476	0.89	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4112	16855	29482	4.93	0.0E+00	A1982597.1	EST_HUMAN	wu04404.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2515975 3'
4112	16855	29483	4.93	0.0E+00	A1982597.1	EST_HUMAN	wu04404.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2515975 3'
4115	16857	29485	0.82	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4115	16857	29485	0.82	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4115	16857	29486	0.82	0.0E+00	BE274217.1	EST_HUMAN	601120778FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867690 5'
4120	16862		2.34	0.0E+00	BE274217.1	EST_HUMAN	Homo sapiens mRNA for KIAA1125 protein, partial cds
4126	16868	29495	0.99	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4126	16868	29496	0.99	0.0E+00	AB032951.1	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4128	16870	29498	2.24	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4135	16877		5.52	0.0E+00	AW675599.1	EST_HUMAN	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:TH12_BOVIN
4140	16882	29511	1.14	0.0E+00	AW408788.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4142	16884	29514	1.26	0.0E+00	8922466	NT	U1HF-BM0-adx-c-020-UI.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083147 5'
4142	16884	29515	1.26	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4151	16893		2.8	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4169	16909	29537	8.97	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu
4169	16909	29538	8.97	0.0E+00	AA401438.1	EST_HUMAN	repetitive element contains element MER35 repetitive element ;
4205	16946		1.01	0.0E+00	AL163303.2	NT	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu
4240	16981	29606	4.08	0.0E+00	J02610.1	NT	repetitive element contains element MER35 repetitive element ;
4255	16996	29625	0.83	0.0E+00	AW936689.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4281	17002	29633	0.74	0.0E+00	4826827	NT	Homo sapiens apolipoprotein B-100 mRNA, complete cds
4281	17002	29634	0.74	0.0E+00	4826827	NT	Human apolipoprotein B-100 mRNA, complete cds
4283	17004	29636	4.7	0.0E+00	AF174590.1	NT	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4270	17010		2.52	0.0E+00	AI189844.1	EST_HUMAN	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4273	17012		4.32	0.0E+00	U14520.1	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4285	17024	29650	1.35	0.0E+00	4505646	NT	Homo sapiens F-box protein Fbx4 (FBL4) mRNA, partial cds
4291	17030	29657	0.76	0.0E+00	6563384	NT	Homo sapiens placenta_8to9weeks_2NH-HP8c9W Homo sapiens cDNA clone IMAGE:1724579 3'
4291	17030	29658	0.76	0.0E+00	6563384	NT	similar to contains MER20 b2 MER20 repetitive element ;
4293	17036	29684	1.58	0.0E+00	U10991.1	NT	Human CBFA3 (Cbfa3) gene, partial cds
			4.32	0.0E+00	U14520.1	NT	Human CBFA3 (Cbfa3) gene, partial cds
			1.35	0.0E+00	4505646	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
			0.76	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
			0.76	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
			1.58	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4297	17036	29665	1.58	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4307	17046	29671	8.31	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4327	17068		1.16	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4337	17078	29704	4.17	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4341	17080	29709	2.88	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4341	17080	29710	2.88	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4342	17081	29711	0.94	0.0E+00	AW169833.1	EST_HUMAN	xg68e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2633514 3' similar to TR:P97365 P97365
4348	17087	29717	1.42	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 64 ;
4348	17087	29718	1.42	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4353	17091	29724	8.62	0.0E+00	7662091	NT	H. sapiens KIAA0390 gene product (KIAA0390), mRNA
4353	17091	29725	8.62	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4366	17104	29740	12.99	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4367	17105	29741	1.14	0.0E+00	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4400	17137	29766	0.98	0.0E+00	7019456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4408	17145		6.5	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4414	17151	29778	1.25	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4414	17151	29778	1.25	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4436	17172		1.81	0.0E+00	AF200629.1	NT	Homo sapiens HPST gene, intron 5
4453	17189	29814	1.43	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cc18-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F1205 5'
4453	17189	29815	1.43	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cc18-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F1205 5'
4458	17192		0.73	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4466	17202	29828	5.68	0.0E+00	AW084964.1	EST_HUMAN	Q09688 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4468	17881		1.57	0.0E+00	8051619	NT	xc68e08.x1 NCL_CGAP_Es02 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW-AHNK_HUMAN
4470	17205	29831	0.93	0.0E+00	AI696998.1	EST_HUMAN	Q09688 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4473	17203		8.82	0.0E+00	AL163207.2	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4475	17210	29835	3.17	0.0E+00	AW381570.1	EST_HUMAN	wc68e02.x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:232603 3' similar to contains MER22.b2
4481	17216	29842	1.99	0.0E+00	AJ278120.1	NT	P TR5 repetitive element ;
4481	17216	29843	1.99	0.0E+00	AJ278120.1	NT	Homo sapiens chromosome 21 segment HS21C007
4483	17218	29845	1.29	0.0E+00	4758467	NT	PM1-HT0305-101199-002-403 HT0305 Homo sapiens cDNA
4484	17219	29846	2.88	0.0E+00	AF109830.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
							Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
							Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
							Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
							Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4493	17229	29858	1.26	0.0E+00	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4494	17230	29859	1.06	0.0E+00	AF111163.1	NT	Homo sapiens pyrim (MEFV) gene, complete cds
4494	17230	29860	1.06	0.0E+00	AF111163.1	NT	Homo sapiens pyrim (MEFV) gene, complete cds
4502	17882	29870	2.56	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4507	17242	29875	6.16	0.0E+00	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4512	17247	29882	4.31	0.0E+00	AF152337.1	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4515	17250	29886	1.32	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4525	17260	29894	15.47	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4532	17267	29900	0.79	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4536	17271	29903	1.61	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4540	17275	29908	2.03	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4544	17279		2.38	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4546	17281	29910	12.72	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4546	17281	29911	12.72	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4563	17298	29926	0.96	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4566	17301	29928	10.33	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4566	17301	29929	10.33	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4581	17316		1.68	0.0E+00	AA174072.1	EST_HUMAN	zfp18g08.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4583	17318		1.46	0.0E+00	7657410	NT	Homo sapiens cdx (odd Ozlen-m, Drosophila) homolog 1 (ODZ1), mRNA
4585	17320		3.16	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4586	17321	29947	1.04	0.0E+00	H92741.1	EST_HUMAN	y92b01.s1 Soares_pheal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4586	17321	29948	1.04	0.0E+00	H92741.1	EST_HUMAN	y92b01.s1 Soares_pheal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4587	17322	29949	2.8	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTIR) gene, complete cds
4588	17323	29950	4.94	0.0E+00	AF183300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4589	17324		1.66	0.0E+00	AB037521.1	NT	Homo sapiens gene for retinoid protein, partial cds
4586	17331	29956	1.53	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4586	17331	29959	1.53	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4597	17332	29960	1.52	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4597	17332	29961	1.52	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds

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4598	17333	29962	1.5	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4605	17340	29970	1.22	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4605	17340	29971	1.22	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4611	17346	29979	5.25	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4617	17352	29987	1.08	0.0E+00	AA418246.1	EST_HUMAN	z66807.s1 Soares_NIH-MPU_S1 Homo sapiens cDNA clone IMAGE:767605 3'
4624	17359		2.27	0.0E+00	AF086641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4629	17364	29998	1.06	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4629	17364	29999	1.06	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4630	17365	30000	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4630	17365	30001	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4631	17366	30002	2.67	0.0E+00	MT74099.1	NT	Human displacement protein (CCAA1) mRNA
4635	17370	30005	1.84	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4635	17370	30006	1.84	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4636	17370	30006	0.82	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4636	12950	25593	0.82	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4636	12950	25594	0.82	0.0E+00	BE278730.1	EST_HUMAN	601158939F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'
4639	17373		1.31	0.0E+00	U56651.1	NT	Mus musculus neurophilin 1 (Nuph1) gene, large exon and 3' end of the intron, and partial cds
4660	17394	30029	1.33	0.0E+00	U56651.1	NT	Human AFNAK nucleoprotein mRNA, 5' end
4665	17399	30033	5.87	0.0E+00	M80902.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4668	17402	30036	2.23	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4668	17402	30037	2.23	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (NKTR) gene, complete cds
4671	17405	30040	1.9	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4673	17407	30042	2.02	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4680	17414	30049	0.95	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4681	17415	30050	0.97	0.0E+00	S71446.1	NT	SCN1A=brain type I sodium channel alpha-subunit (IIIS5 transmembrane region) [human, placenta, Genomic, 1556 nt]
4681	17415	30051	0.97	0.0E+00	S71446.1	NT	SCN1A=brain type I sodium channel alpha-subunit (IIIS5 transmembrane region) [human, placenta, Genomic, 1556 nt]
4692	17426		1.45	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4701	17435	30065	1.05	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4701	17435	30066	1.05	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4709	17441	30073	1.4	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26
4712	17444	30076	0.84	0.0E+00	7019320	NT	Homo sapiens protein x0008 (AD013), mRNA

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4712	17444	30077	0.84	0.0E+00	7019320	NT	Homo sapiens protein0008 (AD013), mRNA
4735	17467	30103	1.88	0.0E+00	AW444637.1	EST_HUMAN	UL-H-B13- α -w-c-04-0-UI.s1 NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294.3'
4740	17472		1.82	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4750	17482		2.28	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
4790	17521		2.79	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4794	17525	30147	2.02	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4798	17527	30149	1.11	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSER9) mRNA, complete cds
4797	17528	30150	1.96	0.0E+00	AF097418.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4798	17529	30151	3.01	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4800	17531	30153	13.57	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4801	17532	30154	1.04	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4805	17536	30159	5.7	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4809	17540	30163	0.97	0.0E+00	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4810	17541	30164	1.84	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4810	17541	30165	1.84	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4812	17543	30167	1.44	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4812	17543	30168	1.44	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4815	17546	30171	2.96	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4823	17554	30176	1.17	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, l 28kD (TAF21) mRNA
4830	17561	30183	1.09	0.0E+00	X92841.1	NT	H.sapiens MICA gene
4832	17563	30185	1.91	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4833	17564	30186	1.81	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4834	17565	30187	2.24	0.0E+00	6677648	NT	Homo sapiens zinc finger protein interacting with K protein 1 (Zik1), mRNA
4835	17566	30188	0.95	0.0E+00	5174560	NT	Mus musculus zinc finger protein expressed with K protein 1 (Zik1), mRNA
4836	17567	30189	1.19	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DP1) (DSP) mRNA
4838	17569	30191	1.81	0.0E+00	7705548	NT	Homo sapiens zinc-finger DNA-binding protein (HUM-HOXY1), mRNA
4842	17572	30196	12.62	0.0E+00	AF055066.1	NT	Homo sapiens opid receptor, delta 1 (OPRD1) mRNA
4844	17574		3.47	0.0E+00	4505508	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4845	17575	30199	2.39	0.0E+00	AF091711.1	NT	Homo sapiens COL4A6 gene for α (IV) collagen, exon 44 and partial cds
4858	17587	30210	1.07	0.0E+00	D63562.1	NT	Homo sapiens COL4A6 gene for α (IV) collagen, exon 44 and partial cds

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4860	17589	30212	1.88	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDP-S) mRNA
4865	17224	29852	1.03	0.0E+00	4506952	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminidase: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4875	17602	30224	3.09	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4875	17602	30225	3.09	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4885	17612	30232	0.95	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4899	17626	30243	1.45	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4906	17633	30248	1.02	0.0E+00	AW452728.1	EST_HUMAN	UI-HB13-ahv-4-02-0-UJ.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068691 3'
4909	17637	30251	1.81	0.0E+00	8922828	NT	Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA
4912	17640	30255	1.09	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
4915	17643		4.69	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
4924	17652		2.95	0.0E+00	BE408663.1	EST_HUMAN	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
4928	17656	30268	3.18	0.0E+00	4758169	NT	Homo sapiens desmoplakin (DPI, DPIP) (DSP) mRNA
4933	17661	30271	1.15	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4938	17666	30274	1.01	0.0E+00	AB028966.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
4947	17674	30283	2.34	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4947	17674	30284	2.34	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4958	17683	30291	0.81	0.0E+00	AA601246.1	EST_HUMAN	nc14g09.s1 NCI CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
4958	17683	30292	0.81	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN ;
4958	17683	30293	0.81	0.0E+00	AA601246.1	EST_HUMAN	nc14g09.s1 NCI CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
4961	17686	30295	1.11	0.0E+00	AF161463.1	NT	E239140 SPALT PROTEIN ;
4961	17686	30296	1.11	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
4973	13019	25661	0.71	0.0E+00	AF185868.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4976	17699		0.84	0.0E+00	AL050253.1	NT	H.sapiens mRNA similar to D29763 mouse mRNA for seizure-related gene product 6. Shares domains with BMPs, Tollid, Sushi repeat proteins
4985	17708	30312	1.63	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
4986	17709	30313	1.5	0.0E+00	Y19186.1	NT	Mus musculus mRNA for aczonin, short spliced variant (acz gene)
4986	17709	30314	1.5	0.0E+00	Y19186.1	NT	Mus musculus mRNA for aczonin, short spliced variant (acz gene)
4994	17717		1.26	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4997	17720		26.03	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5001	17724	30326	0.97	0.0E+00	AA084272.1	EST_HUMAN	zn03g10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546402 5'
5001	17724	30327	0.97	0.0E+00	AA084272.1	EST_HUMAN	zn03g10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546402 5'
5012	16924	29553	0.95	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5012	16924	29554	0.95	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5026	17747	30359	3	0.0E+00	X52988.1	NT	Bacillus amyloqueladens sacB gene for levansucrase (EC 2.4.1.10)
5042	17761	30375	1.04	0.0E+00	AF240835.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5042	17761	30376	1.04	0.0E+00	AF240835.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5045	17764	30380	1.55	0.0E+00	7657074	NT	Homo sapiens ecotropic viral integration site 2A (EVI2A), mRNA
5045	17764	30381	1.55	0.0E+00	7657074	NT	Homo sapiens ecotropic viral integration site 2A (EVI2A), mRNA
5049	17768	30387	1.11	0.0E+00	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5050	17769	30388	14.05	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
5052	17771	30389	1.03	0.0E+00	4557362	NT	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA
5056	17775	30391	2.75	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5056	17775	30392	2.75	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5058	17777	30394	1.07	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5079	17798	30414	1.01	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5079	17798	30415	1.01	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5081	17800	30417	0.76	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5081	17800	30418	0.76	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5088	17807	30423	2.69	0.0E+00	7657008	NT	Homo sapiens deleted in bladder cancer chromosome region candidate 1 (DBCOR1), mRNA
5097	17816	30433	2.05	0.0E+00	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
5109	17827	30444	1.23	0.0E+00	D48802.1	NT	Mus musculus mRNA for leucine-rich repeat protein, partial cds
5110	17828	30445	1.14	0.0E+00	AF227534.1	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo mRNA, complete cds, long splice variant
5111	17829	30446	1.88	0.0E+00	AF227534.1	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo mRNA, complete cds, long splice variant
5112	17830	30447	0.99	0.0E+00	AF245702.1	NT	Homo sapiens toll-like receptor 7 (TLR7) mRNA, complete cds
5115	17833	30449	6.53	0.0E+00	4505068	NT	Homo sapiens microtubule-associated protein 2 (MAP2) mRNA
5116	17834	30450	1.5	0.0E+00	6008002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
5116	17834	30451	1.5	0.0E+00	6008002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
5117	17835	30452	1.6	0.0E+00	AW855818.1	EST_HUMAN	EST367889 MAGD resequences, MAGD Homo sapiens cDNA
5119	17837		1.31	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
5128	17844		1.12	0.0E+00	AJ010179.1	NT	Homo sapiens gabar1 receptor gene, exon 6

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5139	17857	30473	5.57	0.0E+00	AB027013.1	NT	Homo sapiens mRNA for Nucleosome Assembly Protein 1-like 2, complete cds
5150	17861	30477	1.19	0.0E+00	AB035358.1	NT	Homo sapiens mRNA for neuroxin I-alpha protein, complete cds
5151	17868	30481	1.18	0.0E+00	AB029040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds
5154	17871		1.08	0.0E+00	M91803.1	NT	Human sodium channel mRNA
5155	17872	30484	1.37	0.0E+00	5454013	NT	Homo sapiens ring finger protein 15 (RNF15), mRNA
5162	17893		3.44	0.0E+00	AF068093.1	NT	Homo sapiens acinase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5172	17981	30495	2.52	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5172	17981	30496	2.52	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5192	18000	30623	1.29	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
5195	18003	30626	1.77	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDH13), mRNA
5209	18017	30639	3.81	0.0E+00	BE631080.1	EST_HUMAN	RC3-GN0076-310800-013-b03 GN0076 Homo sapiens cDNA
5213	18021	30643	3	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5213	18021	30644	3	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5220	18027	30652	1.66	0.0E+00	X58163.1	NT	H sapiens immunoglobulin heavy chain gene, variable region
5220	18027	30653	1.66	0.0E+00	X58163.1	NT	H sapiens immunoglobulin heavy chain gene, variable region
5299	18104	30763	6.56	0.0E+00	BE675498.1	EST_HUMAN	7f10c08.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3284250 3'
5300	18105	30764	1.75	0.0E+00	BE220753.1	EST_HUMAN	H99a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN
5301	18106	30765	1.93	0.0E+00	BE794412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0054.;
5301	18106	30766	1.93	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5302	18107	30767	0.81	0.0E+00	AI189142.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5308	18111	30770	6.17	0.0E+00	M29908.1	NT	q04a04.x1 Soares_placenta_8tc9weeks_2NblHP8tc8W Homo sapiens cDNA clone IMAGE:1722702 3'
5319	25066	30780	4.68	0.0E+00	11421038	NT	similar to SW:T2D3_DROME P49846 TRANSCRIPTION INITIATION FACTOR TFIIID 85 KD SUBUNIT ;
5329	18132		7.18	0.0E+00	BF685982.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4), mRNA
5330	18133	30791	0.73	0.0E+00	AU134406.1	EST_HUMAN	602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276254 5'
5330	18133	30792	0.73	0.0E+00	AU134406.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5335	18138	30799	1	0.0E+00	BE538857.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5344	18147	30826	1.07	0.0E+00	BE292784.1	EST_HUMAN	601061489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5348	18151	30831	1.69	0.0E+00	BF526328.1	EST_HUMAN	601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310 5'
5348	18151	30832	1.69	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4214272 5'
5367	19491	32513	1.82	0.0E+00	4557364	NT	602071372F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4214272 5'
5370	18171	30858	0.91	0.0E+00	AB007835.1	NT	Homo sapiens Bloom syndrome (BLM) mRNA
							Homo sapiens mRNA for KIAA0466 protein, partial cds

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5370	18171	30859	0.91	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
5374	18174	30863	4.85	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5374	18174	30864	4.85	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5387	18187	30878	1.08	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5387	18187	30879	1.06	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5401	18201	30906	1.88	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5407	18206	30912	0.81	0.0E+00	Z38133.1	NT	H. sapiens mRNA for myosin
5426	18225	30938	0.78	0.0E+00	D61564.1	EST_HUMAN	HUM418D06B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5426	18225	30938	0.78	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5429	18228	30941	2.55	0.0E+00	BF52931.1	EST_HUMAN	602042322F1 NCJ CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179988 5'
5429	18228	30942	2.55	0.0E+00	BF52931.1	EST_HUMAN	602042322F1 NCJ CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179988 5'
5434	18233	30946	2.92	0.0E+00	BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5445	18244	31132	4.37	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5477	18276	31171	1.15	0.0E+00	BE260777.1	EST_HUMAN	601150252F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502909 5'
5486	18285	31196	3.51	0.0E+00	AW887316.1	EST_HUMAN	MRO-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5500	18298	31197	2.33	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5500	18298	31197	2.33	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5521	18319	31219	1.51	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5521	18319	31220	1.51	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5528	18326	31228	4.35	0.0E+00	AF084254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5528	18326	31229	4.35	0.0E+00	AF084254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5535	18333	31239	2.95	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5535	18333	31240	2.95	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5568	18363	31271	0.61	0.0E+00	AI198515.1	EST_HUMAN	Homo sapiens Surf-5 and Surf-6 genes
5570	18367	31277	6.98	0.0E+00	M85719.1	EST_HUMAN	q194g10.x1 Scores, placenta, 86weeks, 2NHP86c9W Homo sapiens cDNA clone IMAGE:1757730 3'
5577	18374	31286	4.83	0.0E+00	AW405472.1	EST_HUMAN	similar to SW-CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR :
5590	18386	31296	1.25	0.0E+00	Z26269.1	NT	UI-HF-BLO-acth-d-02-Q-J11 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3081658 5'
5590	18386	31296	1.25	0.0E+00	Z26269.1	NT	H. sapiens isoform 1 gene for L-type calcium channel, exon 14 adin 16
5601	18396	31306	1.94	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5601	18396	31307	1.94	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5601	18396	31308	1.94	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5605	18401	31315	2.55	0.0E+00	U36261.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13

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5636	18431	31344	1.03	0.0E+00	AB046861.1	Homo sapiens mRNA for KIAA1841 protein, partial cds
5691	18485	31404	1.56	0.0E+00	AJ006345.1	Homo sapiens KVLQ11 gene
5691	18485	31405	1.56	0.0E+00	AJ006345.1	Homo sapiens KVLQ11 gene
5699	18493	31416	1.19	0.0E+00	AJ207616.1	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5717	18509	31430	5.23	0.0E+00	11416801	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
5722	18514	31433	1.21	0.0E+00	BE791173.1	Homo sapiens cDNA clone IMAGE:3938551 5'
5731	18523	31444	1.13	0.0E+00	9998943	601584032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938551 5'
5732	18524	31445	6.59	0.0E+00	BE560082.1	Homo sapiens aniloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
5733	18525	31446	1.67	0.0E+00	10048478	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5734	18526	31447	4.05	0.0E+00	U86961.1	Mus musculus accorin (Acc), mRNA
5734	18526	31448	4.05	0.0E+00	U86961.1	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5752	18544	31466	2.28	0.0E+00	BF33835.1	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5756	18548	31469	1.03	0.0E+00	AF142621.1	602036272F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184321 5'
5757	18549	31470	3.06	0.0E+00	BE273983.1	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
5768	18559	31486	0.88	0.0E+00	BE503096.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5773	18564	31493	1.87	0.0E+00	BF569905.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5778	18569	31497	1.21	0.0E+00	AA454642.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5811	18600	31528	2.38	0.0E+00	AF217289.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5813	18602	31530	1.75	0.0E+00	BE828144.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5818	18607	31535	2.27	0.0E+00	BE958636.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5831	18620	31552	0.55	0.0E+00	BE673986.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5831	18620	31553	0.55	0.0E+00	BE673986.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5836	18625	31559	1.14	0.0E+00	AW278760.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5847	18634	31571	1.16	0.0E+00	BF031742.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5847	18634	31572	1.16	0.0E+00	BF031742.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5859	18646	31587	0.58	0.0E+00	AW470846.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5872	18658	31599	0.77	0.0E+00	BF156670.1	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'

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5872	18659	31600	0.77	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-290900-399-a10 HT0894 Homo sapiens cDNA
5878	18664	31604	3.22	0.0E+00	W33069.1	EST_HUMAN	zc08h08.r1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
5878	18664	31605	3.22	0.0E+00	W33069.1	EST_HUMAN	zc08h08.r1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
5879	18665		2.51	0.0E+00	AF012618.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
5882	18668	31609	3.33	0.0E+00	BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
5887	18675	31620	2.6	0.0E+00	BE889610.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
5905	18690	31639	0.6	0.0E+00	AW752848.1	EST_HUMAN	IL3-CT0220-111199-028-E04 CT0220 Homo sapiens cDNA
5908	18692	31641	1.1	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA
5908	18692	31642	1.1	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA
5909	18693	31643	0.88	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
5909	18693	31644	0.88	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
5909	18693	31645	0.88	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
5923	25081	31661	10.66	0.0E+00	9789986	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
5926	18710	31664	1.2	0.0E+00	AA193508.1	EST_HUMAN	zr40h01.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
5926	18710	31665	1.2	0.0E+00	AA193508.1	EST_HUMAN	zr40h01.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
5948	18730	31689	16.77	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5948	18730	31690	16.77	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5987	18768	31732	0.96	0.0E+00	BE258330.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355563 5'
5997	18778	31740	1.2	0.0E+00	BE156561.1	EST_HUMAN	QV0-HT0368-090200-099-a09 HT0368 Homo sapiens cDNA
6007	18788	31750	0.85	0.0E+00	M38107.1	NT	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6040	18820	31781	1.32	0.0E+00	BE379007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
6048	18826	31787	1.39	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
6066	18845	31809	3.76	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
6094	18872	31839	4.52	0.0E+00	AA204740.1	EST_HUMAN	zq81403.r1 Stragene INT neuron (#37233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
6095	18873	31840	3.97	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6095	18873	31841	3.97	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6129	18907	31875	1.14	0.0E+00	11428367	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6133	18911	31890	2.87	0.0E+00	BE257173.1	EST_HUMAN	601109532F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350622 5'
6147	18924		0.85	0.0E+00	AN86048.1	EST_HUMAN	td91f10.x1 NC1_CGAP_P228 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TRQ14839 Q14839 MI-2 PROTEIN. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6151	18928	31897	1.53	0.0E+00	L35930.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6159	18936	31903	1.22	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6159	18936	31904	1.22	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6170	18947	31919	0.57	0.0E+00	AI198025.1	EST_HUMAN	q150b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT ;
6170	18947	31920	0.57	0.0E+00	AI198025.1	EST_HUMAN	q150b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT ;
6172	18949	31921	0.85	0.0E+00	BF357123.1	EST_HUMAN	MRO-HT0923-220800-102-505 HT0923 Homo sapiens cDNA
6180	18957	31931	1.08	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51296), mRNA
6189	18966	31939	0.65	0.0E+00	D55649.1	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6207	18982	31961	1.03	0.0E+00	AW178142.1	EST_HUMAN	IL3-HT0062-010999-014-A04 HT0062 Homo sapiens cDNA
6228	19002	31978	0.66	0.0E+00	BE674544.1	EST_HUMAN	7e02c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302 3' similar to SW:Y176_HUMAN
6232	19006	31983	1.33	0.0E+00	7662039	NT	Q14681 HYPOTHETICAL PROTEIN KIAA0176 ; Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6246	19020		8.59	0.0E+00	AV650020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'
6254	19028	32003	3.13	0.0E+00	AW575598.1	EST_HUMAN	UI-HF-BL0-acc-g-12-Q-UJ.st NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
6257	19031	32006	6.26	0.0E+00	H01255.1	EST_HUMAN	Y27503.1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:149933 5'
6269	19042	32019	1.6	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
6271	19044	32021	0.65	0.0E+00	AA456375.1	EST_HUMAN	aa14607.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813252 5'
6272	19045	32022	1.3	0.0E+00	AI612841.1	EST_HUMAN	tz57d08.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292687 3' similar to SW:NTCS_HUMAN P53796 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2 ;
6278	19051	32028	4.71	0.0E+00	BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6278	19051	32029	4.71	0.0E+00	BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6282	19055	32035	0.86	0.0E+00	AW748596.1	EST_HUMAN	MRO-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA
6282	19055	32036	0.86	0.0E+00	AW748596.1	EST_HUMAN	MRO-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA
6283	19056		0.6	0.0E+00	U77629.1	NT	Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
6285	19058	32038	15.59	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6285	19058	32039	15.59	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6289	19062	32044	0.8	0.0E+00	BE780453.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871869 5'
6290	19063	32045	1.12	0.0E+00	X92217.1	NT	H.sapiens germ-line immunoglobulin heavy chain, variable region, (13-2)
6304	19076	32062	1.52	0.0E+00	AI989483.1	EST_HUMAN	ws25c07.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2498220 3'
6317	19088	32072	6.91	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
6317	19088	32073	6.91	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6355	19125	32119	0.58	0.0E+00	BF057438.1	EST_HUMAN	7k43h05.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3478496 3' similar to TR:O14553 O14553
6388	19157	32157	1.89	0.0E+00	AW406348.1	EST_HUMAN	R31240.1;
6388	19157	32157	1.89	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BLO-eco-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059831 5'
6418	19186	32184	0.79	0.0E+00	AV719444.1	EST_HUMAN	UI-HF-BLO-eco-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059831 5'
6427	19195	32191	0.98	0.0E+00	BE898340.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GL CEHC06 5'
6427	19195	32192	0.98	0.0E+00	BE898340.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GL CEHC06 5'
6430	19198	32195	2.24	0.0E+00	AF190860.1	NT	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6433	19201	32197	1.17	0.0E+00	11420658	NT	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6440	19208	32204	7.5	0.0E+00	AW163840.1	EST_HUMAN	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
6440	19208	32205	7.5	0.0E+00	AW163840.1	EST_HUMAN	Homo sapiens transformin/transcription domain-associated protein (TRRAP), mRNA
6444	19212	32208	0.97	0.0E+00	W37163.1	EST_HUMAN	Homo sapiens transformin/transcription domain-associated protein (TRRAP), mRNA
6444	19212	32209	0.97	0.0E+00	W37163.1	EST_HUMAN	Homo sapiens transformin/transcription domain-associated protein (TRRAP), mRNA
6459	19226	32226	1.08	0.0E+00	BE794853.1	EST_HUMAN	al96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784169 5' similar to
6466	19233	32233	5.81	0.0E+00	BE799873.1	EST_HUMAN	TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206;
6467	19234	32234	0.56	0.0E+00	BE767955.1	EST_HUMAN	al96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784169 5' similar to
6467	19234	32235	0.56	0.0E+00	BE767955.1	EST_HUMAN	TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206;
6471	19238	32238	6.95	0.0E+00	BE89813.1	EST_HUMAN	z520a06.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:302628 5' similar to
6471	19238	32239	6.95	0.0E+00	BE89813.1	EST_HUMAN	SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6480	19247	32247	5.62	0.0E+00	L24493.1	NT	SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6485	19252	32251	1.98	0.0E+00	AL163204.2	NT	SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6485	19252	32252	1.98	0.0E+00	AL163204.2	NT	SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6491	19258	32259	4.06	0.0E+00	6005963	NT	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6494	19260	32261	4.76	0.0E+00	AI638412.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6495	19261	32262	1.36	0.0E+00	L32832.1	NT	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6507	19272	32273	4.12	0.0E+00	AA434594.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6520	19286		0.99	0.0E+00	BF217200.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6523	19289	32263	1.82	0.0E+00	BE925875.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
							601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
							Human antigen CD27 gene, exons 1-2
							Homo sapiens chromosome 21 segment HS21C004
							Homo sapiens chromosome 21 segment HS21C004
							Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
							1631f11.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE
							P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR;
							Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
							zw52c03.r1 Soares total fetal Nb2HF8_gw Homo sapiens cDNA clone IMAGE:773668 5'
							601895317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
							QV3-BN0047-300800-278-c08 BN0047 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6554	19319	32325	1.11	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6554	19319	32326	1.11	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6571	19335	32348	1.6	0.0E+00	AU125928.1	EST_HUMAN	Homo sapiens cDNA clone NT2RM4002430 5'
6573	19337	32348	1.88	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-280700-001-h10 NN0174 Homo sapiens cDNA
6573	19337	32349	1.88	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-280700-001-h10 NN0174 Homo sapiens cDNA
6594	19357	32371	1.87	0.0E+00	BE142363.1	EST_HUMAN	CM0-HT0143-270999-062-d08 HT0143 Homo sapiens cDNA
6614	19377	32391	1.44	0.0E+00	BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6614	19377	32392	1.44	0.0E+00	BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6638	19400	32415	8.38	0.0E+00	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6640	19402	32417	1.93	0.0E+00	BF085687.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6678	19595	32683	3.49	0.0E+00	AA190755.1	EST_HUMAN	z88c03.r1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:827292 5'
6690	19607	32647	0.94	0.0E+00	U39573.1	NT	Human salivary peroxidase mRNA, complete cds
6693	19610	32649	0.91	0.0E+00	BE671987.1	EST_HUMAN	7449007.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:322037 3' similar to TR:Q9Z285 Q9Z285 TEKTN.
6703	19618	32660	6.69	0.0E+00	A1940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6703	19618	32661	6.69	0.0E+00	A1940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6714	19628	32674	1.91	0.0E+00	11435628	NT	Homo sapiens CD6 antigen (CD6), mRNA
6726	19560	32592	0.99	0.0E+00	AL042443.1	EST_HUMAN	DKFZp434D2021.1 434 (synonym: hss3) Homo sapiens cDNA clone IMAGE:1565761 3' similar to
6729	19563	32595	0.9	0.0E+00	A1168270.1	EST_HUMAN	0010001.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3842080 5'
6734	19568	32600	0.83	0.0E+00	BE734087.1	EST_HUMAN	TR:Q26823 Q26823 TEKTN C1.;
6752	17921	30556	1.88	0.0E+00	BE566381.1	EST_HUMAN	601567370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
6761	17930	30565	11.84	0.0E+00	BE867889.1	EST_HUMAN	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682267 5'
6761	17930	30566	11.84	0.0E+00	BE867889.1	EST_HUMAN	601436677F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6768	19510	32535	2.2	0.0E+00	BE560162.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6768	19510	32536	2.2	0.0E+00	BE560162.1	EST_HUMAN	7b4903.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
6790	19534	32582	1.25	0.0E+00	BF088378.1	EST_HUMAN	Q08379 GOLGIN-95.;
6796	19540	32588	2.48	0.0E+00	AA195108.1	EST_HUMAN	Q08379 GOLGIN-95.;
6803	19464		12.37	0.0E+00	11034810	NT	CM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA z34g03.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665332 5' Homo sapiens calenlin (catharin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA

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6805	19466	32487	1.08	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
6807	19468	32490	0.6	0.0E+00	BE313075.1	EST_HUMAN	601150862F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503391 5'
6807	19468	32491	0.6	0.0E+00	BE313075.1	EST_HUMAN	601150862F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503391 5'
6822	19483	32505	2.69	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6837	19499		2.32	0.0E+00	J03069.1	NT	Human MYCL2 gene, complete cds
6845	19545	32573	3.52	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6845	19545	32574	3.52	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6848	19546	32575	1.18	0.0E+00	M38113.1	NT	Human neurofibromatosis type 1 gene, exon x8
6858	17935	30571	3.2	0.0E+00	11420775	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
6859	17936	30572	0.74	0.0E+00	AI419689.1	EST_HUMAN	ig53cd06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN. ;
6859	17936	30573	0.74	0.0E+00	AI419689.1	EST_HUMAN	ig53cd06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN. ;
6863	17940	30576	0.78	0.0E+00	BE256708.1	EST_HUMAN	601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356330 5'
6874	17950	30546	0.58	0.0E+00	BE904955.1	EST_HUMAN	601496743F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898739 5'
6884	17960	30514	1.05	0.0E+00	AU118478.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003679 5'
6887	17963	30518	8.08	0.0E+00	BE262941.1	EST_HUMAN	601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5'
6888	17964	30519	2.26	0.0E+00	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6888	17964	30520	2.26	0.0E+00	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6889	17965	30521	3.26	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6889	17965	30522	3.26	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6894	17970	30527	1.06	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6899	19637	32681	1.03	0.0E+00	BE762770.1	EST_HUMAN	QV3-NT0022-140600-223-f01 NT0022 Homo sapiens cDNA
6904	19642	32687	2.37	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6908	19646	32692	4.53	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
6913	19650	32696	0.79	0.0E+00	AW502362.1	EST_HUMAN	U1HF-BR0p-aka-d-10-0-U1r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
6913	19650	32697	0.79	0.0E+00	AW502362.1	EST_HUMAN	U1HF-BR0p-aka-d-10-0-U1r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
6922	19658	32704	0.7	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2211 5'
6922	19658	32705	0.7	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2211 5'
6929	19695	32711	5.87	0.0E+00	BF306896.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
6934	19698	32715	2.33	0.0E+00	U41302.1	NT	Human chromosome 18 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
6972	19454	32474	1.18	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7008	19700	32754	0.65	0.0E+00	AB026883.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds

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7008	19700	32755	0.65	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7013	19705	32761	1.07	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7013	19705	32762	1.07	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7019	19711	32768	1.2	0.0E+00	AW954806.1	EST_HUMAN	EST366876 MAGE sequences, MAGEC Homo sapiens cDNA
7020	19712	32768	0.9	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354568 5'
7033	19725	32781	0.98	0.0E+00	L01973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7041	19732	32791	0.64	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7041	19732	32792	0.64	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7047	19738	32799	2.73	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001555 5'
7062	19753	32818	0.95	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7084	19755	32820	0.56	0.0E+00	AA312125.1	EST_HUMAN	EST182818 Jurkat T-cells VI Homo sapiens cDNA 5' end
7069	19760		2.57	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'
7070	19761	32825	0.94	0.0E+00	4758839	NT	Homo sapiens netrin 1 (NTN1), mRNA
7079	19770	32834	1.32	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7079	19770	32835	1.32	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7100	17981	30495	2.54	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7100	17981	30496	2.54	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7122	19810	32876	5.01	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7122	19810	32877	5.01	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7137	19824	32881	0.55	0.0E+00	AF227744.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform ae (CACNA1G) mRNA, complete cds
7156	19843	32911	37.67	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares placenta_8tc6weeks_2NBHP8b9W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element ;
7158	19843	32912	37.67	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares placenta_8tc6weeks_2NBHP8b9W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element ;
7158	19845	32914	0.88	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7158	19845	32915	0.88	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7161	19848	32918	4.65	0.0E+00	11428392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7161	19848	32919	4.65	0.0E+00	11428392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7163	19850		15.23	0.0E+00	BF337375.1	EST_HUMAN	602035089F1 NC1 CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4182839 5'
7165	19852	32921	2.85	0.0E+00	AA128453.1	EST_HUMAN	zr60009.1 Stratiogene muscle 837209 Homo sapiens cDNA clone IMAGE:582601 5' similar to TR:G808562 G808562 NEBULIN ;

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7170	19856	32927	0.7	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7170	19856	32928	0.7	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7208	19893	32969	1.09	0.0E+00	BE295499.1	EST_HUMAN	601174576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528794 5'
7210	19895	32970	1	0.0E+00	11427965	NT	Homo sapiens hypothetical protein (FLJ20261), mRNA
7213	19898		1.42	0.0E+00	AU118607.1	EST_HUMAN	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
7214	19899	32973	1.99	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7214	19899	32974	1.99	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7226	19911	32984	0.87	0.0E+00	AF245505.1	NT	Homo sapiens adiclin mRNA, complete cds
7232	19917	32989	8.04	0.0E+00	X70172.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7234	19919	32991	8.51	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7234	19919	32992	8.51	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7247	19932	33007	0.86	0.0E+00	AW956503.1	EST_HUMAN	EST368573 MAG2 resequences, MAGD Homo sapiens cDNA
7249	19934	33009	0.56	0.0E+00	BE672445.1	EST_HUMAN	7a60h08.x1 NCI_QGAP_G08 Homo sapiens cDNA clone IMAGE:3223187 3' similar to gb.M54911_rna1 IG
7250	19935	33010	2.52	0.0E+00	AW950516.1	EST_HUMAN	HEAVY CHAIN PRECURSOR V-II REGION (HUMAN);
7273	19957	33033	0.57	0.0E+00	AF001543.1	EST_HUMAN	EST382586 MAG2 resequences, MAGA Homo sapiens cDNA
7273	19957	33034	0.57	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa, S.C.) Homo sapiens cDNA clone kappa_200
7273	19957	33035	0.57	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa, S.C.) Homo sapiens cDNA clone kappa_200
7292	19975		0.56	0.0E+00	M90354.1	NT	Human BTF3 protein homolog gene, complete cds
7293	19976	33053	0.96	0.0E+00	BE408293.1	EST_HUMAN	601302679F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'
7305	19988	33084	0.6	0.0E+00	AW402542.1	EST_HUMAN	UHLF-BKO-eas-g 07-0-UJ.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054924 5'
7322	20005		1.43	0.0E+00	R87430.1	EST_HUMAN	ym88h10.r1 Soares adult brain N2b4fH55Y Homo sapiens cDNA clone IMAGE:186051 5'
7323	20006	33083	1.88	0.0E+00	AW239326.1	EST_HUMAN	xb39a05.y1 NCI_QGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR-Q08050 Q08050
7342	20023		1.31	0.0E+00	AU117553.1	EST_HUMAN	HNF3/FH TRANSCRIPTION FACTOR GENESIS ;
7344	20025	33101	3.67	0.0E+00	11427135	NT	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001681 5'
7366	20046	33125	0.58	0.0E+00	BF229235.1	EST_HUMAN	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7372	20052	33133	0.67	0.0E+00	L32832.1	NT	MRO-AN0083-270900-004-07 AND083 Homo sapiens cDNA
7397	20075	33154	1.18	0.0E+00	BF306996.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7397	20075	33155	1.18	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7406	20083	33166	0.92	0.0E+00	AU118767.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7460	20133	33223	4.16	0.0E+00	AI752581.1	EST_HUMAN	AU118787 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
							cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random

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7460	20133	33224	4.16	0.0E+00	A1752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7535	20205	33301	1.83	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7535	20205	33302	1.83	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7543	20213	33313	1.14	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7557	20227	33330	1.1	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
7570	20239	33343	2.28	0.0E+00	AW672785.1	EST_HUMAN	ba01e06.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823106 5' similar to SW:P101_PIG O02696
7570	20239	33344	2.28	0.0E+00	AW672785.1	EST_HUMAN	PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT ; ba01e06.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823106 5' similar to SW:P101_PIG O02696
7586	20254	33360	1.97	0.0E+00	A1825504.1	EST_HUMAN	PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT ; wb17g05.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363 AIBC1. ;
7586	20254	33361	1.97	0.0E+00	A1825504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363 AIBC1. ;
7594	20262	33370	1.51	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7599	20265	33373	1.09	0.0E+00	N76126.1	EST_HUMAN	za86a03.x1 Soares, Tetra Lung, NBHL19W Homo sapiens cDNA clone IMAGE:299456 3'
7604	20270	33377	5.87	0.0E+00	BF217605.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
7613	20279	33387	5.41	0.0E+00	AU126622.1	EST_HUMAN	AU126622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
7633	25117	33408	0.97	0.0E+00	AW069274.1	EST_HUMAN	cr42a09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42a09 3'
7633	25117	33407	0.97	0.0E+00	AW069274.1	EST_HUMAN	cr42a09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42a09 3'
7636	20301	33409	6.26	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABC43), mRNA
7643	20308	33416	1.13	0.0E+00	AV758467.1	EST_HUMAN	AV758467 BM Homo sapiens cDNA clone BMFBGG05 5'
7645	20309	33417	6.31	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7645	20309	33418	6.31	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7646	20310	33419	1.18	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7646	20310	33420	1.18	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7647	20311	33421	0.71	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7647	20311	33422	0.71	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7680	20344	33456	1.81	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884288 5'

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7680	20344	33457	1.81	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3884258 5'
7720	20384	33498	0.63	0.0E+00	W52673.1	EST_HUMAN	zz90f10.r1 Pancreatic islet Homo sapiens cDNA clone IMAGE:338443 5'
7734	20398	33513	0.56	0.0E+00	AW402332.1	EST_HUMAN	U1-HF-BKO-aal-b-06-0-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3053915 5'
7735	20400	33515	0.76	0.0E+00	AA760692.1	EST_HUMAN	nz13a08.s1 NCL_CGAP_GCBT1 Homo sapiens cDNA clone IMAGE:1287638 3' similar to gb:U01828 MICROTUBULE-ASSOCIATED PROTEIN 2 (HUMAN);
7735	20400	33516	0.76	0.0E+00	AA760692.1	EST_HUMAN	nz13a08.s1 NCL_CGAP_GCBT1 Homo sapiens cDNA clone IMAGE:1287638 3' similar to gb:U01828 MICROTUBULE-ASSOCIATED PROTEIN 2 (HUMAN);
7752	20448	33572	0.84	0.0E+00	AU133187.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5'
7812	20507	33630	0.82	0.0E+00	BE313013.1	EST_HUMAN	601150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'
7824	20519	33645	1.13	0.0E+00	AA149791.1	EST_HUMAN	z001c06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566410 5'
7837	20532	33659	0.84	0.0E+00	BF026628.1	EST_HUMAN	601872310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
7849	20544	33672	0.45	0.0E+00	AA017021.1	EST_HUMAN	ze33n08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360831 5'
7866	20561	33688	2.31	0.0E+00	BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
7881	20576	33703	10.46	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7881	20576	33704	10.46	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7909	20604	33734	0.74	0.0E+00	AW674581.1	EST_HUMAN	bb34d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O64652 F17K2.26 PROTEIN;
7909	20604	33735	0.74	0.0E+00	AW674581.1	EST_HUMAN	bb34d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O64652 F17K2.26 PROTEIN;
7916	20611	33741	3.91	0.0E+00	AA397551.1	EST_HUMAN	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
7918	20613	33742	1.41	0.0E+00	AW387131.1	EST_HUMAN	MRO-ST0031-061059-003-a11 ST0031 Homo sapiens cDNA
7921	20616		0.73	0.0E+00	AB020691.1	NT	Homo sapiens mRNA for KIAA0884 protein, partial cds
7922	20617	33744	7.02	0.0E+00	AU142402.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
7926	20621	33748	1.63	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
7926	20621	33749	1.83	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
7942	20637	33764	1.09	0.0E+00	W95278.1	EST_HUMAN	z05d01.r1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
7942	20637	33765	1.09	0.0E+00	W95278.1	EST_HUMAN	z05d01.r1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
7944	20639		6.89	0.0E+00	BF673098.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
7948	20643		0.67	0.0E+00	AU134114.1	EST_HUMAN	AU134114 OVARC1 Homo sapiens cDNA clone OVARC1001266 5'
7962	20657	33782	0.95	0.0E+00	BF525534.1	EST_HUMAN	602069632F1 NCL_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4212727 5'
7962	20657	33783	0.95	0.0E+00	BF525534.1	EST_HUMAN	602069632F1 NCL_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4212727 5'
7962	20657	33813	1.59	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
7992	20687	33814	1.59	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'

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8035	20730		1.32	0.0E+00	BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:3887773 5'
8057	20751	33892	2.48	0.0E+00	AW500549.1	EST_HUMAN	U1HF-BN0-ak4-01-01-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077498 5'
8065	20759	33898	16.05	0.0E+00	AW157233.1	EST_HUMAN	au93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR:O60483 O60483 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1]; xa07d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567639 3' similar to contains element OFR repetitive element;
8082	20776	33906	0.68	0.0E+00	AW072395.1	EST_HUMAN	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8099	20783	33924	1.09	0.0E+00	11421722	NT	
8102	20796	33927	1.07	0.0E+00	W01816.1	EST_HUMAN	z336405.t1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:294633 5'
8104	20798	33929	1.22	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8104	20798	33930	1.22	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8115	20809	33943	1.46	0.0E+00	AI271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8154	20848	33980	0.95	0.0E+00	AI367350.1	EST_HUMAN	q95c12.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14873 Q14873 KIAA0184 PROTEIN.;
8165	20859	33991	2.63	0.0E+00	BE874157.1	EST_HUMAN	7478604.x1 NCL_CGAP_L24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O95793 O95793 STAUEN PROTEIN.;
8167	20861	33993	1.19	0.0E+00	AI885671.1	EST_HUMAN	w60b10.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR;
8180	20874	34009	1.07	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8180	20874	34010	1.07	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8189	20883	34020	1.63	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8189	20883	34021	1.63	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8191	20885	34023	3.2	0.0E+00	AA403192.1	EST_HUMAN	z66802.t1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD.;
8191	20885	34024	3.2	0.0E+00	AA403192.1	EST_HUMAN	z66802.t1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD.;
8231	20925		4.53	0.0E+00	AA3398511.1	EST_HUMAN	z73a08.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);
8240	20934	34071	0.55	0.0E+00	BE837593.1	EST_HUMAN	RC2-FN0094-120600-013-h07 FN0094 Homo sapiens cDNA
8241	20935	34072	1.17	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8241	20935	34073	1.17	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8260	20954	34092	1.88	0.0E+00	BE612588.1	EST_HUMAN	601452412F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856179 5'
8260	20954	34093	1.88	0.0E+00	BE612588.1	EST_HUMAN	601452412F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856179 5'
8275	20969	34110	1.52	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8275	20969	34111	1.52	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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8286	20980	34120	1.3	0.0E+00	A1884477.1	EST_HUMAN	wn33a11.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
8293	20987	34126	1.27	0.0E+00	AA502294.1	EST_HUMAN	he25d10.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1138434
8298	20992		0.59	0.0E+00	11416798	NT	G1138434 KIAA0187 PROTEIN. ;
8305	20999	34137	1.02	0.0E+00	A1580780.1	EST_HUMAN	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
8308	21002		1.84	0.0E+00	BE890797.1	EST_HUMAN	ta04f11.x1 Scores pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:2043117 3'
8334	21027	34163	0.72	0.0E+00	AW245765.1	EST_HUMAN	601431238F.1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
8334	21027	34164	0.72	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8335	21028	34165	2.24	0.0E+00	4758695	NT	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8335	21028	34166	2.24	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8339	21032	34169	0.59	0.0E+00	U88084.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8339	21032	34170	0.59	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8404	21097	34233	0.66	0.0E+00	AJ251780.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8409	21102	34239	2.63	0.0E+00	X98922.1	NT	Homo sapiens NESP55, GNAS1 antisense (partial) and XLalphas (partial) genes
8409	21102	34240	2.63	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8409	21102	34241	2.63	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8424	21117	34255	0.68	0.0E+00	U82979.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8465	21157	34300	0.88	0.0E+00	AF022855.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
8465	21157	34301	0.88	0.0E+00	AF022855.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8468	21160	34303	2.28	0.0E+00	AU131671.1	EST_HUMAN	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8483	21175	34320	0.65	0.0E+00	11426572	NT	AU131671 NT2RP3 Homo sapiens cDNA clone NT2RP3003016 5'
8487	21179		1.92	0.0E+00	AW513513.1	EST_HUMAN	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8489	21181	34323	14.55	0.0E+00	D52650.1	EST_HUMAN	xx46601.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
8520	21212	34356	4.04	0.0E+00	BE378495.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02
8526	21218	34360	2.58	0.0E+00	AA410545.1	EST_HUMAN	5'
8528	21220		2.91	0.0E+00	BF313946.1	EST_HUMAN	601236488F.1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8535	21227	34369	0.52	0.0E+00	11424387	NT	z32e04.1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724082 5'
8540	21232	34374	1.46	0.0E+00	AW139673.1	EST_HUMAN	601800571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
8540	21232	34375	1.46	0.0E+00	AW139673.1	EST_HUMAN	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA

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8545	21237			0.0E+00	A1640190.1	EST_HUMAN	wa30b10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299579 3' similar to TR:O15044
8564	21256	34393	0.49	0.0E+00	BF377897.1	EST_HUMAN	O15044 KIAA0335.
8574	21266	34406	0.76	0.0E+00	AL163301.2	NT	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
8580	21272	34410	0.59	0.0E+00	BE260272.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
8585	21277	34414	2.51	0.0E+00	BF700165.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'
8585	21277	34415	2.51	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8585	21277	34416	2.51	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8600	21292	34434	0.53	0.0E+00	A1458722.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8626	21318	34460	0.86	0.0E+00	AL449770.1	EST_HUMAN	ik13h11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150949 3'
8631	21323	34464	7.75	0.0E+00	AA92527.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Starvies GS) Homo sapiens cDNA
8637	21329	34472	3.09	0.0E+00	10947037	NT	or80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072.60S
8637	21329	34473	3.09	0.0E+00	10947037	NT	RIBOSOMAL PROTEIN L7A (HUMAN);
8660	21352	34489	1.3	0.0E+00	Y11107.3	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8662	21354	34501	1.62	0.0E+00	BE278917.1	EST_HUMAN	Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41
8672	21364		1.91	0.0E+00	AV718377.1	EST_HUMAN	6011566330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
8679	21371	34516	3.33	0.0E+00	AW337277.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5'
8685	21377	34521	1.12	0.0E+00	AU124051.1	EST_HUMAN	xw73c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587
8761	21453	34601	1.05	0.0E+00	AU140704.1	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
8771	21463	34610	0.86	0.0E+00	AB007923.1	NT	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
8776	21468	34614	0.54	0.0E+00	R17132.1	EST_HUMAN	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000089 5'
8776	21468	34615	0.54	0.0E+00	R17132.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
8780	21472	34617	4.43	0.0E+00	AW592233.1	EST_HUMAN	yg09e09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31674 5'
8780	21472	34618	4.43	0.0E+00	AW592233.1	EST_HUMAN	yg09e09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31674 5'
8815	21507	34652	0.47	0.0E+00	AU128804.1	EST_HUMAN	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
8827	21519	34664	1.04	0.0E+00	AV714764.1	EST_HUMAN	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
8843	21535	34679	2.79	0.0E+00	AL040428.1	EST_HUMAN	AU128804 NT2RP2 Homo sapiens cDNA clone NT2RP2004245 5'
8843	21535	34680	2.79	0.0E+00	AL040428.1	EST_HUMAN	AV714764 DGB Homo sapiens cDNA clone DGBAJA06 5'
8849	21540	34686	1.17	0.0E+00	AF133901.1	NT	DKFZp434C1814_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814 3'
8851	21542	34689	2.03	0.0E+00	AB040945.1	NT	DKFZp434C1814_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814 3'
8858	21549	34696	0.65	0.0E+00	BF875505.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814 3'
							Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
							Homo sapiens mRNA for KIAA1512 protein, partial cds
							602138483F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274708 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HIT BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8880	21551			0.0E+00	BF058289.1	EST_HUMAN	7k2b03.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476692 3' similar to TR-O36448 O36448 S GAG.
8889	21580	34720	3.97	0.0E+00	11422857	NT	Homo sapiens tumor protein p73 (TP73), mRNA
8898	21589	34729	1.19	0.0E+00	K01241.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
8905	21596	34737	4.27	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8905	21596	34737	4.27	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8905	21598	34738	4.27	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8910	21601	34744	1.79	0.0E+00	AV660739.1	EST_HUMAN	AV660739 GLC Homo sapiens cDNA clone GLOC612 3'
8916	21607	34750	2.88	0.0E+00	7706638	NT	Homo sapiens polyomavirus (PKDL), mRNA
8921	21612	34755	0.5	0.0E+00	BE763326.1	EST_HUMAN	601588304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'
8922	21613	34756	0.73	0.0E+00	AB030377.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
8922	21613	34757	0.73	0.0E+00	AB030377.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
8934	21625	34779	0.91	0.0E+00	H73937.1	EST_HUMAN	yu03h08.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:232767 5'
8944	21635	34780	4.57	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
8944	21635	34780	4.57	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
8954	21645	34795	0.46	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
8954	21645	34796	0.46	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
8957	21648		0.45	0.0E+00	M89986.1	NT	Human polymorphic loci in Xq28
8959	21650	34800	3.66	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
8980	21670	34820	2.03	0.0E+00	AI061395.1	EST_HUMAN	an29s04.x1 Geaster Wilms tumor Homo sapiens cDNA clone IMAGE:1700084 3'
8985	21675	34824	1.95	0.0E+00	AI954607.1	EST_HUMAN	wq34a12.x1 NCL CGAP_QC8 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW-MGB3_HUMAN O15480 MELANOMA-ASSOCIATED ANTIGEN B3
8989	21679	34828	4.65	0.0E+00	9256595	NT	Homo sapiens protocadherin alpha 8 (PCDH8), mRNA
9000	21690	34840	1.42	0.0E+00	AW958311.1	EST_HUMAN	EST370381 MAGE resequences, MAGE Homo sapiens cDNA
9011	21701	34851	2.48	0.0E+00	9835487	NT	Human endogenous retrovirus, complete genome
9028	21716	34869	1.53	0.0E+00	AU142662.1	EST_HUMAN	AU142662 Y79AA1 Homo sapiens cDNA clone Y79AA1000878 5'
9042	21732	34887	1.76	0.0E+00	11438993	NT	Homo sapiens MAP kinase activating death domain (MADD), mRNA
9043	21733		1.18	0.0E+00	BE410768.1	EST_HUMAN	601301676F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'
9056	21745	34904	1.83	0.0E+00	BF002024.1	EST_HUMAN	7g97m12.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TRQ8UH82 Q9U462 HYPOTHETICAL 42.5 KD PROTEIN
9070	21759	34920	1.1	0.0E+00	AB011150.1	NT	Homo sapiens mRNA for KIAA0578 protein, partial cds
9071	21760	34921	7.72	0.0E+00	BE794823.1	EST_HUMAN	601589294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'
9075	21764	34926	0.99	0.0E+00	BE810282.1	EST_HUMAN	RC3-PT0151-280600-011-c05 PT0151 Homo sapiens cDNA
9075	21764	34927	0.99	0.0E+00	BE810282.1	EST_HUMAN	RC3-PT0151-280600-011-c05 PT0151 Homo sapiens cDNA
9078	21767	34930	2.93	0.0E+00	AU136226.1	EST_HUMAN	AU136229 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'

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9083	21772	34935	1.27	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9083	21772	34936	1.27	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9102	21790	34953	0.62	0.0E+00	AB011166.1	NT	Homo sapiens mRNA for KIAA0584 protein, partial cds
9106	21794	34957	1.4	0.0E+00	AA344601.1	EST_HUMAN	EST150505 Gall bladder 1 Homo sapiens cDNA 5' end
9106	21794	34958	1.4	0.0E+00	AA344601.1	EST_HUMAN	EST150505 Gall bladder 1 Homo sapiens cDNA 5' end
9164	21834	34998	1.13	0.0E+00	AW673469.1	EST_HUMAN	bs54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275
9164	21834	34999	1.13	0.0E+00	AW673469.1	EST_HUMAN	bs54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275
9198	21867	35031	1.62	0.0E+00	BE207063.1	EST_HUMAN	KIAA0522 PROTEIN ;
9198	21867	35032	1.62	0.0E+00	BE207063.1	EST_HUMAN	KIAA0522 PROTEIN ;
9209	22088	35260	1.61	0.0E+00	BF348013.1	EST_HUMAN	ba0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus
9244	21923	35093	2.77	0.0E+00	BE712515.1	EST_HUMAN	Bcl-xL mRNA, complete cds (MOUSE);
9277	22031	35201	0.88	0.0E+00	BF034377.1	EST_HUMAN	ba0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus
9277	22031	35202	0.88	0.0E+00	BF034377.1	EST_HUMAN	Bcl-xL mRNA, complete cds (MOUSE);
9283	22037	35209	0.5	0.0E+00	AI906351.1	EST_HUMAN	QV2-HT0698-250700-282-608 HT0698 Homo sapiens cDNA clone IMAGE:4158300 5'
9288	22040	35211	0.81	0.0E+00	5803069	NT	601455116F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3859035 5'
9288	22040	35212	0.81	0.0E+00	5803069	NT	601455116F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3859035 5'
9288	21963	35137	1.5	0.0E+00	AL042278.1	EST_HUMAN	RC-BT108-040399-032 BT108 Homo sapiens cDNA clone IMAGE:1651249 3' similar to
9331	21998	35171	1.28	0.0E+00	AI088043.1	EST_HUMAN	TR:Q14677 Q14677 KIAA0171 PROTEIN ;
9338	20409	33524	0.72	0.0E+00	BF309982.1	EST_HUMAN	601802245F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138068 5'
9340	20411	33527	2.51	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9340	20411	33528	2.51	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9342	20413	33531	9.88	0.0E+00	AI290909.1	EST_HUMAN	qtm09a08.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN
9342	20413	33532	9.88	0.0E+00	AI290909.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A ;
9343	20414	33533	1.99	0.0E+00	AW953836.1	EST_HUMAN	qtm09a08.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN
9370	21945	35117	3.07	0.0E+00	AF153468.1	NT	P28316 60S RIBOSOMAL PROTEIN L23A ;
							EST1366028 MAGC resequences, MAGC Homo sapiens cDNA
							Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9373	21948	35121	0.86	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9373	21948	35122	0.86	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9382	22044		7.32	0.0E+00	BE255829.1	EST_HUMAN	601106942F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350722 5'
9385	22047	35219	1.09	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9385	22047	35220	1.09	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9387	22049	35221	12.62	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072
9409	22071	35243	2.98	0.0E+00	BE263191.1	EST_HUMAN	6005 RIBOSOMAL PROTEIN L7A (HUMAN);
9427	22105	35278	4.29	0.0E+00	C06158.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
9427	22105	35279	4.29	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9429	22107	35282	2.63	0.0E+00	BE746215.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9439	22117	35293	2.14	0.0E+00	11437282	NT	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9439	22117	35294	2.14	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9459	22009	35179	1.44	0.0E+00	BE900549.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9475	22128	35307	1.01	0.0E+00	AV701829.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9489	22142	35322	2.62	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
9522	22175	35359	0.94	0.0E+00	BE082977.1	EST_HUMAN	Homo sapiens keratin 2e (KRT2E) gene, complete cds
9541	22194	35379	1.74	0.0E+00	AW500293.1	EST_HUMAN	RC2-BT0842-130300-017-g01 BT0842 Homo sapiens cDNA
9541	22194	35380	1.74	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9550	22203	35386	1.45	0.0E+00	AF029308.1	NT	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9550	22203	35387	1.45	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
9552	22205	35388	0.89	0.0E+00	BE783272.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
9552	22205	35389	0.89	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9561	22214	35400	0.54	0.0E+00	W56829.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9561	22214	35401	0.54	0.0E+00	W56829.1	EST_HUMAN	z18e11.1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9572	22225	35410	1.83	0.0E+00	AB035356.1	NT	z18e11.1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9578	22229	35415	0.8	0.0E+00	A1124780.1	EST_HUMAN	Homo sapiens mRNA for neurixin I-alpha protein, complete cds
9578	22231	35415	3.59	0.0E+00	AW500526.1	EST_HUMAN	am56a1.1 x1 Johnson frontal cortex Homo sapiens cDNA clone IMAGE:1539548 3'
9624	22277	35466	1.53	0.0E+00	AF009668.1	NT	UI-HF-BN0-akg-c-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:307384 5'
							Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9652	22304	35499	2.23	0.0E+00	S78466.1	NT	AIIGF=androgen-induced growth factor AIIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9652	22304	35500	2.23	0.0E+00	S78466.1	NT	AIIGF=androgen-induced growth factor AIIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9655	22307	35505	2.93	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:388860 5'
9674	22326	35521	1.84	0.0E+00	AW368135.1	EST_HUMAN	CM2-CT0311-301189-043-H11 GT0311 Homo sapiens cDNA
9682	22343	35537	0.46	0.0E+00	11436432	NT	Homo sapiens mullerlin (MIMRN), mRNA
9683	22344	35538	0.51	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
9702	22353	35548	0.54	0.0E+00	BE206710.1	EST_HUMAN	bb26c01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2964000 3'
9719	22370	35568	2.57	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9719	22370	35569	2.57	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9728	22379	35581	0.77	0.0E+00	AW500936.1	EST_HUMAN	UI-HF-BPOp-ar-f05-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'
9733	22384	35586	9.08	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
9733	22384	35587	9.08	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
9734	22385	35588	0.48	0.0E+00	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
9734	22385	35589	0.48	0.0E+00	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
9747	22398	35603	1.73	0.0E+00	7682067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9765	22416	35623	1.59	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120.r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434L0120 5'
9770	22421	35629	1.53	0.0E+00	AL041084.2	EST_HUMAN	DKFZp434B2416.r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434B2416 5'
9780	22431	35636	2.54	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9781	22432	35637	2.37	0.0E+00	AF152308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
9808	22459	35664	2.63	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9808	22459	35665	2.63	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9824	22475	35678	1.81	0.0E+00	BF092888.1	EST_HUMAN	MR4-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA
9854	22504	35704	2.41	0.0E+00	BE280763.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138788 5'
9864	22514	35710	0.86	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
9864	22514	35711	0.86	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
9873	22523	35717	3.03	0.0E+00	AW236269.1	EST_HUMAN	nm72801.x1 NCJ_CQAP_GML1 Homo sapiens cDNA clone IMAGE:2695977 3' similar to gb:202152_cds1 L
9874	22524	35718	1.06	0.0E+00	AA341305.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN);
9904	22553	35748	0.97	0.0E+00	AW964113.1	EST_HUMAN	EST146740 Fetal kidney II Homo sapiens cDNA 5' end
9915	22564	35759	7.01	0.0E+00	AU143873.1	EST_HUMAN	EST378186 MAGe resequences, MAGe Homo sapiens cDNA
9915	22564	35760	7.01	0.0E+00	AU143873.1	EST_HUMAN	AU143873 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9918	22567	35763	2.98	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
9921	22569	35765	2.75	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL) mRNA
9921	22569	35766	2.75	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL) mRNA
9956	22604	35809	3	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
9956	22604	35810	3	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
9972	22620	35824	2.08	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7/importin7 and partial ZNF143 gene
9972	22620	35824	2.08	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7/importin7 and partial ZNF143 gene
9972	22620	35825	2.08	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7/importin7 and partial ZNF143 gene
9977	22625	35832	1.04	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GK Homo sapiens cDNA clone GKCDXA07 5'
9977	22625	35833	1.04	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GK Homo sapiens cDNA clone GKCDXA07 5'
9983	22631	35840	0.74	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
9985	22633	35843	3.11	0.0E+00	AA196387.1	EST_HUMAN	z31601.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:628197 5'
10011	22659	35873	1	0.0E+00	AA131248.1	EST_HUMAN	z31601.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10011	22659	35874	1	0.0E+00	AA131248.1	EST_HUMAN	z31601.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10056	22704	35922	1.44	0.0E+00	AF179308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10101	22749	35964	0.92	0.0E+00	BE880658.1	EST_HUMAN	601491565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893657 5'
10112	22760	35972	6.22	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10112	22760	35973	6.22	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10117	22765	35977	0.97	0.0E+00	AU127403.1	EST_HUMAN	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 5'
10127	22775	35988	0.87	0.0E+00	BE958511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10127	22775	35989	0.87	0.0E+00	BE958511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10144	22792	36007	0.68	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10154	22802	36020	0.67	0.0E+00	AA311624.1	EST_HUMAN	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10155	22803	36021	1.01	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
10166	22814	36032	0.67	0.0E+00	BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'
10169	22817	36035	1.13	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10179	22827	36041	1.72	0.0E+00	AB029290.1	NT	Homo sapiens mRNA for actin binding protein ABP820, complete cds
10180	22828	36042	0.46	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10180	22828	36043	0.46	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10187	22835	36048	6.02	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10187	22835	36049	6.02	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10193	22841	36056	1.06	0.0E+00	AA704457.1	EST_HUMAN	z19008.s1 Soares_fetal_liver脾脾_INFLS_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gb:IM14123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10195	22843	36057	0.74	0.0E+00	M22921.1	NT	Human beta 1.4-galactosyl-transferase mRNA, complete cds
10197	22845	36060	5.45	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184939 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10197	22845	36061	5.45	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184939 5'
10222	22870	36082	0.93	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10222	22870	36083	0.83	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10252	22900	36110	0.55	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DCB Homo sapiens cDNA clone DCBBD09 5'
10252	22900	36111	0.55	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DCB Homo sapiens cDNA clone DCBBD09 5'
10282	22930	36143	2.36	0.0E+00	AI631818.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR-Q61204
10282	22930	36144	2.36	0.0E+00	AI631818.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR-Q61204
10288	22938	36149	0.49	0.0E+00	11545730	NT	Q61204 NOTCH2-LIKE:
10298	22945	36159	1.52	0.0E+00	T03078.1	EST_HUMAN	Homo sapiens Gigaionh (GAN), mRNA
10323	22970	36190	0.64	0.0E+00	AU122429.1	EST_HUMAN	FB23A4 Fetal brain, Striatum Homo sapiens cDNA clone FB23A4 3'end
10329	22978	36196	0.46	0.0E+00	6005921	NT	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002388 5'
10348	22995	36214	2.5	0.0E+00	BF436218.1	EST_HUMAN	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10349	22998		0.97	0.0E+00	AV654765.1	EST_HUMAN	inab45e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
							AV654765 GLC Homo sapiens cDNA clone GLCD2C07 3'
							xu74601.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb.M69086 MOESIN (HUMAN):
10369	23015	36231	2.75	0.0E+00	AW517960.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484703 5'
10374	23020	36236	8.82	0.0E+00	BE549213.1	EST_HUMAN	Homo sapiens hypothetical protein DKFZp781P1010 [DKFZp781P1010], mRNA
10389	23035	36251	0.75	0.0E+00	11438005	NT	601467419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
10414	23060	36279	2.79	0.0E+00	BE781742.1	EST_HUMAN	RC2-BT0642-150200-012-403 BT0642 Homo sapiens cDNA
10435	23081	36307	1.9	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-403 BT0642 Homo sapiens cDNA
10435	23081	36308	1.9	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10442	23088	36316	0.68	0.0E+00	Y08032.1	EST_HUMAN	tt54e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2244812 3'
10448	23094	36325	0.86	0.0E+00	A1656890.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10454	23100	36331	1.33	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10454	23100	36332	1.33	0.0E+00	BE743215.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10459	23105	36335	2.49	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10459	23105	36336	2.49	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10481	23127	36355	0.57	0.0E+00	H39805.1	EST_HUMAN	jp01a10.t1 Scores breast3NH8st Homo sapiens cDNA clone IMAGE:186138 5'
10508	23154	36380	1.01	0.0E+00	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10510	23156	36382	0.45	0.0E+00	AF081364.1	NT	Synthetic construct CD30 ligand-exon1 A fusion protein (CD30L-E1A fusion) mRNA, partial cds
10519	23165	36392	1.02	0.0E+00	BE172254.1	EST_HUMAN	MRQ-HT0559-270300-008-e12 HT0559 Homo sapiens cDNA
10519	23165	36393	1.02	0.0E+00	BE172254.1	EST_HUMAN	MRQ-HT0559-270300-008-e12 HT0559 Homo sapiens cDNA
10532	23229	36463	2.76	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAGG05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10532	23229	36464	2.76	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
10534	23231		2.13	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
10542	23238	36472	7.02	0.0E+00	AW963563.1	EST_HUMAN	EST375636 MAGE resequences, MAGH Homo sapiens cDNA
10555	23251	36487	3.19	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10555	23251	36488	3.19	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10559	23255	36492	2.09	0.0E+00	AW057621.1	EST_HUMAN	wy81109.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR:Q60568 Q60568 VDX;
							TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
10567	23262	36499	1.6	0.0E+00	BE243270.1	EST_HUMAN	wb28a12.x1 NCLGAP_GC8 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element
10568	23263	36500	2.85	0.0E+00	AI652239.1	EST_HUMAN	MSR1 MSR1 repetitive element
10568	23263	36501	2.85	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCLGAP_GC8 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element
10573	23268	36506	1.54	0.0E+00	BF306642.1	EST_HUMAN	MSR1 MSR1 repetitive element
10580	23275	36512	5.06	0.0E+00	11545911	NT	MSR1 MSR1 repetitive element
10580	23275	36513	5.06	0.0E+00	11545911	NT	MSR1 MSR1 repetitive element
10596	23290	36528	1.98	0.0E+00	AW404795.1	EST_HUMAN	MSR1 MSR1 repetitive element
10600	23294	36533	3.17	0.0E+00	11424829	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10601	23295	36534	7.47	0.0E+00	4504538	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10601	23295	36535	7.47	0.0E+00	4504538	NT	UHF-BLO-acm-d-04-0-U1r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
10602	23296	36536	3.68	0.0E+00	AI991827.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
10605	23299	36540	4.48	0.0E+00	BE882109.1	EST_HUMAN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10609	23303	36542	8.24	0.0E+00	BE891630.1	EST_HUMAN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10612	23306	36544	1.66	0.0E+00	8923939	NT	wu32008.x1 Soares Dieckgreffe NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3906885 5'
10612	23306	36545	1.66	0.0E+00	8923939	NT	601434622F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919638 5'
10619	23312	36551	1.4	0.0E+00	AB014608.1	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10619	23312	36552	1.4	0.0E+00	AB014608.1	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10628	23321	36559	1.31	0.0E+00	BE903304.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
							Homo sapiens mRNA for KIAA0708 protein, partial cds
10631	18484	31403	1.65	0.0E+00	AA195905.1	EST_HUMAN	Homo sapiens mRNA for KIAA0708 protein, partial cds
10652	23343	36581	5.53	0.0E+00	BE793498.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
10660	23351	36588	1.79	0.0E+00	BE729706.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10660	23351	36589	1.78	0.0E+00	BE729706.1	EST_HUMAN	601588829F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
10661	23352	36590	33.99	0.0E+00	AV727362.1	EST_HUMAN	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'
							601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'
							AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10661	23352	36591	33.99	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCQH06 5'
10674	23365	36608	9.59	0.0E+00	AW516055.1	EST_HUMAN	xy04g10.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852228 3' similar to gb:M60854 40S
10680	23371	36613	3.18	0.0E+00	AU135741.1	EST_HUMAN	RIBOSOMAL PROTEIN S16 (HUMAN);
10686	23377	36617	3.41	0.0E+00	AW593333.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'
10686	23377	36618	3.41	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element;
10686	23377	36619	3.41	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element;
10688	23379	36620	1.89	0.0E+00	Z34897.1	NT	hg13d02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element;
10689	23380	36621	2.97	0.0E+00	F13069.1	EST_HUMAN	H.Sapiens mRNA for H1 histamine receptor
10700	23391	36629	1.79	0.0E+00	D10083.1	NT	HSC3IC031 normalized infant brain cDNA Homo sapiens cDNA clone c-31c03
10706	23396	36634	1.33	0.0E+00	4758281	NT	Homo sapiens RGH1 gene, retrovirus-like element
10706	23396	36635	1.33	0.0E+00	4758281	NT	Homo sapiens Epha7 (EPHA7) mRNA
10718	23407	36648	2.13	0.0E+00	AW338094.1	EST_HUMAN	Homo sapiens Epha7 (EPHA7) mRNA
10719	23408	36649	4.62	0.0E+00	AW451230.1	EST_HUMAN	xw6601.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);
10719	23408	36650	4.62	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B13-ali-a-01-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
10721	13021		11.67	0.0E+00	4506632	NT	UI-H-B13-ali-a-01-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
10723	23411	36652	2.53	0.0E+00	AB014567.1	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
10738	23425	36670	1.98	0.0E+00	BE298449.1	EST_HUMAN	Homo sapiens mRNA for KIAA0667 protein, partial cds
10754	23439	36683	2.04	0.0E+00	AB011117.1	NT	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
10763	23447		1.71	0.0E+00	AU124106.1	EST_HUMAN	Homo sapiens mRNA for KIAA0545 protein, partial cds
10771	23454	36697	1.45	0.0E+00	AB029040.1	NT	AU124106 NT2RM2 Homo sapiens cDNA clone NT2RM2001875 5'
10776	23459	36702	4.04	0.0E+00	BE792155.1	EST_HUMAN	Homo sapiens mRNA for KIAA1117 protein, partial cds
10777	23460		59.14	0.0E+00	BF684061.1	EST_HUMAN	Homo sapiens mRNA for KIAA1117 protein, partial cds
10778	23461	36703	1.3	0.0E+00	BE269288.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'
10781	23464	36706	5.6	0.0E+00	AU118386.1	EST_HUMAN	602147405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'
10786	23469	36710	6.53	0.0E+00	A1149809.1	EST_HUMAN	601186342F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544259 5'
10786	23469	36711	6.53	0.0E+00	A1149809.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
10787	23470	36712	3.04	0.0E+00	AW391837.1	EST_HUMAN	qf43c03.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
							qf43c03.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
							QV4-ST0234-121199-032-b08 ST0234 Homo sapiens cDNA

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10788	23481	36721	4.39	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10798	23481	36722	4.39	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10807	23490	36726	9.57	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR), mRNA
10814	23497	36733	1.42	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-d06 UM0093 Homo sapiens cDNA
10814	23497	36734	1.42	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-d06 UM0093 Homo sapiens cDNA
10815	23498	36735	1.6	0.0E+00	BF340309.1	EST_HUMAN	602037014F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4184979 5'
10817	23500	36738	52.94	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
10821	23504	36743	2.37	0.0E+00	AB029040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds
10824	23507	36746	1.89	0.0E+00	AB007892.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
10828	23510	36750	3.47	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
10832	23514	36755	1.55	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-407 FT0134 Homo sapiens cDNA
10832	23514	36756	1.55	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-407 FT0134 Homo sapiens cDNA
10838	23520	36762	1.47	0.0E+00	W21828.1	EST_HUMAN	57E10 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
10854	23534	36779	136.91	0.0E+00	AA740782.1	EST_HUMAN	MSR1 repetitive element
10857	23537	36783	2.05	0.0E+00	AW468922.1	EST_HUMAN	h604h04.X1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
10863	23543	36790	2.91	0.0E+00	AF252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
10879	23559	36806	7.34	0.0E+00	CO5089.1	EST_HUMAN	CO5089 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4817
10886	23566	36814	2.31	0.0E+00	AA746375.1	EST_HUMAN	ce56h01.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
10888	23566	36815	2.31	0.0E+00	AA746375.1	EST_HUMAN	ce56h01.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
10895	23575	36825	3.74	0.0E+00	M78448.1	EST_HUMAN	EST00598 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBCC28
10895	23575	36825	3.74	0.0E+00	M78448.1	EST_HUMAN	EST00598 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBCC28
10895	23575	36826	3.74	0.0E+00	M78448.1	EST_HUMAN	DKFZp761J2118.11 761 (synonym: hary2) Homo sapiens cDNA clone DKFZp761J2116 5'
10898	23578	36827	6.82	0.0E+00	AL157608.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
10910	23590	36836	5.81	0.0E+00	AL116988.1	EST_HUMAN	AV683656 GKC Homo sapiens cDNA clone GKCNC03 5'
10924	23604	36853	1.64	0.0E+00	AV693656.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
10932	23612	36862	2.09	0.0E+00	BF366553.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
10955	18399	31311	2.73	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neurexin II, complete cds
10955	18399	31312	2.73	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neurexin II, complete cds
10960	23636	36887	2.64	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
10960	23636	36887	2.64	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
10960	23636	36888	2.64	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
10961	23637		1.4	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAD06 5'
10980	23655	36908	4.07	0.0E+00	BE898423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10989	23663	36919	1.95	0.0E+00	AW500307.1	EST_HUMAN	U1HF-BNO-akg-4-02-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
10989	23663	36920	1.85	0.0E+00	AW500307.1	EST_HUMAN	U1HF-BNO-akg-4-02-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							b678c04.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048486 5' similar to gb:Y00345_cds1 POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M. musculus mRNA for poly(A) binding protein (MOUSE);
10992	23666	36923	2.39	0.0E+00	BE018293.1	EST_HUMAN	602043377F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181083 5'
11016	23688	36949	1.77	0.0E+00	BF528907.1	EST_HUMAN	602043377F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181083 5'
11016	23688	36950	1.77	0.0E+00	BF528907.1	EST_HUMAN	602043377F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181083 5'
11016	23688	36951	1.77	0.0E+00	BF528907.1	EST_HUMAN	602043377F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181083 5'
11028	25133	36964	1.27	0.0E+00	AW387766.1	EST_HUMAN	MR4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA
11028	25133	36965	1.27	0.0E+00	AW387766.1	EST_HUMAN	MR4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA
11034	23705	36973	1.53	0.0E+00	4758281	NT	Homo sapiens EphA7 (EPHA7) mRNA
11035	23708	36974	8.73	0.0E+00	BE897953.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
11037	23708	36977	1.89	0.0E+00	AI459545.1	EST_HUMAN	ac88g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11037	23708	36978	1.89	0.0E+00	AI459545.1	EST_HUMAN	ac88g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11051	23721	36992	2.76	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120.t1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L0120 5'
11083	23753	37028	1.81	0.0E+00	10880982	NT	Homo sapiens gephyrin (GPH), mRNA
11085	23755	37031	3.98	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
11086	23766	37032	2.67	0.0E+00	BF206661.1	EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
11091	23761	37036	12.22	0.0E+00	AW207734.1	EST_HUMAN	U1H-BI2-age-h-01-0-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11096	23766	37040	4.23	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11096	23766	37041	4.23	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
							ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B 55KDA-ASSOCIATED PROTEIN ;
11098	23768	37043	2.69	0.0E+00	BE206946.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B 55KDA-ASSOCIATED PROTEIN ;
11098	23768	37044	2.69	0.0E+00	BE206946.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B 55KDA-ASSOCIATED PROTEIN ;
11110	23780	37055	1.9	0.0E+00	11528409	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
11124	23793	37059	1.62	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11127	20052	33133	1.5	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11131	23769	37074	3.84	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-H04 HT0230 Homo sapiens cDNA
11131	23769	37075	3.84	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-H04 HT0230 Homo sapiens cDNA
							bs54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
11154	23821	37101	1.96	0.0E+00	AW673466.1	EST_HUMAN	bs54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
11154	23821	37102	1.96	0.0E+00	AW673466.1	EST_HUMAN	bs54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;

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11176	23843	37128	6.21	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-aok-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085028 3'
11178	23843	37128	6.21	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-aok-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085028 3'
11185	23850	37136	1.57	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5'
11189	23854	37140	1.82	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11189	23854	37140	1.82	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11190	23855	37142	1.57	0.0E+00	BF088811.1	EST_HUMAN	RC3-GN0089-100900-011-c06 GN0089 Homo sapiens cDNA
11192	23857	37143	5.5	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11192	23857	37144	5.5	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11199	23864	37150	1.94	0.0E+00	D87682.1	NT	Human mRNA for KIAA0241 gene, partial cds
11204	23868		5.95	0.0E+00	BF240536.1	EST_HUMAN	601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5'
11218	23881	37166	2.04	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11218	23881	37167	2.04	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11222	23885	37170	4.17	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11222	23885	37171	4.17	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11230	23893	37179	1.8	0.0E+00	AA772837.1	EST_HUMAN	ae74g04.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969942 3'
11241	23903	37182	1.62	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11241	23903	37183	1.62	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11244	23906	37198	6.16	0.0E+00	4503544	NT	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
11251	23913	37205	1.36	0.0E+00	BF576267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11254	23916	37209	5.84	0.0E+00	AW328173.1	EST_HUMAN	dr04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11258	23920		71.88	0.0E+00	M55083.1	NT	Human gamma actin-like pseudogene, complete cds
11284	23926	37216	2.93	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11284	23926	37217	2.93	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11271	23932	37225	105.87	0.0E+00	BF362462.1	EST_HUMAN	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA
11291	23952	37249	2.34	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11291	23952	37250	2.34	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11296	23956		3.03	0.0E+00	BE897051.1	EST_HUMAN	601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3824577 5'
11296	23957		1.73	0.0E+00	4503786	NT	Homo sapiens fyn-related kinase (FRK) mRNA
11310	23969	37271	3.55	0.0E+00	8923688	NT	Homo sapiens golgin-like protein (GLP), mRNA
11313	23972		2.69	0.0E+00	BF207682.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11314	23973		2.03	0.0E+00	BE257744.1	EST_HUMAN	601116705F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357384 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11327	24018	37321	4.02	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
11327	24018	37322	4.02	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
11329	24020	37324	3.88	0.0E+00	AW753028.1	EST_HUMAN	QV0-CT0225-101299-071-106 CT0225 Homo sapiens cDNA
11334	24025		3.06	0.0E+00	AA558707.1	EST_HUMAN	h42c08.st NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11335	18000	30623	3.84	0.0E+00	A1934954.1	EST_HUMAN	wp06p08.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2464094 3'
11336	24026	37330	7.45	0.0E+00	AW327895.1	EST_HUMAN	dp02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
11355	25134	37348	1.89	0.0E+00	AW292776.1	EST_HUMAN	UI-H-BW0-aj-d-07-0-UI.st NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2728509 3'
11362	23173	36401	2.2	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
11368	23975	37276	1.73	0.0E+00	BE254068.1	EST_HUMAN	601113903F.1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354600 5'
11371	23978	37278	1.74	0.0E+00	BE965909.2	EST_HUMAN	601169089R.1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11371	23978	37279	1.74	0.0E+00	BE965909.2	EST_HUMAN	601169089R.1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11372	23979	37280	4.52	0.0E+00	BE185656.1	EST_HUMAN	IL5-H-T0731-020500-077-105 HT0731 Homo sapiens cDNA
11373	23980		1.29	0.0E+00	BF513960.1	EST_HUMAN	UI-H-BW1-amy-a-05-0-UI.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071121 3'
11387	23993	37294	7.81	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G178 5'
11387	23993	37295	7.81	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G178 5'
11397	24003	37306	5.89	0.0E+00	A1923116.1	EST_HUMAN	wn83g03.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11401	24050	37353	3.42	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 Q13686 ALKB HOMOLOG PROTEIN. ;
11401	24050	37354	3.42	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 Q13686 ALKB HOMOLOG PROTEIN. ;
11406	24055	37360	1.84	0.0E+00	BE910546.1	EST_HUMAN	601501060F.1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902928 5'
11416	23183	36413	7.9	0.0E+00	BE676347.1	EST_HUMAN	7127f12.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3285918 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR 1. ;
11419	23186	36416	1.79	0.0E+00	BE615668.1	EST_HUMAN	601278335F.1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11419	23188	36417	1.79	0.0E+00	BE615668.1	EST_HUMAN	601278335F.1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11426	23193	36424	1.61	0.0E+00	AV757420.1	EST_HUMAN	AV757420 BM Homo sapiens cDNA clone BMFAGH03 5'
11457	24061	37367	1.52	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
11461	24064	37370	10.31	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11461	24064	37371	10.31	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11476	24077	37387	4.69	0.0E+00	AU138211.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'

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11491	24092	37404	1.92	0.0E+00	BE622317.1	EST_HUMAN	60144106F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
11518	24118	37428	1.42	0.0E+00	A039634.1	EST_HUMAN	tr94c10.x5 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165778 3'
11528	24129	37434	13.79	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11529	24129	37435	13.79	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11538	24139	37447	1.81	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11539	24139	37448	1.81	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11542	24142	37451	2.08	0.0E+00	AW006022.1	EST_HUMAN	wz81h01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:J53H10.2 CE11040 ZINC FINGER, C2H2 TYPE:
11546	25135	37455	3.49	0.0E+00	BF002333.1	EST_HUMAN	7h22b10.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458 TRIO.:
11571	24170	37485	2.88	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
11571	24170	37486	2.88	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
11582	24181		2.41	0.0E+00	AW863777.1	EST_HUMAN	MR3-SN0010-310300-107-b03 SN0010 Homo sapiens cDNA
11601	24200	37521	4.76	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11601	24200	37522	4.76	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11608	24206	37529	5.87	0.0E+00	U86253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
11612	24210	37533	2.29	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11612	24210	37534	2.29	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11632	24228	37553	2.22	0.0E+00	BE794758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11634	24231	37554	45.09	0.0E+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11640	24237	37560	1.62	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
11640	24237	37561	1.62	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
11644	24241	37565	1.65	0.0E+00	AF053543.1	NT	Homo sapiens glutathione transferase zeta 1 (GSTZ1) gene, exons 6 and 7
11646	24243		1.56	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
11653	24250	37572	14.06	0.0E+00	BE409993.1	EST_HUMAN	601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
11654	24251	37573	1.46	0.0E+00	BE148650.1	EST_HUMAN	MR0-HT0241-150500-011-02 HT0241 Homo sapiens cDNA Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11655	24252	37574	2.69	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11655	24252	37575	2.69	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11657	18187	30878	1.29	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11657	18187	30879	1.29	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11658	24254	37576	5.6	0.0E+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'
11658	24254	37577	5.6	0.0E+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11662	24258		1.83	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11664	17806	30593	1.5	0.0E+00	AF272683.1	NT	Homo sapiens gephyrin mRNA, complete cds
11667	24262	37586	1.71	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP4000929 5'
11670	24265	37588	1.35	0.0E+00	BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
11687	24282	37604	2.5	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11687	24282	37605	2.5	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11728	25136		15.74	0.0E+00	BF309120.1	EST_HUMAN	60189034F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
11737	24330	37654	11.96	0.0E+00	BE287175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532968 5'
11751	24342	37671	1.3	0.0E+00	BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
11751	24342	37672	1.3	0.0E+00	BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
11757	24348	37678	1.43	0.0E+00	BE257812.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'
11757	24348	37679	1.43	0.0E+00	BE257812.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'
11785	24375	37705	1.69	0.0E+00	BE257898.1	EST_HUMAN	601114240F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'
11790	24380	37710	1.88	0.0E+00	AW749184.1	EST_HUMAN	PM1-BT0348-151299-001-c11 BT0348 Homo sapiens cDNA
11790	24380	37711	1.88	0.0E+00	AW749184.1	EST_HUMAN	PM1-BT0348-151299-001-c11 BT0348 Homo sapiens cDNA
11792	24382	37713	2.23	0.0E+00	AW367811.1	EST_HUMAN	MRO-HT0168-271199-005-g03 HT0168 Homo sapiens cDNA
11792	24382	37714	2.23	0.0E+00	AW367811.1	EST_HUMAN	MRO-HT0168-271199-005-g03 HT0168 Homo sapiens cDNA
11797	24387	37720	2.46	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
11797	24387	37721	2.46	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
11808	14946		1.31	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11821	18891	37859	2.45	0.0E+00	U07223.1	NT	Human beta2-chimaerin mRNA, complete cds
11822	24407	37741	5.54	0.0E+00	Z31706.1	NT	H.sapiens GLAST1 gene for glial glutamate transporter, exon8
11835	24419		2.26	0.0E+00	A1656185.1	EST_HUMAN	tt38f02.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2243067 3' similar to SW:CG2G_HUMAN
11837	24421	37762	2.31	0.0E+00	AU132394.1	EST_HUMAN	P51959 G2/MITOTIC-SPECIFIC CYCLIN G1.
11879	25399	30600	2.27	0.0E+00	BE312542.1	EST_HUMAN	AU132394 NT2RP3 Homo sapiens cDNA clone NT2RP3004339 5'
11893	25257		3.89	0.0E+00	A1180983.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
11902	24468		1.6	0.0E+00	AB011398.1	NT	ql7b12.x1 Soares fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
11921	24482		4.9	0.0E+00	AL163246.2	NT	Homo sapiens gene for AF-6, complete cds
11929	24488		4.1	0.0E+00	11417862	NT	Homo sapiens chromosome 21 segment HS21C046
11947	24501		3.05	0.0E+00	5802973	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11982	25218	30816	2.59	0.0E+00	AF240788.1	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
11993	25228		5.39	0.0E+00	AL041931.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
							DKFZp434K0819_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434K0819 5'

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12015	25369		3.12	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
12023	24551		3.91	0.0E+00	AL046544.1	EST_HUMAN	DKFZp434G218.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218.5
12037	25261		1.68	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
12076	25390		1.52	0.0E+00	N54484.1	EST_HUMAN	yv40e08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to
12089	24594		5.88	0.0E+00	AF106656.1	NT	SW_P0L_BAEVM P10272 POL POLYPROTEIN ;
12092	13593	26262	3.39	0.0E+00	4507500	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
12092	13593	26263	3.39	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12100	25264		2.21	0.0E+00	10092587	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12129	13318		2.04	0.0E+00	AF003528.1	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
12218	25198	30814	2.63	0.0E+00	AW590082.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12229	25248		1.34	0.0E+00	BE080210.1	EST_HUMAN	hg31e08.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2847234 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
12273	25258		4.43	0.0E+00	AF068757.1	NT	RC6-BT0711-290300-011-D05 BT0711 Homo sapiens cDNA
12308	24732		3.36	0.0E+00	9635487	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12351	25252		2.41	0.0E+00	AI204914.1	EST_HUMAN	Human endogenous retrovirus, complete genome
12383	24778		1.68	0.0E+00	AI904646.1	EST_HUMAN	en05e04.x1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12405	14718	27436	1.51	0.0E+00	6912457	NT	QV-BT065-020399-103 BT065 Homo sapiens cDNA
12405	14718	27437	1.51	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12423	24789	31039	2.08	0.0E+00	AF036365.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12435	14424	27119	2.76	0.0E+00	H30132.1	EST_HUMAN	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12435	14424	27120	2.76	0.0E+00	H30132.1	EST_HUMAN	yc59e08.r1 Soares breast 3NHBat Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089
12446	24816		10.66	0.0E+00	D50659.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12448	24818	31020	2.51	0.0E+00	11418189	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12448	24818	31021	2.51	0.0E+00	11418189	NT	Human gamma-cytoplasmic actin (ACTGP6) pseudogene
12464	14817	27549	1.53	0.0E+00	4758489	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12502	24856		1.5	0.0E+00	AW684999.1	EST_HUMAN	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12538	13953	26817	2.09	0.0E+00	8922593	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12544	24884		1.88	0.0E+00	11526291	NT	h18e06.x1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2878154 3'
12568	16069	28718	4.24	0.0E+00	4895312	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
							Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
							Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12576	17905	30592	3.05	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12582	24905		2.12	0.0E+00	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
12622	24927	31009	2.06	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
12648	25410		2.68	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12654	13390	26021	2.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12729	24999	30972	1.5	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12735	25004		4	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
12790	25042	30967	1.76	0.0E+00	AW025032.1	EST_HUMAN	w83c07.x1 NCL CGAP_Kld3 Homo sapiens cDNA clone IMAGE:2527596 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ; contains TAR1.13 TAR1 repetitive element ;
12808	13890	26550	1.37	0.0E+00	9966844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12818	25251		1.39	0.0E+00	AF083824.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 8

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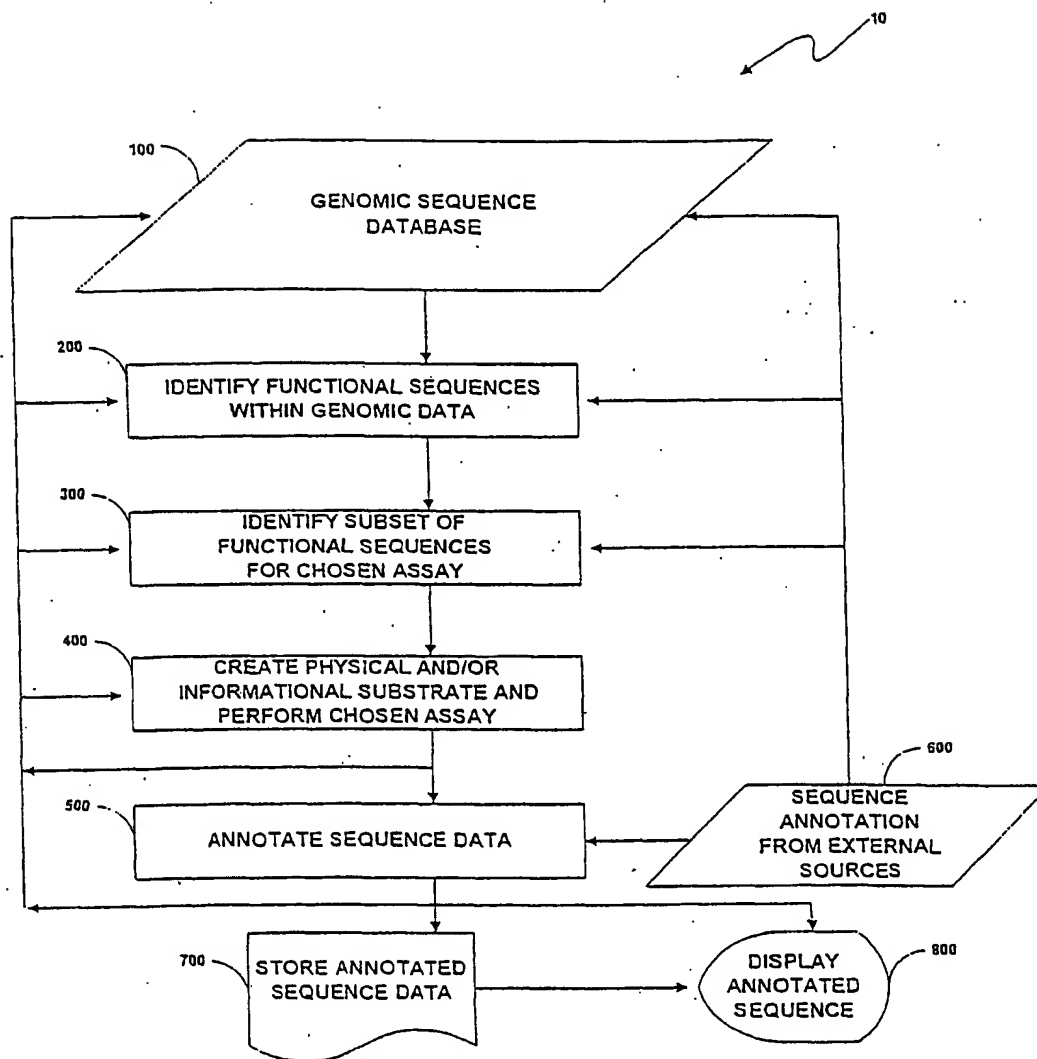


Fig. 1

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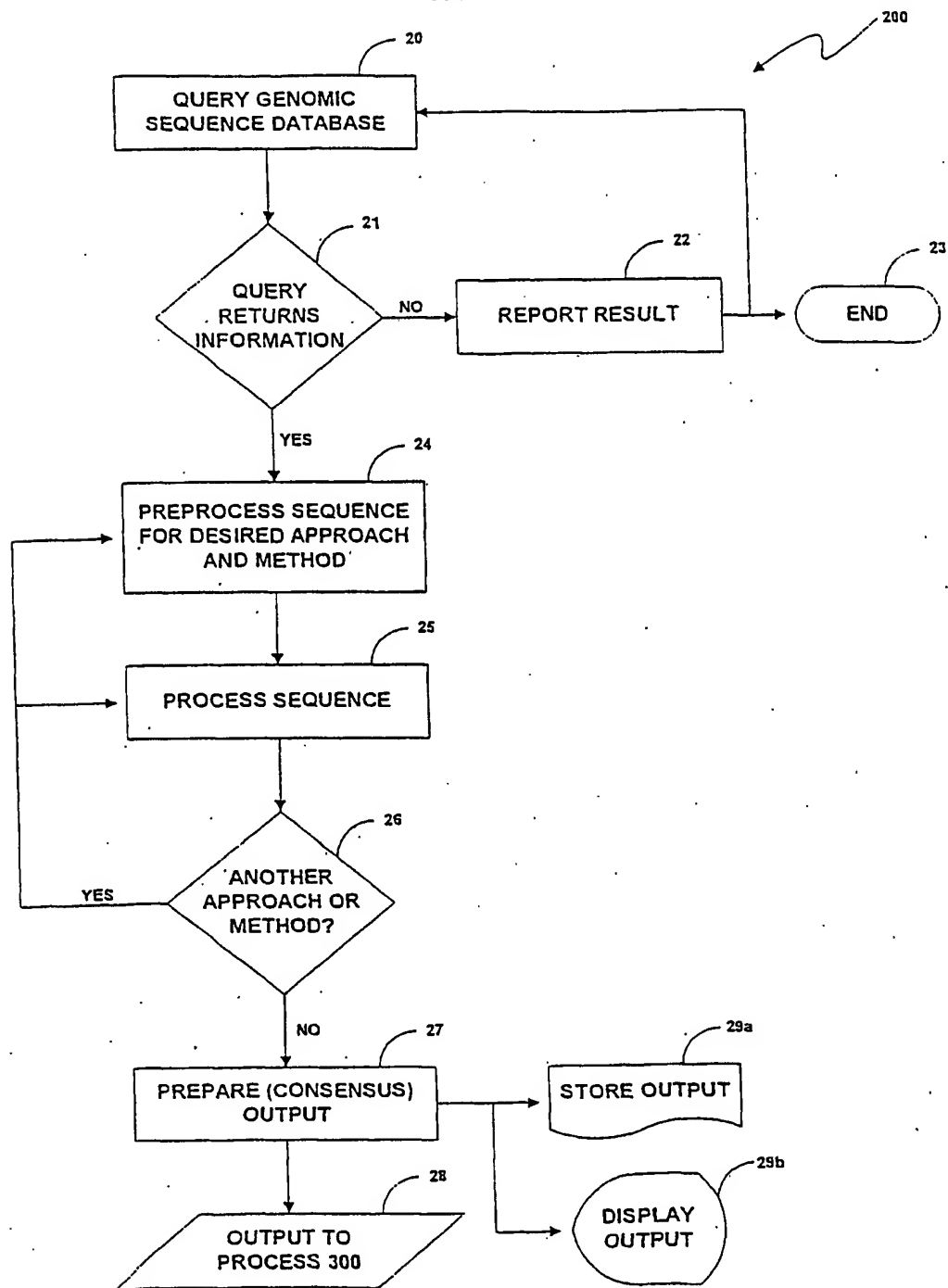


Fig. 2

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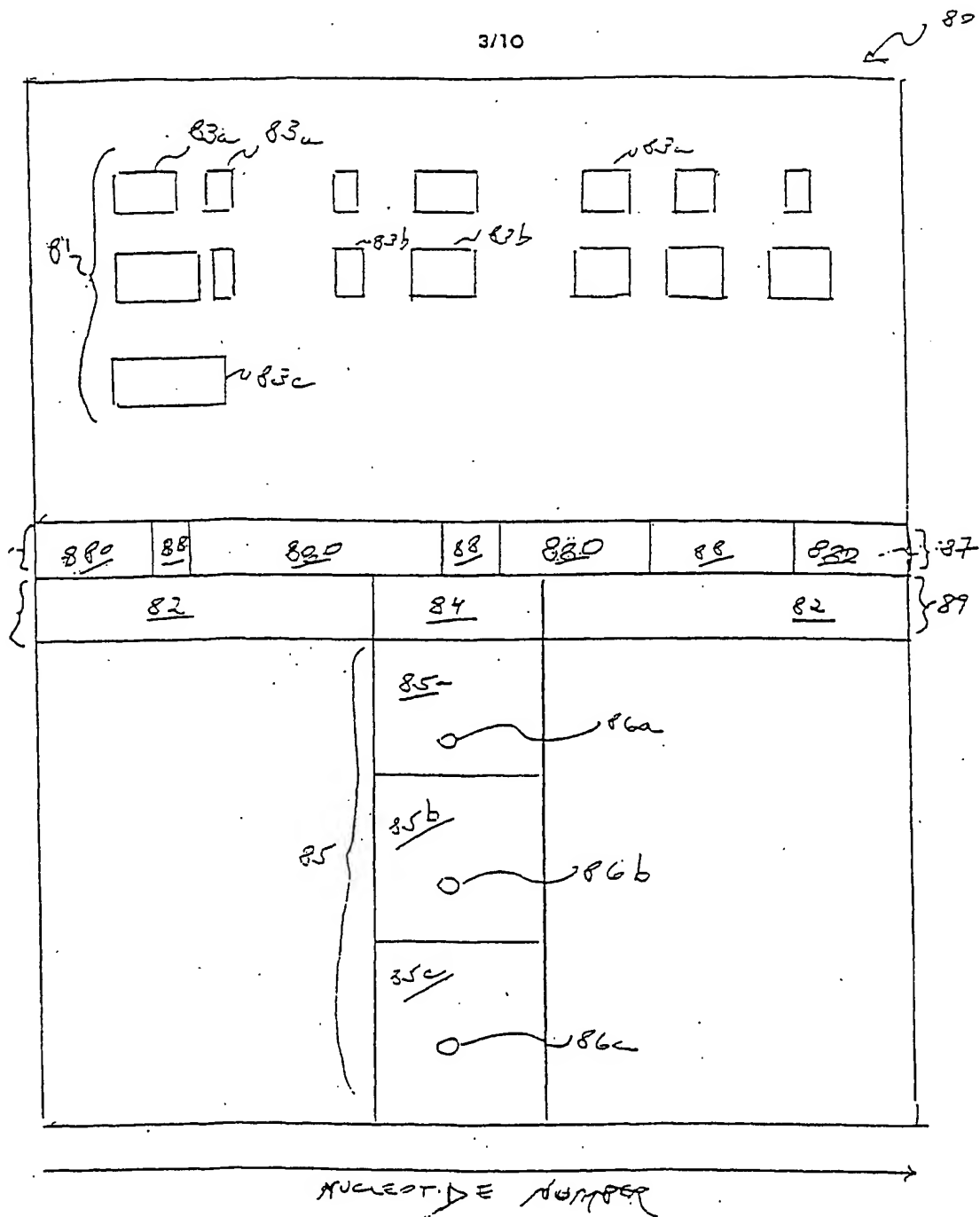


Fig. 3

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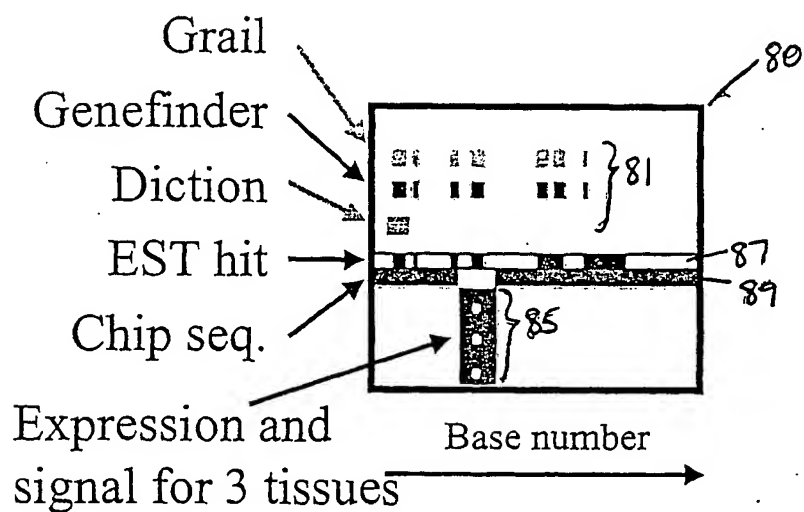


Fig. 4

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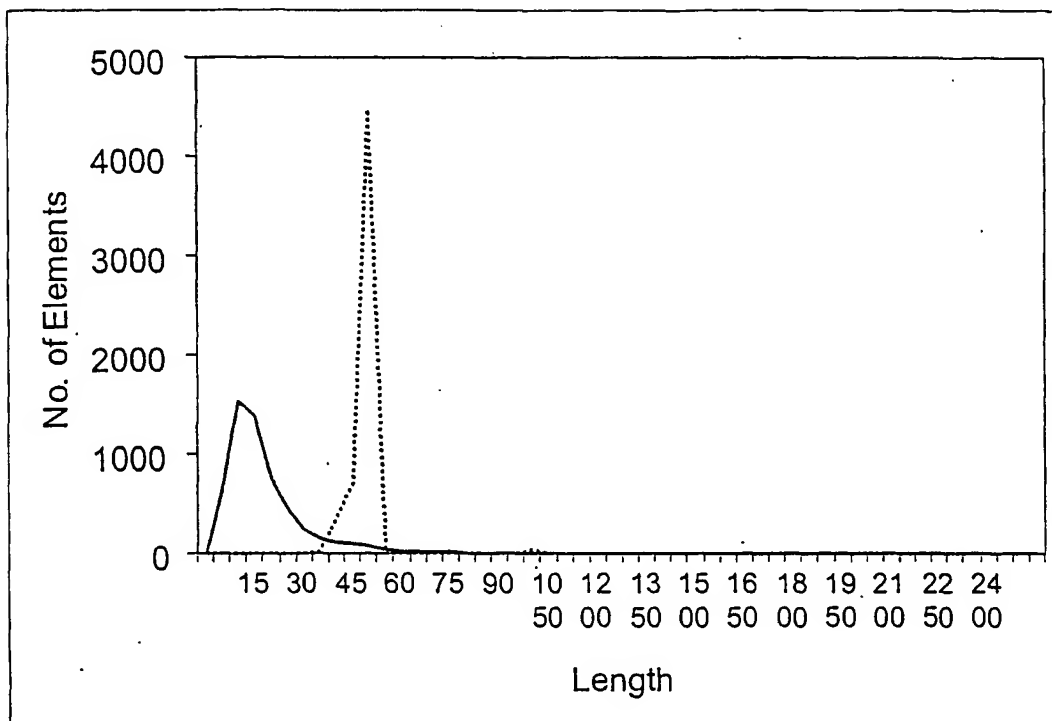


Fig. 5

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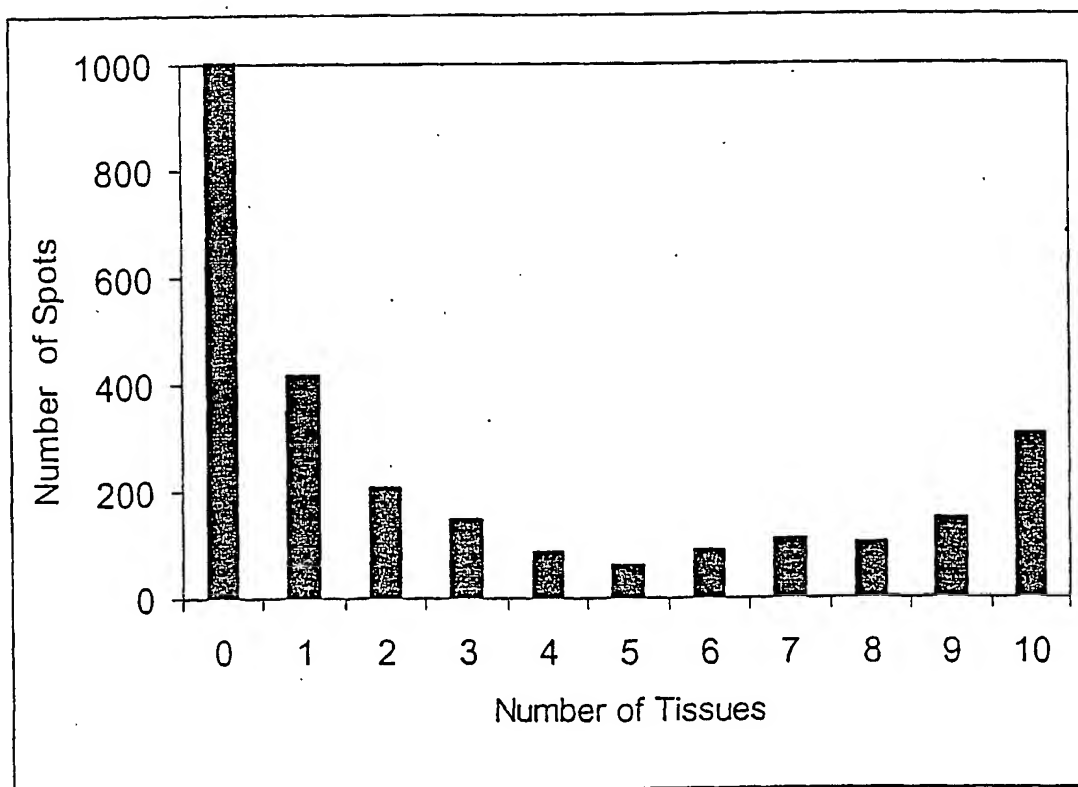
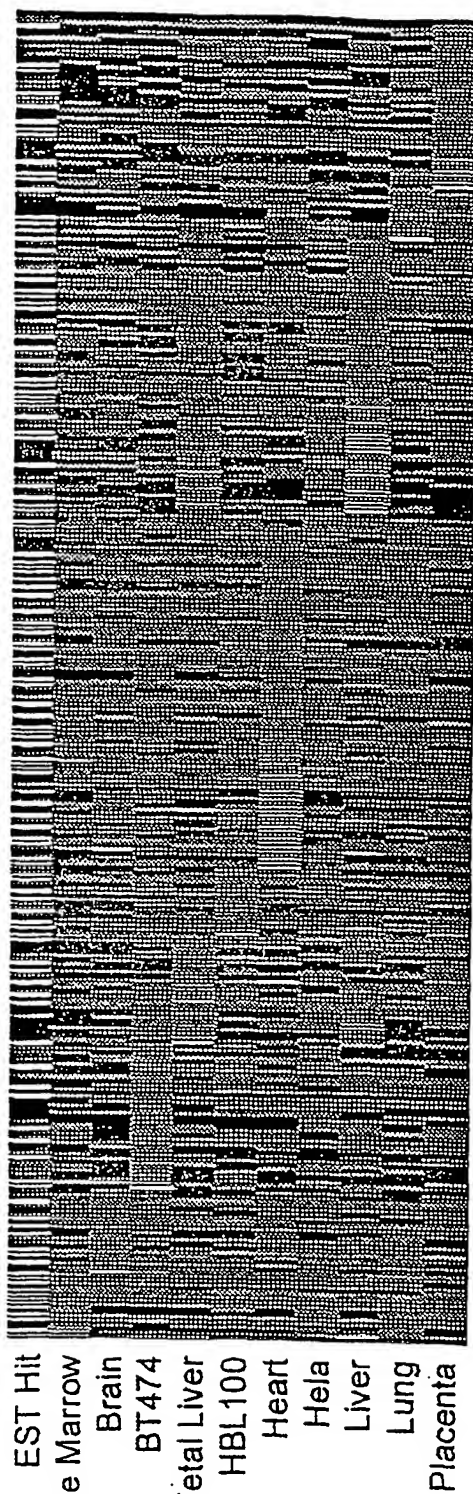


Fig. 6

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EST Hit
Bone Marrow
Brain
BT474
Fetal Liver
HBL100
Heart
Hela
Liver
Lung
Placenta

Fig. 7a

ratio legend

>9
8
7
6
5
4
3
2
1



Fig. 7b

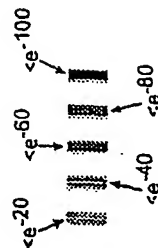


Fig. 7c

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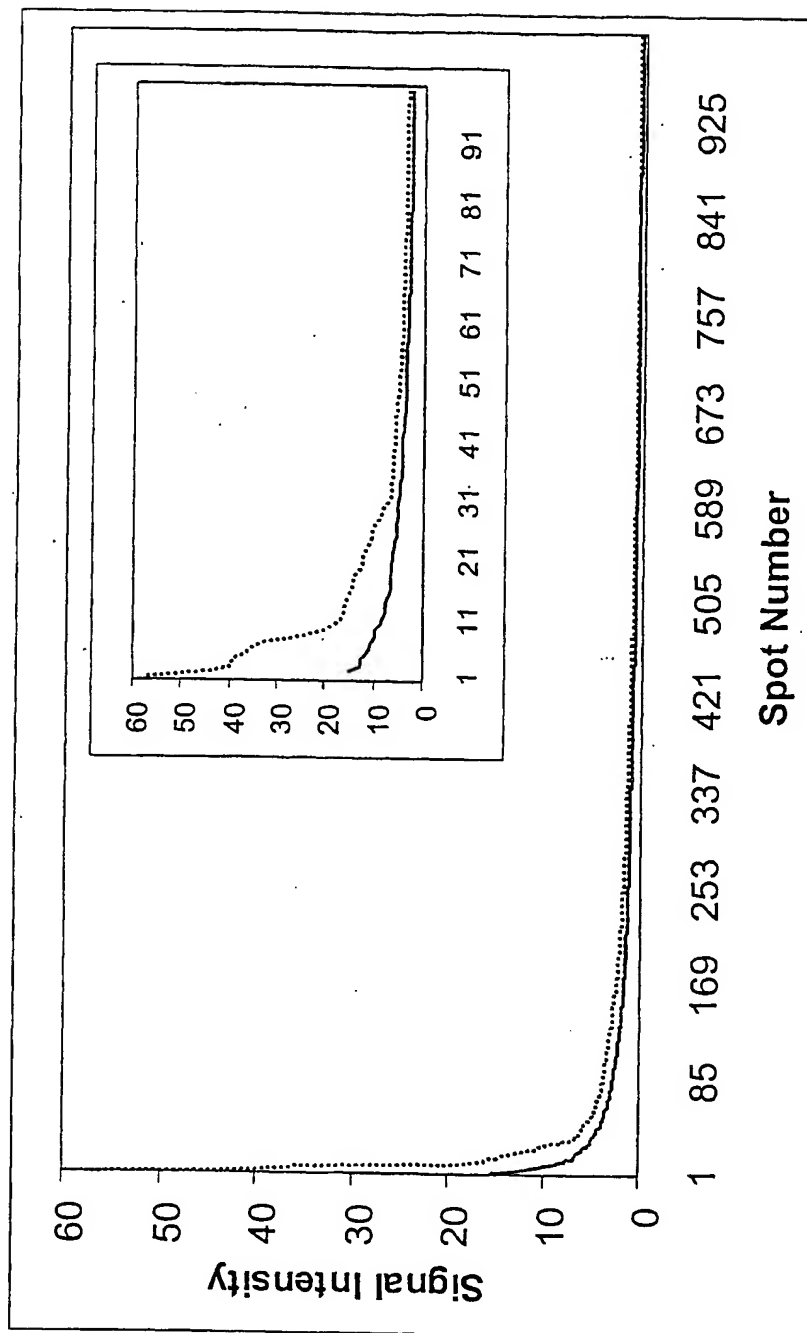


Fig. 8

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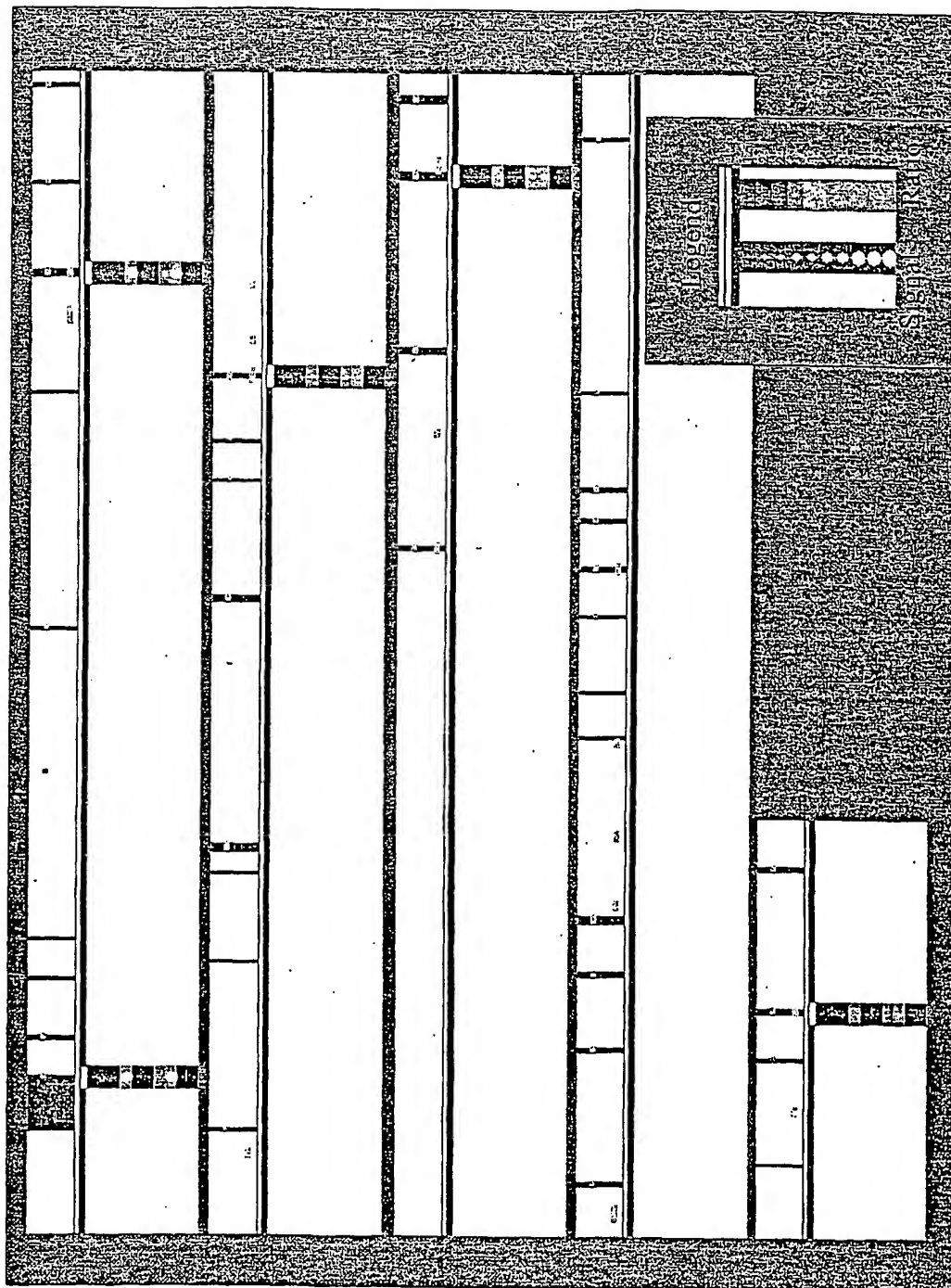


Fig. 9

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Fig. 10

